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gtgggaatgt actatggagc agctttgttc atgtacatac ggccacatc tgatcgctcc 600
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<210> 802

<211> 635

<212> DNA

<213> Unknown (H38g652 nucleotide)

<220>

<223> Synthetic construct

<400> 802

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<210> 803

<211> 670

<212> DNA

<213> Unknown (H38g653 nucleotide)

<220>

<223> Synthetic construct

<400> 803

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aattgtttcc tccattctga gggtttcttc gtcagggtgg aggtataaag ccctctccac 540
ctgtgggtct cacgtgtcag ttgtttgctg agtttatgga acaggcgttg gagggtaacct 600
cagttcggat gtgtcatttt ccccagaaa ggggtgcagt gcctcagtga tgtacgcggt 660
tgtcaccccc 670

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<210> 804

<211> 648

<212> DNA

<213> Unknown (H38g654 nucleotide)

<220>

<223> Synthetic construct

<400> 804

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ctaatacccc	tgacactcat	ccttatatca	tatgctttta	ttgtccgagc	agtattgagg	480
atacagtcctg	ctgaaggctg	acaaaaagca	tttgggacat	gtgggttcca	tctaattgtg	540
gtgtctcttt	ttaatagtac	agccgtctct	gtgtacctgc	aaccaccttc	gcccagctcc	600
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<210> 805

<211> 655

<212> DNA

<213> Unknown (H38g655 nucleotide)

<220>

<223> Synthetic construct

<400> 805

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ggaggcatgg	aagacagaca	tgctcctgag	tgtgatggcc	tatgaccggg	tcgtagccat	180
ctgtcaccct	ctatatcatt	cagccatcat	gaatccgtgt	ttctgtgggt	tcctactttt	240
gttgtctttt	ttttttctca	gtcttttaga	cgcccagctg	cacaacttga	ttgccttaca	300
aatgacctgc	ttcaaggatg	tggaaattcc	taatttcttc	tgtgaccttc	ctcaactccc	360
ccatcttgca	tggtgtgaca	ccttcaccaa	taacataatc	atgtattttc	ctgctgccat	420
atttggtttt	cttcccatct	cggggaccct	tttctcttac	gataaaaattg	tttccctccat	480
tctgagggtt	tcacatcag	gtgggaagta	taaagccttc	tccacctatg	gggtctcacct	540
gtcagatggt	tcctgatttt	atggaacagg	cggtggaggg	tacctcagtt	cagatgtgtc	600
atcttccccg	agaaagactg	cagtggcctc	agtgatgtac	acagtgggtca	cccc	655

<210> 806

<211> 662

<212> DNA

<213> Unknown (H38g656 nucleotide)

<220>

<223> Synthetic construct

<400> 806

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ggagacacgg	aagagagaca	tgttcctgag	tgtgggtggc	tatgaccggg	ttgtagccat	180
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gccttacaaa	tgacctgctt	caaggatgtg	gaaattccta	atctctcttg	ggaaccttct	360
caactccccc	atcttgcatg	ttgtgacatc	ttcaccagga	acatcaacct	gtatttccct	420
gctgccatat	ttgggtttct	tcccatctcg	gggacgcttt	tctcttgcta	taaaattggt	480
tccttcatte	tgagggtttc	atcatcaggt	gggaagtata	aaccttctcc	gcctgtgggt	540
ctcatctgtc	agttgtttac	tgatttttatg	gaacaggctt	tggagggtac	ctcagttcag	600
atgtgtcatc	ttccccgaga	aagactgcag	tggcctcagt	gatgtacgca	gtggtcaccc	660
cc						662

<210> 807

<211> 647

<212> DNA

<213> Unknown (H38g657 nucleotide)

<220>

<223> Synthetic construct

<400> 807

gtgctggatg	tggatgtat	cactgtcact	gttcctgcaa	tgttgggtcg	tctcttgtec	60
cacaagtcca	caatttccta	tgacgcctgc	ctctcccagc	tcttcttctt	ccacettctg	120
gctgggatgg	actgttcctt	gctgaccgcc	atggcctatg	accgactcct	ggccatctgc	180
cagccccca	cctacagcac	ccgcatgagt	cagacagtcc	agaggatgtt	ggtggctgcg	240
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tctgtctcta	gcacccaact	caatgagctg	ctgctctttg	tagcagcagc	cttcattggt	420
gtggcaccct	tggcttctcat	cagtgtgccc	tatgcccattg	tggtagctgc	tgtgctgcaa	480
atcgctccgc	tgagggcaga	aagaaggcct	tctccacatg	tggctcccac	ctcactgtgg	540
tgggcatctt	ctatgggaca	ggtgtcttca	gctacatgag	gctgggttca	gtggaatctt	600
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<210> 808

<211> 635

<212> DNA

<213> Unknown (H38g658 nucleotide)

<220>

<223> Synthetic construct

<400> 808

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ggttgtgtcg	acatttttgt	tttgactgtc	atggcttttg	atcgctgtgc	tgctatctgc	180
caacccctcc	gttacactgt	catcatgagt	gctaattgctt	atactgtgct	ggcatcactg	240
tcttgggttg	gggcccctggg	tcatttcctt	gttcagaccc	tctgacctt	ccagctgccc	300
ttctgtaatg	ctcagggttat	agaccattac	ttttgtgatg	tccacccagt	cctaaaaactt	360
gcctgtgtcg	atacaactct	ggtaaataatg	ttgggtgggtg	ccaacagtgg	tctcatctcc	420
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actttcttct	ttgttccgtg	tatctttatt	tatctccatc	cactactttc	ccattggata	600
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<210> 809

<211> 648

<212> DNA

<213> Unknown (H38g659 nucleotide)

<220>

<223> Synthetic construct

<400> 809

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ggagacctgg	agagcttctt	ccttgtggcc	atggcctatg	accgctatgt	ggccatctgc	180
ttccccctgc	actacaccgc	catcatgagc	cccatgctct	gtctcgccct	ggtggcgctg	240
tcttgggtgc	tgaccacctt	ccatgccatg	ttacacactt	tactcatggc	caggttgtgt	300
ttttgtgcag	acaatgtgat	ccccactttt	ttctgtgata	tgtctgctct	gctgaagctg	360
gccttctctg	acactcgagt	taatgaatgg	gtgatattta	tcatgggagg	gctcattctt	420
gtcatcccat	tcctactcat	ccttgggtcc	tatgcaagag	ttgtctcctc	catcctcaag	480
gtcccttctt	ctaagggtat	ctgcaaggcc	ttctctactt	gtggctccca	cctgtctgtg	540
gtgtcactgt	tctatggaac	cgttattggt	ctctacttat	gctcatcagc	taatagtctt	600
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<210> 810

<211> 438

<212> DNA

<213> Unknown (H38g660 nucleotide)

<220>

<223> Synthetic construct

<400> 810

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ggaaacagcc	tgatcctctt	cgctaccatc	actcagccca	gcctccacga	accaatgtac	180
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atgctgagta	tattctgggt	caatgtgagg	gaaatcagct	ttaatgcctg	cttgtcccac	300
atgttcttta	ttaaattctt	cactgtcatg	gaatcctcag	tgctgttggc	catggctttt	360
gacgttttgg	tgccgtctct	atccccttag	tatgccatga	tttaactgac	tcagatagct	420
aaaatgagtg	cagtgtat					438

<210> 811

<211> 1002

<212> DNA

<213> Unknown (H38g661 nucleotide)

<220>

<223> Synthetic construct

<400> 811

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gacgtcccc	acctagagct	gacgtctctt	gtggttgctc	tcactcttta	tctgctgact	120
cttcttgcca	acatgaccat	tgtcttgctt	tcagctctgg	attcccggct	gcacacacca	180
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aacacttgca	gctcgcactc	aattgttgtc	tctctcttct	atggtacaat	catatacatg	780
tacctccagc	cagcaaatac	ttattcccag	gaccagggca	agtttcttac	ccttttctac	840
acaattgtca	ctcccagtgt	taaccccctg	atctatacac	taagaaacaa	agatgttaaa	900
gaggccatga	agaaggtgct	aggggaaggg	agtgcagaaa	tatagtaagg	ggtgattaaa	960
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<210> 812

<211> 827

<212> DNA

<213> Unknown (H38g662 nucleotide)

<220>

<223> Synthetic construct

<400> 812

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tgggtgaatc	acaggggaaga	ttagcagtg	gggctgcttc	ctacaggctt	actttattca	180
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catttccata	tggcaaatct	catgttatca	cacgttgctt	tctgcctcca	ccaagaaatc	420
atgagactgg	cttggtgctga	cataacttcc	aataaaacttt	accctgtaat	tttgatctct	480
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taagttgtgt	ccttatctcc	tatgttacgg	tgatgggttt	gacattcatt	tacaaatttg	660
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ctttaatgaa	ccctgtcatc	tacagcatca	aaaccaagca	aatacaatat	ggcattatcc	780
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<210> 813

<211> 657

<212> DNA

<213> Unknown (H38g663 nucleotide)

<220>

<223> Synthetic construct

<400> 813

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ggaggcatgg	aagaaagaca	tgctcctgag	tgtgagggcc	tatgaccggt	ttgtagccat	180
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<210> 814

<211> 655

<212> DNA

<213> Unknown (H38g664 nucleotide)

<220>

<223> Synthetic construct

<400> 814

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cacagcagag	tcattctcta	tgcaggctgc	ctgactcaga	tgtctctctt	tgccattttt	120
ggaggcatgg	aagagacaca	tgctcctgaa	tgtgatggcc	tatgtccggt	ttgtagccat	180
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aatgacctgc	atcaaggatg	tggaaattcc	taatttcttc	tgtgacctt	ctcaactccc	360
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gtcagttgtt	tgcttatttt	atggaaaagt	cgttgggggg	tacctgagtt	cagatgtgtc	600
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<210> 815

<211> 646

<212> DNA

<213> Unknown (H38g665 nucleotide)

<220>

<223> Synthetic construct

<400> 815

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ggagacaagg	tcattctcta	caatgcattg	gctgctcaaa	tggtcttttt	tgacgccttt	120
gccactgtgg	aaaatttccct	cttggcctcg	atggcctatg	accgccatga	tgcatgtgtc	180
aaacccttac	attacaccac	caccatgaca	acaagtgtgt	gtgcatgtct	ggctataatc	240
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gcactcggct	tcaggatacc	agaaggcttt	gtccacctgt	gcctcccacc	tcactgcagt	540
catcatcttc	tatgggacta	ttatctccat	gtacttacag	cccagctctg	gtcactccat	600
ggacacagac	aaactggcat	ctgtgtccta	tactatgatc	atcccc		646

<210> 816

<211> 649

<212> DNA

<213> Unknown (H38g666 nucleotide)

<220>

<223> Synthetic construct

<400> 816

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acagcagagt	catctcctac	gcaggctgcc	tgactcagat	gtctctcttt	gccatttttg	120
gaggcatgga	agagagacat	gctcctgagt	gtgatggcct	atgaccgggt	tgtagccatc	180
tgtcaccctc	tatatcattc	agccatcatg	aaccctgtgt	tctgtggctt	cctagttttg	240
ctgtcttttt	tttctttctt	tttctcagct	gcacaacttg	attgccttaa	aaatgacctg	300
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atgttgtgac	accttcacca	ataagataat	catgtatttc	cctgctgcca	tatttggttt	420
tcttcccatc	tcagggaccc	ttttctctta	ctctaaaatt	gtttctctca	ttctgagggt	480
ttcatcatca	ggtgggaagt	ataaagcctt	ctccacctgt	gggtctcacc	tgtcagttgt	540
ttgtctgagt	tatggaacag	gcgttggagg	ttacctcagt	tcagatgatg	tgctcatctc	600
ccccagaaag	ggtgcagtgg	cctcagtgat	gtacacgggtg	gtcaccccc		649

<210> 817

<211> 651

<212> DNA

<213> Unknown (H38g667 nucleotide)

<220>

<223> Synthetic construct

<400> 817

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tttgtctaca	ctgagtgtct	catcttggtg	atgatgtcct	acgatcggta	catggctatc	180
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gggatccagt	ctggggaggg	ccgcagaaaag	gccttctcca	cctgctcctc	ccacctttgc	540
atggtggggac	tcttcttttg	cagcgccatt	gtcatgtaca	tgccccccaa	gtccccccac	600
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<210> 818

<211> 646

<212> DNA

<213> Unknown (H38g668 nucleotide)

<220>

<223> Synthetic construct

<400> 818

ctagtggact	tttgttactc	ttcagctgtc	actcccacag	tcatagctgg	gtctggtata	60
ggagacgagg	tcattcttta	cagtgcagt	gctgctcaaa	tggtcttttt	tgcagccttt	120
gccactgtgg	aaaatttctt	cttggcctca	atggcctatg	accgctatga	tgcagtgtgc	180

aaacccctac	attacaccac	caccatgaca	acaagtgtgt	gtgcatgtct	ggctataatc	240
tggtatgtct	gtgggtttctt	gaatgcctcc	atacacattg	gggaaacatt	gtctctcttt	300
ctgaatgtcc	aatgaagtcc	attgcatttt	ctgtgatgtt	ccaccagtca	tggtctgtgc	360
ttgctgtgat	agacatgtga	atgagctagt	tctcatttat	gtagccagtt	tcaatatctt	420
ttctgccatc	ctagtaatcc	tggtctccta	cctattcata	tttatcacca	tcctagagat	480
gcactcagct	tcaggatacc	agaaggcttt	gtccaactgt	gcctcccacc	tcactgcagt	540
catcatcttc	tatgggacta	ttatcttcat	gtacttacag	cccagctctg	gtcactccat	600
ggacacagac	aaactggcat	ctgtgttcta	tactatgatc	atcccc		646

<210> 819

<211> 933

<212> DNA

<213> Unknown (H38g669 nucleotide)

<220>

<223> Synthetic construct

<400> 819

atggctgctg	agaattcctc	cttcgtgaca	cagttttatcc	tcgcaggctt	aactgaccac	60
ccgggagtc	agatccccct	cttcttctctg	tttctagget	tctacgtggg	caactgtggg	120
gggaacctgg	gcttgataac	cctgataagg	ctcaactctc	acttgacac	ccctatgtac	180
ttcttctct	ataacttgct	cttcatagat	ttctgctatt	ccagtgttat	caactccaaa	240
atgctgatga	gctttgtctt	aaagaagaac	agcatctcct	acgcagggtg	tatgactcag	300
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gttgttgtgg	gcattgatat	tggtgtgccc	acagtcacca	tcttcatttc	ctatgctctc	660
attctctcca	gcattctcca	cattgattcc	acggagggca	ggtccaaagc	cttcagcacc	720
tgcagctccc	acataattgc	agtttctctg	ttctttgggt	caggagcatt	catgtacctc	780
aaaccccttt	ctctttttagc	tatgaaccag	ggcaagggtg	cttccctatt	ctataccact	840
gtggtgcccc	tgtctaaccc	attaatttat	agcctgagga	ataaggacgt	caaagttgct	900
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<210> 820

<211> 927

<212> DNA

<213> Unknown (H38g670 nucleotide)

<220>

<223> Synthetic construct

<400> 820

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ggcaacttgg	gcttgatcac	cttaattggg	ataaatccta	gccttcacac	ccccatgtac	180
tttttctct	tcaacttgct	ctttatagat	ctctgttatt	cctgtgtgtt	tacccccaaa	240
atgctgaatg	actttgtttc	agaaagtatc	atctcttatg	tgggatgtat	gactcagcta	300
tttttctct	gtttctttgt	caattctgag	tgtatgtgt	tgggtatcaat	ggcctatgat	360
cgtatgtgg	ccatctgcaa	ccccctgctc	tacatgggtc	ccatgtcccc	aagggtctgc	420
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<210> 821
 <211> 887
 <212> DNA
 <213> Unknown (H38g671 nucleotide)

<220>
 <223> Synthetic construct

<400> 821
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 cataatttta tgtccctaaa ttctcacctt cataccccca cacacttttt cctcttcacg 180
 ctatccttca ttgatgtctg ctattcattt gtctgtacca caaaaattcc aatgggcttt 240
 atctcagaga ggaacatcat ctcccttttg ggatggccaa cgtagctata tttcttttgc 300
 atctttgtca aagaacctaa aaatggggtc attgtgggaa taatgttctc agccaagatg 360
 cttgtagccg agagataatg gactagtcgt tgatgtgaaa ctagaaaatg cacatggccc 420
 tagaaaggtc tgatttttaga atgggataaa caggatctgc tacaagaaa catttaatca 480
 tattcttgta ttacagcgat tatttccaga gatagtggg ctgcagagct ttgggacaag 540
 gttccttagc gaagcaagac acactctcta gaattgcaca tgtactttta aaagtctgtt 600
 acatattata atatgttttt atatttgga acagaaaaaa ataagttatt tatatcacia 660
 atcatagaaa atggatcttt acaaaatctt catgttttgc gggttactca caagaaaaat 720
 tttctccgct catttctact tctcaaatgg ttcaaggaaa aatgctcctt aaaggatata 780
 tctgattctg gagaatgagc ttacctatgt gtgcaatttt tatctttgtc agaagatact 840
 actaccttct gaaaaagttg aaaacactgc tttataagaa cagctat 887

<210> 822
 <211> 939
 <212> DNA
 <213> Unknown (H38g672 nucleotide)

<220>
 <223> Synthetic construct

<400> 822
 atgctggcta gaaacaactc cttagtact gaatttattc ttgctggatt aacagatcgt 60
 ccagagttcc ggcaaccctt ctttttctctg tttctagtgg tctacattgt caccatggta 120
 ggcaaccttg gcttgatcat tcttttcggg ctaaattctc acctccacac accaatgtac 180
 tatttctct tcaatctctc cttcattgat ctctgttact cctctgtttt cactcccaaa 240
 atgctaataga actttgtatc aaaaaagaat attatctcct atgttgggtg catgactcag 300
 ctgtttttct ttctcttttt tgtcatctct gaatgctaca tgttgacctc aatggcatat 360
 gatcgctatg tggccatctg taatccattg ctgtataagg tcaccatgtc ccatcaggtc 420
 tgttctatgc tcaacttttg tgcttacata atgggattgg ctggagccac ggcccacacc 480
 ggggtgcatg ttagactcac cttctgcagt gctaatatca tcaaccatta cttgtgtgac 540
 atactcccc tctccagct ttctgcacc agcacctatg tcaacgaggt ggttgttctc 600
 attgttggtg gtattaatat catggtaccc agttgtacca tctcatttc ttatgttttc 660
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 tgtagctctc atgtcattgc tctgtctctg ttttttgggt cagcggcatt catgtatatt 780
 aaatattctt ctggatctat ggagcaggga aaagtttctt ctgttttcta cactaatgtg 840
 gtgcccagtc tcaatcctct catctacagt ttgaggaaca aggatgtcaa agttgcactg 900
 aggaaagctc tgattaaaat tcagagaaga aatatattc 939

<210> 823
 <211> 1071
 <212> DNA
 <213> Unknown (H38g673 nucleotide)

<220>
 <223> Synthetic construct

<400> 823
 atgaattggg taaataagag tgtccacacag gagttcattc tgttagtttt ctcagatcaa 60

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ccatggctag agattccacc ctttgtgatg tttctgtttt cctatatctt gacaatcttt 120
ggcaatctga caataattct tgtgtcacat gtggatttca aactccacac ccctatgtac 180
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tgtggctccc atctaattgt ggtgtcactt ttttatggta cagctatctc catgtacctg 780
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agcttttgcta aagacacagt gcttacttac cttactaact tctccgcaag ttgtcctatt 1020
tttgtcatta ctatagaaaa ctattgtaat ctccctcaaa gaaaatttcc t 1071

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<210> 824

<211> 991

<212> DNA

<213> Unknown (H38g674 nucleotide)

<220>

<223> Synthetic construct

<400> 824

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ccagatctcc aactccctct gttcttctg tttctagtgt atggctcactg cgttgggaaa 120
tttggcttgg taactctcgt tgtgctcaat tcacaccttc ataccccat gtacttttctc 180
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atgaacttca taacacagaa ggatattatc tcccacatgg ggtgcatgtc ccagcttttc 300
ttttttcttt attttttttt ggtatttctg aatgctatgt gctcacctca atggcctatg 360
atcagcatgt caccatgatc accatgtagc catctgtaac ccacttttgt ataattatgc 420
catgtccccc aaagtgtact ctcaccttat gcttgggtta tacttgctag ctttttctag 480
tgccatggcc cacactggat gcatgctgag actgaccttc tgtgatgcaa acaccatcca 540
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tgaacacctg cagttccaac ctaattgctg tttctcttag tttggatcgt gtgcatttat 780
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caccaataca gctcccttga tgaacccctt aatctacagt ttgatgaata aaatgttcaa 900
ctttctctga gaaaaaac cttagtagaa aaaattttga ctagaaatag tatcttctctg 960
tgcattgatt ttaggacag ggagcttctg t 991

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<210> 825

<211> 997

<212> DNA

<213> Unknown (H38g675 nucleotide)

<220>

<223> Synthetic construct

<400> 825

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atggctcctg gaaatggctc tttgatgaat gaattcattc tgggtggggtt aacagactag 60
ccagatcttt aactccctct gttcttcatg tttcttgtaa tgtatgttgt cactgtgata 120
agaaactttg tcttggtaat tctaactatg cgaaattcac gtcttcacac tcccaagtac 180
tttttctttt cttaaattgt cttcacagac ctctgttatt cttctgtgtt tatactccaa 240
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gacgtcaatg gcctatgatt gctgtgtggc catctgttac ccacttctt atcacattgc 420

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catgtccctt	aaagtgtgtt	tcagccttat	gcttggttcc	tacttcctat	ccttttctgg	480
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ttacttccgt	gacatccctc	ctgtgttcca	gctctcctgc	accagcacct	acatcaatga	600
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tgtaaatttt	gccatgggaa	aatctctgag	taggagaatg	tttttgccat	aaacaacatt	960
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<210> 826

<211> 939

<212> DNA

<213> Unknown (H38g676 nucleotide)

<220>

<223> Synthetic construct

<400> 826

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gggaacattc	tcatcatcat	tgccacagtc	tttactccaa	gtctccatac	ccccatgtat	180
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atgttggagg	gtttgctttt	agaaagaaaag	accatttccct	ttgacaactg	catcacacag	300
ctcttcttcc	tacatctctt	tgcctgtgcc	gagatctttc	tgctgatcat	tgtggcgtat	360
gatcgttacg	tggctatctg	cactccactc	cactacccca	atgtgatgaa	catgagagtc	420
tgtatacagc	ttgtctttgc	tctctgggtg	gggggtactg	ttcactcact	agggcagacc	480
ttcttgacta	ttcgtctacc	ttactgtggc	cccaacatta	ttgacagcta	cttctgtgat	540
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ccagacacca	gcttctccat	tgacaagggtg	gtgtctgtct	tctacacagt	ggtcacccct	840
ttgctgaatc	ccttcattta	caccttgagg	aatgaggagg	taaaaagtgc	catgaagcag	900
ctcaggcaga	gacaagtttt	tttcacgaaa	tcatataca			939

<210> 827

<211> 992

<212> DNA

<213> Unknown (H38g677 nucleotide)

<220>

<223> Synthetic construct

<400> 827

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gggaatttgg	gcttggtaac	tctgattgtg	ttcagttcac	actttcatgc	acccatgtac	180
ttttttcttt	ttagttttage	ttttatagac	cactttttatt	cttctgtgtt	tattccaaaa	240
atgctgatga	acttcataac	agagaagaat	attatttccct	atgcgggttg	catgtcagct	300
ttttttcttt	tttttttttt	tttttttttt	ttatttctga	atgctatgtt	ttgacgtcaa	360
tggtctctga	tcactagtgg	ccatggccat	ctgttaaccg	cttctgtata	acattgccat	420
gtccctctaa	gtgtgttcca	gccatattgct	tggttccctac	ttctggccct	tttctggggc	480
catggcccat	accaggtgca	tgctgaaact	gacctcctgt	gaggcaaaaca	ccatcaacca	540
ctacttctgt	gacacccttc	atctgctcca	gctctcttgc	accagcacct	acgtcagtga	600
gttgatgggt	ttcattgcag	caggcatcat	tttcaactgtg	cccagtatca	ccatctttat	660
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acattgatgt	agttcccatg	ataaactcct	caatttacag	cttaagaaac	aatgatgtta	900

aacttgccctg gagaaaaatc ctaagttgga gaaaatttcc atttgaaact atctctctcc 960
atgcatatag ttacaggaca aggagattct gt 992

<210> 828

<211> 966

<212> DNA

<213> Unknown (H38g678 nucleotide)

<220>

<223> Synthetic construct

<400> 828

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ttcccctgcc tgctgcaggg agaccaagat cctcctcttt gtggtcttct ccctcatcta	120
ccttctgacc ctcatgggta acacatccat catctgcgct gtgtgggtcaa gccagaaact	180
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ttttactgca cagcaacccc attctttaat cccctgacct acagtctctg gaacaaagat	900
atgacagatg cccttaaaaa agtgcctggga gtgccatcaa aagaaatata ttggaacaca	960
ctgaaa	966

<210> 829

<211> 1003

<212> DNA

<213> Unknown (H38g679 nucleotide)

<220>

<223> Synthetic construct

<400> 829

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ctgacactga ttgggaatgt tctcattgtc ataactatta tctatgacca ccggtcccat	180
actcccattg atttcttctc cagcaacctg tcttttattg atgtctgcca ctccactgtc	240
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tgtgtgaccc agatgttctt cctgcacctc tttgcctgca cagagatctt cctcctcacc	360
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aactggaagg tatgtgtgct gctggctgtg gccctctgga caggaggggac catccactcc	480
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agatcctcat tgtctccaac agtggattga tctccgtggg ctgttttgtg gtcctggtgg	660
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ccctgtccac ctgtgcagcc catctcactg tagttacact gttcctggga cactgcactc	780
tcatctattc ccgcccaccc accagcctcc cagaggacaa ggcagtatct gtgtttttca	840
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gtgccttaaa caagttagtg gggagaaaag agagaaaaga agaaaaatga aaatgtctac	960
gtccttagga tacgtggtgc tccaaattaa agaagcgctc tgc	1003

<210> 830

<211> 478

<212> DNA

<213> Unknown (H38g680 nucleotide)

<220>

<223> Synthetic construct

<400> 830

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ctgtaaggac	acatccttag	cccagagggt	agggttttaca	aatgttggtc	ttttgtctct	180
catttgcttt	tttctcatcc	ttgtttccta	tacttgcatt	gggatttcca	tatcaaaaat	240
ccgctcagca	gagggcaggc	agcgggcctt	ctccacctgc	agcgctcacc	tcactgcaat	300
cctttgtgct	tatgggccag	tcategttat	ctatctacaa	cccaatccca	gtgccttgct	360
tggttccata	attcagatat	tgaataatct	ggtaacccca	atgttgaatc	cactaatcta	420
tagccttagg	aataaggatg	taaaatcaga	tcagccctga	ggaatgtatt	tcccaaga	478

<210> 831

<211> 400

<212> DNA

<213> Unknown (H38g681 nucleotide)

<220>

<223> Synthetic construct

<400> 831

ttactatttt	taatgttctt	tattacttcc	ttgggtcata	aattccatct	gatatcattt	60
cccttcagtc	aacaaaccac	ctaacaaaaa	tactttataa	tttttgaagt	atgactctgc	120
tgataacata	cactcacagc	attaatttat	tgttaaatgt	ccttggtcta	gggtatagac	180
ctattttag	ggtataccct	ttagtcccag	agtattgttc	ttatttctag	ggcggtgtcc	240
ttctgggttt	tcattagaaa	gcctaagttt	ttaccgaacc	tctttcactt	ggcagcactt	300
gcatttaaaa	ttctattgcc	ctagttagag	gtaactgcta	aaatcttttc	tctcagccat	360
ctggctgctg	ttttctactt	actttcttag	agtcttgtct			400

<210> 832

<211> 933

<212> DNA

<213> Unknown (H38g682 nucleotide)

<220>

<223> Synthetic construct

<400> 832

atgggtactt	caaaccattc	ttcaggggct	gagtttatac	tggcagggtt	gacacaacgc	60
ccagaacttc	aactgccact	cttctctctg	ttccttggaa	tatatgtggt	cacagtgggtg	120
gggaacctgg	gcatgatctt	cttaattgct	ctcagttctc	aactttaccc	tccagtgtat	180
tattttctca	gtcatttgte	tttcattgat	ctctgtact	cctctgtcat	tacccttaag	240
atgctggtga	actttgttcc	agaggagAAC	attatctctt	ttctggaatg	cattactcaa	300
ctttatttct	tccttatttt	tgtaatgca	gaaggctacc	ttctgacagc	catggaatat	360
gaccgttatg	ttgctatctg	tcgcccactg	ctttacaata	ttgtcatgtc	ccacagggtc	420
tgttccataa	tgatggctgt	ggtatactca	ctgggttttc	tgtggggcac	agtccatact	480
acccgcatgt	cagtgttgte	attctgtagg	tctcatacgg	tcagtcatta	tttttgtgat	540
attctcccct	tattgactct	gtcttgctcc	agcaccaca	tcaatgagat	tctgtgttcc	600
attattggag	gagttataac	cttagcaact	acactggcgg	tccttatctc	ttatgctttc	660
attttctcta	gtatccttgg	tattcattcc	actgaggggc	aatccaaagc	ctttggcact	720
tgtagctccc	atctcttggc	tgtgggcate	ttttttgggt	ctataacatt	catgtatttc	780
aagccccctt	ccagcactac	tatggaaaaa	gagaagggtg	cttctgtgtt	ctacatcaca	840
ataatcccca	tgtctgaatcc	tctaattctat	agcctgagga	acaaggatgt	gaaaaatgca	900
ctgaagaaga	tgactagggg	aaggcagtca	tcc			933

<210> 833

<211> 948

<212> DNA

<213> Unknown (H38g683 nucleotide)

<220>

<223> Synthetic construct

<400> 833

atggtgatcc	tgtcctggga	aaaccaaacg	atgagagtgg	aattcgtgct	tcaaggattc	60
tcttccatca	gacagttaaa	tattttcctc	tttatgataa	ttttagtttt	ctacatctta	120
actgtttctg	gaaacatcct	cattgtcctt	ctagttttag	tcagacatca	tctccacacc	180
cctatgtact	tcctcctggg	gaacttgtec	tgtctggaga	tctgggtatac	ctctaacatc	240
atccccaaaa	tgttgctgat	tatcatagct	gaatagaaga	ctatctctgt	ggctggctgg	300
ctggcacaat	tctacttctt	cggatccctg	gctgccacgg	agtgcctctt	gctcaetgtg	360
atgtcctatg	atcgctacct	agccatctgc	cagcctcttt	gctaccgtgt	cctcatgact	420
ggcccccttt	gcatcaggct	agctgctggc	tcttggttct	gctgcttctt	ccttacagca	480
atcaccatgg	tcttgctatg	tagactaacc	ttctgtggac	cctatgaaac	tgatcacttc	540
ttttgtgact	tcacccctct	gggttcattc	tcctgcatgg	atacctcagt	gactgagacc	600
attgcctttg	ccacctcttc	tgcagtaact	ctgacccat	ttctcctcat	tgtagcctcc	660
tactcctgcy	tcctttctgc	tatcctaaga	atcccatctt	gcacaggcca	gaaaaaggcc	720
ttctccacct	gctcttccca	cctcaetgtg	gtcatagtgt	tttatgggac	actgattgcc	780
acataccttg	tgccctcagc	caactcatcc	caactcttgt	gcaaagggtc	ctctctgctc	840
tacatcatcc	tgacacccat	gtttaacccc	atcatttata	gcctgagaaa	tagagacatc	900
catgaagctc	tgaagaagtg	cttgaggaag	aagtcagggt	tttgcctt		948

<210> 834

<211> 946

<212> DNA

<213> Unknown (H38g684 nucleotide)

<220>

<223> Synthetic construct

<400> 834

ccagtgagga	ccttggagac	tactaatatc	actggatttg	tgaatgagtt	catcctcttg	60
ggcttcccc	gccgtggga	gatccagatc	ctcctttttg	tggtcttctc	tctcatctac	120
cttctgaccc	tcctaggtaa	cacatccatc	atctgtgctg	tgtggtcaag	ccagaaactc	180
cacacaccta	tgtacatcct	actggccaat	ttctccttcc	tggagatctg	ctgtgtcagt	240
tctgacgtgc	ccataatggc	agccaatctc	atctcccaga	cacagagcat	ctcctgtgct	300
ggctgcctgc	tcgggttcta	cttcttctcc	atgtgtgctg	cagagtgcct	atttctgtca	360
gtgatgtctt	ttgatagggt	tcctgccatt	tgtagacctt	tgactatcc	caccttaatg	420
acccatcacg	tttgtgtca	ttttgtgat	cttctgctgg	gtgggtggct	gtctctgggt	480
attgacccct	ttgacactaa	tatctcaggt	gctcttttgt	ggtccaaaca	ctatcgacca	540
ttttttctgt	gatctggcac	ctttgctggc	actgtcttgt	gctccaatac	ctggaattac	600
tctgacttgt	ggtatcatta	gcgctctcat	catctttctt	accttcttgt	atataccttg	660
gacttatttc	tgtgttctaa	gcacagtgtc	acaggtgcct	tcaggcttag	gaaggcataa	720
ggctttctca	acttgtggct	gtcaccttgc	tgtagtgtct	ctcttctatg	gttctcttat	780
gggtgatgtat	gttagccag	gttctgggga	ctatcatggg	ataaagaaat	ttgcgacctt	840
gttctatact	ttgtcaactc	cattctttta	tcctctgac	tacagtttcc	ggaacaagga	900
tatgaaagag	gcactaaaga	aatttctgag	gaatcgccac	actgtc		946

<210> 835

<211> 946

<212> DNA

<213> Unknown (H38g685 nucleotide)

<220>

<223> Synthetic construct

<400> 835

cttatagcta	caggaaactg	gacaagaata	agtaagttaa	tctcatgag	cttctcttcc	60
ctgcctactg	aaatacagtc	attactcttt	ctgacatttc	taaccatcta	cctggtcacc	120
ctgatgggaa	actgcctcat	cattctgggt	accctagctg	acccatgct	acacagcccc	180
atgtacttct	tcctcagaaa	cttatctttc	ctggagattg	gcttcaacct	agtcattgcy	240

cccaacatgc	tgtggaccct	gcttgcccag	gacacaacca	tctccttccct	tggctgtgcc	300
acttagatgt	atttcgtctt	cttctttggg	gtggctgaat	gcctcctcct	ggctaccatg	360
gcatatgacc	gctatgtggc	catctgcagt	ccttgcacta	cccagtcac	atgaacccaa	420
ggactcttgc	caaactggct	gctacctcct	ggttcccagg	ctttcctgta	gctactgtgc	480
agaccacatg	gctcttcagt	tttccattct	gtggcaccaa	caagggtgaac	cacttcttct	540
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ccatcgctcg	aaccattctg	gtggtcatga	tcccctgctt	gctgatcttg	tgttcctata	660
ctcacattgc	tgctgccatc	ctcaagatcc	catcagctaa	aggggaagaat	aaagcctttt	720
ctacatgttc	ctcacacctc	cttgttgtct	ctctttttcta	tatatcatta	agcctcacct	780
acttcgggac	taaatacaat	aattcacctg	agggcaagaa	gctgctatca	ttgtcctaca	840
ctgttatgac	tcccattgtg	aaccccatga	tctacagcct	gagaaataac	gagggtgaaga	900
atgccctcag	caggacgggc	tctaaggccc	tagccctcag	aaactg		946

<210> 836

<211> 973

<212> DNA

<213> Unknown (H38g686 nucleotide)

<220>

<223> Synthetic construct

<400> 836

atggctgtgg	aaaatgactc	ttcagtgaca	agagtttatt	cttttgggat	taacagacca	60
gcctgagatc	taattgcccc	tgtttttcct	gttcttgggtg	aactatatga	ccaccatggt	120
gggcaacttg	agtttaatta	atctaatttg	cctgaattca	caccttcaca	ctcccatgta	180
ttttttcctt	ttcaatctgt	ccttcattga	tctctgttat	tcatttgtct	ttacccccaa	240
aatgctgatg	agctttatct	cagagaggaa	catcatctcc	tttccaggat	gcgtaactca	300
gctctttttc	ttctgctttt	ttgtccactc	tgagtgtctat	gtgctgacag	ccatggccta	360
tgatcgctat	gtggccatct	gcaaaccctc	tctgtacatg	gtcaccacgt	cccctcagat	420
ctgttctcta	ctgatgcttg	gttcatatgt	gatgggggtt	gctggggcca	tgggtccacac	480
agagtgtatg	atgaagctca	tcttttgtga	ctccaacgtc	atcaaccatt	acatgtgtga	540
catcttccca	ctgctccagc	tctcctgcag	cagcacctag	gccaatgagc	tgggtgatgtc	600
tgttattgta	ggcacagttg	ttatagtatc	aagcctcatt	atcttaattct	cttatgcttt	660
gattcttttc	aatatccttc	acatgtcctc	agccgagggt	tgggttcaaag	ccatcggtac	720
ctgtggctcc	cacataataa	ctgttggcct	attctatgaa	tttgggctga	tcactcatgt	780
taagttatca	tctgattggg	atatgggtca	ggggaagttt	ctctcagtg	tttacacgaa	840
tgaggtagcc	atgctgaacc	ccctcattta	tagcctcagg	aacaaggatg	tcaaacttgc	900
tctaaaggaa	accctaaata	aaattacaaa	ctgagtagag	ccaatggtgc	tgccttagcc	960
cctctccaat	tgc					973

<210> 837

<211> 992

<212> DNA

<213> Unknown (H38g687 nucleotide)

<220>

<223> Synthetic construct

<400> 837

atgagataga	taaatacagac	acaagtgata	gaattcctcc	ttctgggact	ctctgatggg	60
ccacacaccg	agcagctgct	atttatcgta	ttattgggtg	tctacctggt	cactgtgctt	120
ggaaatctgc	ttctaacttc	ccttgttcat	gttgactccc	aacttcacac	acccatgtat	180
ttttttctct	gcaacttgtc	tctggctgac	ctctatttct	ctaccaacat	acttcctcag	240
gcactagtcc	acctgctttc	cataaacaac	ctcattgcat	tcacactttc	tctaactcaa	300
cttctctttt	tctctatttt	tgggtgaccc	agtgcgccct	tattgcagtg	atgtcctata	360
atccctatgt	tgcaatctgc	aatcctctgc	attaccctaa	catcatgacc	tggaaagtgt	420
gtgtccagct	ggcaacagga	tcatggacca	gtggcattct	ggtgtctgtg	gtagacacca	480
ccttcacact	gaggctaccc	taccgaggca	gtaacagcat	tgctcatttc	ttttgtgagg	540
ccctgcact	attgatctta	gcattccacag	acacccatgc	atcagagatg	gccattttatc	600
ttacgggggt	tgtgattctc	ctcatacctg	tttttctgat	tctggtatcc	tatggccgta	660
tcatagtaac	tgtggtcaag	atgaagtcaa	ctgtggggag	tctcaaggca	ttttctacct	720

gtggctccca	cctcatggtg	gtcatacttt	taaattggatc	agcaatactc	acttgcata	780
cacccaagtc	ttccaaacag	cagtaaaaat	cggtgtctgt	tttctatgca	atagtaactc	840
ccatgcttaa	ccccctcatc	tatagcctga	gaaacaagga	tgtgaaggca	gctctgagga	900
aagtagccac	aaggaatttc	ccatgaaggc	ttggaatctc	acactgacag	tgagctcaga	960
gaaccttttg	gcttcctact	tcaaagactt	gc			992

<210> 838

<211> 549

<212> DNA

<213> Unknown (H38g688 nucleotide)

<220>

<223> Synthetic construct

<400> 838

atggaaaaaa	gcaataatag	cactttgttt	attctcttgg	ggttttccca	aaataagaac	60
attgaagtcc	tctgctttgt	attatatttt	ttttgctaca	ttgctatttg	gatgggaaac	120
ttactcataa	tgattttctat	cacgtgcacc	cagctcattc	accaacccat	gtattttcttc	180
ctcaattacc	tctcactctc	cgacctttgc	tacacatcca	cagtgaaccc	caaattaatg	240
gttgacttac	tggcagaaag	aaagaccatt	tcctataata	actgtatgat	acaactcttt	300
accacccatt	tttttggagg	catagagatc	ttcattctca	cagggatggc	ctatgaccgc	360
tatgtggcca	tttgcaagcc	cctgcactac	accattatta	tgagcaggca	aaagtgtaac	420
acaatcatca	tagtttgggt	tactggggga	tttatacatt	ctgccagtca	gtttctcttc	480
accatctctg	taccattttg	tggcccaaat	gatatagatc	actactctcg	cgatgtgtat	540
cctttgctg						549

<210> 839

<211> 670

<212> DNA

<213> Unknown (H38g689 nucleotide)

<220>

<223> Synthetic construct

<400> 839

ttgcctgaca	tcggtttcac	ctccaccacg	gtccccaaga	tgagcgtgga	catccagtct	60
cacagcagag	tcattctccta	tgcaggctgc	ctgactcaga	tgtctctctt	tgccattttt	120
ggaggcatgg	aagagagaca	tgctcctgag	gtgatggcct	atgacctggt	tgtagccatc	180
tgacaccttc	tatategttc	agccatcttg	aaccctgttg	tcctgtggct	cctagatttg	240
ttgtctttgt	tgttggtttt	tttttttttc	tctcagctct	ttagactccc	agctgcacaa	300
cttgattgcc	ttacaaatga	cctgcttcaa	ggatgtggaa	attccgaatt	tcttctggga	360
accttctcaa	ctcccccatc	ttgcatgttg	tgacaccttc	accaggaaca	acaacatgta	420
tttccctgct	gccgtatttg	gttttcttcc	catctcgggg	acctttttct	cttactgtaa	480
aattgtttcc	tccattctga	gggtttcctc	atcaggtggg	aagtacaaac	cttctccacc	540
tgtgggtctc	acctgtcagt	tgtttgctga	ttttatggag	caggcgttgg	agggtacctt	600
ggttcagatg	tgatcatctt	cccagaaaag	gggtgcagtgg	cctcagtgac	gtacgtacac	660
ggtggtcacc						670

<210> 840

<211> 645

<212> DNA

<213> Unknown (H38g690 nucleotide)

<220>

<223> Synthetic construct

<400> 840

atggacgtca	ggctcatctg	caccaccgta	cccaagatgg	ccttcaacta	cttgtctggc	60
agcaagtcca	tttctatggc	tggtgtgccc	acacaaattt	tcttctgtgt	atcactgctt	120
ggctctgaat	gctttctgtt	ggctgttatg	tcttatgact	gctacattgc	catttgccac	180
cctctaagat	acaccaatct	catgagaccc	aaaatttgta	gacttatgac	tgcccttctc	240

tggatcctgg	gctctacaga	tggaatcatt	tatgctgtag	ccacattttc	cttctcctac	300
tgtgggtctc	gggaaatagc	ccacttcttc	tgtgagttac	cttccctact	aatcctctca	360
tgcaatgaca	cgtcaatatt	tgaaaagggt	attttcattt	gctctatagt	aatgcttggt	420
ttccctgttg	caatcatcat	tgcttcctat	gctggagtta	ttctggctgt	cattcacatg	480
ggatctggag	agggtcgtcg	caaagctttc	acgacctgtt	cctctcacct	catggtggtg	540
ggaatgttct	atggagcagg	tttgttcatg	tacatacagc	ccacatctga	tcgctcccca	600
acgcaggaca	agctgggtgc	tgtattctac	accatcctca	ctccc		645

<210> 841

<211> 380

<212> DNA

<213> Unknown (H38g691 nucleotide)

<220>

<223> Synthetic construct

<400> 841

aatctcctcc	ccgtgtggac	ccctggaagc	agggtgtccct	tcattgatcac	aaattttctgt	60
ctccgagaag	caaggcatgt	cctttcccaa	gaaacttttc	cagaatcaca	aacttttcct	120
actctttgca	gggatgaatg	tattttctgca	gactgtgatg	gcctatgacc	actttgtggc	180
catctgtcac	cccctgcact	acagggtcat	catgaatcct	gggatctttg	gactgtgggt	240
tctggtgtcc	tggagcatga	gtgccctgaa	ttcctcactg	caaagcagaa	tgtgttgcag	300
ctgtccttct	gcacaaaactt	ggaaatcccc	ccattttttt	ctgtgaactt	aatcagttga	360
tcctgcttgc	ctgtttctaac					380

<210> 842

<211> 648

<212> DNA

<213> Unknown (H38g692 nucleotide)

<220>

<223> Synthetic construct

<400> 842

tttgttgatt	tctgttattc	caccacgatt	acacccaaac	tgctggagaa	cttggtttgtg	60
gaagatagaa	ctatctcctt	cacaggatgc	atcatgcagt	tattctttgt	ctgcatattt	120
gtagtaacag	aaacattcat	gctggcagtg	atggcctatg	accgatatgt	ggcgggtgtg	180
aaccctcttc	tctacacagt	tgcaatgtac	cagaggcttt	gctccttggt	agtggctacg	240
tcatactggt	gggggatagt	ctgttccctg	acacttacct	agtttctact	ggaattatcc	300
ttcagaggaa	ataatatcat	taataacttt	gtctgtgagc	acgctgccgt	cgttgctgtg	360
tcttggtctg	acccctgtgt	gagccaggag	atcactttag	tttctgccac	attcaatgaa	420
ataagcggcc	tggatgatcat	tctcactccc	tatgctttca	tttttatcac	tgtcatgaag	480
acgccttcca	ctggggggcg	caagaaagcg	ttctccacgt	ctgcctccca	cttgacggcc	540
attaccattt	tccatgggac	tatccttttc	ctctactgtg	ttcctaacte	caaaagtctg	600
tggctcatgg	tcaagggtggc	ctctgtcctt	tacacagtgg	tcattccc		648

<210> 843

<211> 643

<212> DNA

<213> Unknown (H38g693 nucleotide)

<220>

<223> Synthetic construct

<400> 843

ttgccagaca	ttggttttcac	cttggccacg	gtccccaaga	tgattgtaga	catgcaatca	60
catagcagaa	tcatctccca	tgcaggctgt	ctgacacaga	tacctttctt	tgctcttttt	120
gtatgtatag	atgacatgct	cctgactgtg	atggcctatg	actgatttgt	ggccatctgt	180
caccccttgc	actacccagt	catcatgaat	cctcacctct	gtgtcttctt	agtgttgatg	240
tcttttctct	tagcctgttg	gattcctagc	tgcacaactg	gattgttaca	attcacctgc	300
ttcaagaatg	tggaaatctc	taattttttc	tgtgactgat	ctcaacttct	caaccttgcc	360

tgttctgact	gtcatcagta	acatatccat	acgttttagat	agtactatat	ttgggtttct	420
tcccatattca	gggatccctt	tgtcttacta	taaaattgtg	ccctccattc	taagaattcc	480
attgtcagat	gggaagtata	aagccttctc	cacctgcggc	tctcacctgg	caattgtttg	540
cttattttat	ggaacaggca	ttggcatgta	cctgacttca	gctgtgtcac	cagccccag	600
gaatggtgtg	gtggcatcag	tgttgtagcg	tatggtcacc	ccc		643

<210> 844

<211> 652

<212> DNA

<213> Unknown (H38g694 nucleotide)

<220>

<223> Synthetic construct

<400> 844

ttgcctgaca	tcgggtttcac	ccccaccacg	gtccccaaga	tgattgtgga	catccagtct	60
cacagcagag	tcattctatgc	aggctgcctg	actgtgatgt	ctctctttgc	catttttgga	120
ggcatggaag	agacacatgc	tcctgaatgt	gatggcctat	gtccggtttg	tagccatctg	180
tcaccctcta	tatcattcag	ccatcatgaa	cccggtgttc	tgtggcttct	tacttttgtt	240
gtcttttttt	tttctcggtc	tttttagacgc	ccagctgcac	aacatgattg	ccttacaaat	300
gacctgcttc	aaggatgtgg	aaattcctaa	tttcttctgt	gaccttctc	aactcccca	360
tcttgcatgt	tgtgacacct	tcaccaataa	cataatcatg	tattttcctg	ctgccatatt	420
tggttttctt	cccatctcgg	ggaccctttt	ctcttactat	gaaattgttt	cctccattct	480
gagggtttca	tcataagggtg	ggaagtataa	ggccttcgcc	acctgtgggt	ctcacctgtc	540
agtcgtttgc	tgattttatg	gaacaggcgt	tggagggtac	ctcagttcag	atgtgtcatc	600
ttccccgaga	aagactgcag	tggcctcagt	gatgtacgca	gtggtcaccc	cc	652

<210> 845

<211> 692

<212> DNA

<213> Unknown (H38g695 nucleotide)

<220>

<223> Synthetic construct

<400> 845

ttgcctgaca	tcgggtttcac	ctccaccaca	gtcgccaaga	tgattgtgga	catccagtct	60
cacagcagag	tcattctcta	tgcaggctgc	ctgactcaga	tgtctctctt	tgccattttt	120
ggaggcatgg	aagagagaca	tgctcctgag	tgtgatggcc	tatgaccggt	ttgtagccat	180
ctgtcaccct	ctatatcgtt	cagccatctt	gagcccgta	ttctgtgcct	tcctagattt	240
gttgtctttg	ttttgttttg	ttttgttttg	ttttgttttg	ttttgttttg	ctcagctctt	300
tagactccca	gctgcacaac	ttgattgcct	tacaaatgac	ctgcttcaaa	gatgtggaaa	360
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ccaggaacat	caacatgtat	ttccctgctg	ctgtatttgg	ttttcttccc	atctcgggga	480
ccttttctct	tacaatggag	taaaattgtt	tcctccactc	tgaggggttc	atcatcaggt	540
gggaagtata	aaccttctcc	acctgtgggt	ctcacctgtc	agttgtttgc	tgattttgtg	600
gaacaggcgt	tggagggtac	ctcggttcag	atgtgtcatc	ttccccgaga	aagagtgcag	660
tggcctcagt	gatgtacacg	gtggtcaccc	cc			692

<210> 846

<211> 939

<212> DNA

<213> Unknown (H38g696 nucleotide)

<220>

<223> Synthetic construct

<400> 846

atgctggcta	gaaacaactc	cttagtgact	gaatttatcc	ttgctggatt	aacagatcgt	60
ccagagttcc	ggcaaccctt	ctttttcctg	ttcctagtga	tctacattgt	caccatggta	120
ggcaaccttg	gcttgatcac	tcttttcggt	ctaaattctc	acctccacac	accaatgtac	180

tatttccctct	tcaatctctc	cttcattgat	ctctgttact	cctctgtttt	cactcccaaa	240
atgctaataga	acttttgtgc	aaaaaagaat	attatctcca	atgttggtg	catgactcgg	300
ctgttttttct	ttctcttttt	cgctatctct	gaatgttaca	tgttgacctc	aatggcatat	360
gatecgctatg	tggccatctg	taatccattg	ctgtataagg	tcaccatgtc	ccatcagggtc	420
tgttctatgc	tcacttttgc	tgtttacata	atgggattgg	ctggagccac	ggcccacacc	480
gggtgcatgc	ttagactcac	cttctgcagt	gctaatatca	tcaaccatta	cttgtgtgac	540
atactcccc	tcctccagct	ttcctgcacc	agcacctatg	tcaacgaggt	ggttgttctc	600
attgttgtgg	gtactaatat	cacggtaccc	agttgtacca	tcctcatttc	ttatgttttc	660
attgtcacta	gcattcttca	tatcaaatcc	actcaaggaa	gatcaaaagc	cttcagtact	720
tgtagctctc	atgtcattgc	tctgtctctg	ttttttgggt	cagcggcatt	catgtatatt	780
aaatattctt	ctggatctat	ggagcagggg	aaagtttctt	ctgttttcta	cactaatgtg	840
gtgcccattgc	tcaatcccc	catctacagt	ttgaggaaca	aggatgtcaa	agttgcactg	900
aggaaagctc	tgattaaaat	tcagaggaga	aatatattc			939

<210> 847

<211> 924

<212> DNA

<213> Unknown (H38g697 nucleotide)

<220>

<223> Synthetic construct

<400> 847

atgaccatgg	aaaattatcc	tatggcagct	cagtttgtct	tagatgggtt	aacacagcaa	60
gcagagctcc	agctgcccct	cttccctcctg	ttcctgggaa	tctatgtggt	cacagtagtg	120
ggcaacctgg	gcatgattct	cctgattgca	gtcagccctc	tacttcacac	ccccatgtac	180
tatttccctca	gcagcttgct	cttcgtcgat	ttctgtctatt	cctctgtcat	tactcccaaa	240
atgctgggtga	acttcctagg	aaagaagaat	acaatccttt	actctgagtg	catgggtccag	300
ctcttttttct	ttgtgggtctt	tgtgggtggct	gaggggttacc	tcctgactgc	catggcatat	360
gatecgctatg	ttggcatctg	tagcccactg	ctttataatg	cgatcatgtc	ctcatgggtc	420
tgtcactcgt	tagtgcctggc	tgccttcttc	ttgggctttc	tctctgcctt	gactcataca	480
agtgccatga	tgaactgtc	cttttgcaaa	tcccacatta	tcaaccatta	cttctgtgat	540
gttcttcccc	tcctcaatct	ctcctgctcc	aacacacacc	tcaatgagct	tctacttttt	600
atcattgcgg	ggtttaaac	cttgggtgcc	accctagctg	ttgctgtctc	ctatgccttc	660
atcctctaca	gcatecttca	catccgctcc	tcagagggcc	ggtccaaagc	ttttggaaca	720
tgcagctctc	atctcatggc	tgtgggtgatc	ttctttgggt	ccattacctt	catgtatttc	780
aagccccctt	caagtaactc	cctggaccag	gagaaggtgt	cctctgtatt	ctacaccacg	840
gtgatcccca	tgctgaaccc	tttaatatat	agtctgagga	ataaggatgt	gaagaaagca	900
ttaaggaagg	tcttagtagg	aaaa				924

<210> 848

<211> 984

<212> DNA

<213> Unknown (H38g698 nucleotide)

<220>

<223> Synthetic construct

<400> 848

atggcacctg	gaaatggctc	tttcgtgact	gaattcatte	tggcgggatt	aacacatcag	60
ccagatctcc	agtcctctct	gttcttccctg	tttctagtaa	tctatgtggt	cactctgttg	120
ggaaaacttg	gcttggtaac	tctaattggg	ctgaactcac	accttcatac	ccccatgtac	180
ttcttccctct	ttaacttgct	cttcatagat	ctctgttatt	cttctgtgtt	tacacccaaa	240
atgctaataga	actttatttc	agagaagaat	attatctcct	tcaaggggtg	catgacccaa	300
cttttctttt	tctgtttttt	ttggtcattt	ctgaatgtta	tgtgctgacg	tcaatggcgt	360
atgatcgctg	tggccatctg	taaccactt	ctgtatcaca	ttgccatgtc	tcctacagtg	420
tgtctccagcc	ttatgttttg	ttcctatttg	atggcctttt	ctggtgccat	ggcccacact	480
ggatgcacgc	tgagactgac	tttctgtgat	gcgaacacca	tcgatcacta	cttctgtgac	540
atcctccctc	tgtctcagct	ctcctgcacc	agcacctaca	tcaatgagct	ggtgggttttc	600
actgtgggtt	gcataacat	cattgtgccc	actgttacca	tctttatctc	ttatggtttc	660
atcctctcca	gcatectcca	tatcagttcc	aaggagggca	ggtccaaagc	tttcagcact	720

tgcagttccc	atataattgc	tgtttctctg	ttctttggat	caggtgcatt	tatgtatctc	780
aacctatctt	ctgctgggtc	catggataag	agaaaattat	cttctgtctt	ttatacaaat	840
gtggttccca	tgttgaaccc	cttaatctac	agcctgagga	acaaagatgt	taaatttgcc	900
ctaagaaaag	ccctgagtag	taggaaactt	tgataagtaa	tagtatgtgt	ctgtgtgtat	960
agtcacaaga	cagggatatt	ctgt				984

<210> 849

<211> 940

<212> DNA

<213> Unknown (H38g699 nucleotide)

<220>

<223> Synthetic construct

<400> 849

atgaaaccag	ggaatgagac	acaaatttca	caattccttc	tcctgggact	ttcagaggaa	60
ccagaattgc	agcccttcc	ctttgggcta	tttctgtcca	tgtacctggt	caccgtgctc	120
gggaacctgc	tcatcatcct	ggccacaatc	tcagactccc	acctccacac	ccccatgtac	180
ttcttcctct	ccaacctgtc	ctttgcagac	atctgttttg	tgtctaccac	tgtcccaaaag	240
atgctgggtga	acatccagac	acagagcaga	gtcatcacct	atgcagactg	catcacccag	300
atgtgctttt	ttatactctt	tgtagtgttg	gacagcttac	tcctgactgt	gatggcctat	360
gaccgggtttg	tggccatctg	tcacccctcg	cactacacag	tcattatgaa	ctcctggctc	420
tgtggactgc	tgggttctggt	gtcctggatc	gtgagcatcc	tatattctct	gttacaagc	480
ataatggcat	tgcagctgtc	cttctgtaca	gaattgaaaa	tccttcattt	tttctgtgaa	540
cttaatcagg	tcattccacct	tgccgtgtcc	gacactttta	ttaatgacat	gatgatgaat	600
tttacaagtg	tgtctgtggg	tgggggatgc	ctcgtctggaa	tattttactt	actttaagat	660
actttgttgc	atatgttcga	tctcatcagc	tcaggggatg	aataaagcac	tttccacctg	720
tgcattctcac	ctctcagttg	tctccttatt	ttattgtaca	ggcgtagggtg	tgtaccttag	780
ttctgtctgca	accataact	cactctcaaa	tgctgcagcc	tcgggtgatgt	acactgtggt	840
cacctccatg	ctgaacccct	tcattctacag	cctgaggaat	aaagacataa	acagagctct	900
gaatcgattc	ttcagagagc	agaaacagga	gggccatttt			940

<210> 850

<211> 971

<212> DNA

<213> Unknown (H38g700 nucleotide)

<220>

<223> Synthetic construct

<400> 850

cacacagagc	cacggaatct	cacaggtgtc	tgagaattcc	tcctcctggg	actctcagag	60
gatccagaac	tgcagtcggg	cctcgctttg	ctgtccctgt	ccctgtccct	gaatctggtc	120
acggtgctga	ggaacctgct	cagcatcctg	gctgtcagct	ctgactcccc	cctccacacc	180
cccattgtact	tcttcctctc	caacctgtgc	tgggtctgaca	tcgggtctcac	ctcggccacg	240
gttcccaagg	tgattctgga	tatgcagtcg	catagcagag	tcattctctca	tgtgggctgc	300
ctgacacaga	tgtctttctt	ggtccttttt	gcatgtatag	aaggcatgct	cctgactgtg	360
atggcctatg	gctgctttgt	agccatctgt	cgccctctgc	actaccagct	catagtgaat	420
cctcacctct	gtgtcttctt	cgttttgggtg	tcctttttcc	ttaacctgtt	ggattcccag	480
ctgcacagtt	ggatttgtgt	acaattcacc	atcatcaaga	atgtggaaat	ctctaatttt	540
ttctgtgacc	cctctcagct	tctcaacctt	gctgttctcg	acagcgtcat	caatagcata	600
ttcatatatt	tcgatatgtac	tatgtttggt	ttctctccca	tttcagggat	ccttttctct	660
tactataaaa	ttgtcccttc	cattctaaagg	atgtcatcgt	cagatgggaa	gtataaagcc	720
ttctccacct	atggctctca	cctaggaggt	gtttgtctgt	tttatggaac	agtcattggc	780
atgtacctgg	cttcagccgt	gtcaccaccc	cccaggaatg	gtgtgggtggc	atcagtgtatg	840
taggctgtgg	tcacccccat	gctgaacctt	ttcatctaca	gcctgagaaa	caggacata	900
caaagtgcc	tgcggagggt	gcgcagcaga	acagtcgaat	ctcatgatct	gttccatcct	960
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<210> 851

<211> 1014

<212> DNA

<213> Unknown (H38g701 nucleotide)

<220>

<223> Synthetic construct

<400> 851

```

cccattgagc agggaaatta caccagggtg aaggaatctc ttttttcaag gactgaccca      60
gtcccaagag ctgagcttgg tcttatttct tttcttattt tttgtgtact cagcaactgt      120
gctgggtaac ctctcatca tggctgtggt gacctgtgag tctcgccttc acacccccac      180
gtacttctcg ctctgcaatc tctctgtgtt gggtatctgc ttctcctcca tcactgtctcg      240
gaagggtgcta atagaccttt caagcagaaa gaccatctcc ttcaatggtt gcatgacaca      300
gatgtttttc ttccacctcc tcggtgggac agacgttttt tctctctttg tgatggcggt      360
tgaccaatac atggccatct tcaagccctt gcactgtgtg accatcgtga gtaggggaca      420
gtgctccctt acatcgtgag tagggggcgt gagtgaggcg caggcctcat catggcttcc      480
tgggtggggg gtttgtccac tccattgtgc aggtatttct gttgtctcca ctcccttctg      540
tggacatcat atgattgatg gtttctactg tgatgtcccc caggctctca aacttgccctg      600
caccacacac tttgtcttgg aggtcttaat gatttccaat aatggcttga tctctatgct      660
gtggttcata tttctcctca tatcttacac ggtcatcttg atgatgttga ggtctcacac      720
tgaggaaggc aggaggaaaag ccatcgccac ctgcacctcc cacatcactg tggtgacctt      780
gcatttcgtg ccctgcacat atgtgcatgc ccagccttca ctgccctccc cacggacaga      840
gctgtctcca tcacctttac agtcattatt cctgtcctga accccatgat ctacaccttg      900
aggaaccagg agatgaagtc agccttgagg aggcggaaga aaagaccttc tggaaaggga      960
tagatgctac gaagtccaga ttggaaaatc agaactgaaa agtatttctt cata      1014

```

<210> 852

<211> 1004

<212> DNA

<213> Unknown (H38g702 nucleotide)

<220>

<223> Synthetic construct

<400> 852

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tctaataacc cgcagaattt aacagatgtc tctttattcc tcctcctaga agctcagagg      60
atccagaaca gcagcctgtc ctgctgggc tgttccctgtc catgtgcctg gtcacgggtgc      120
tggggaacct gtcacatcct ctggccgtca gccctgactc ccacctccac acccccatgt      180
acctcttctt ctccaacctg tccttgccctg acatcggttt cacctccagc atgggtcccca      240
agatgattgt ggacatctaa tctcacagca gactcatctc ctaggcaggc tgccctgactc      300
ccatgtctct ctttgccatt tttggaggca tgggaagagag acatgtctct gagtgtgatc      360
cctatgaccc gtttgtagcc atctgtcacc ctctatatca ttcagccatc atgaaccctg      420
gtttctgtgg ctttctagtt ttgttgtctt ttttttctca gtctctttta gacgccagg      480
tgcacaactt gattgcctta caaatgacct gcttcaagga tgtggaaatt cctaatttct      540
tctgggaacc ttctcaactc ccccatcttg catgttgcca caccttcacc aataacataa      600
tcatgtatct ccctgtctgc atatttggtt ttcttcccat ctcggggacc cttttctctt      660
actataagat tgtttcctcc attctgaggg ttcatcctc aggtgggaag tataaggcgt      720
gtccacacct tgggtctcac ctgtcagttg ttgtctgatt ttatggaaca ggcttttggg      780
ggtacctcag ttcagatgtg tcatcttccc cgggaaaggc tgcagtggcc tcagtgtatg      840
acacggtggt ccccccatg ccgaacctct tcatctacag cctgagaaac agggatatta      900
aaagcgtcct gcggcgcccg cacggcagca cagtctaag tcaatatctc cttatctgtt      960
ccatgccttt tgtagtgtgg gttaaaaaag gcagcaaggc caaa      1004

```

<210> 853

<211> 945

<212> DNA

<213> Unknown (H38g703 nucleotide)

<220>

<223> Synthetic construct

<400> 853

```

atgaaaaaact gtaccagggt aaaagaattt attttccttg gcctaaccce gaatggggac      60
acaagattgg tcctatttct ttctactctc ttgggtgtaca tgacgactct gctgggaaac      120
ctcctcatca tggtcactgt cacctgtgaa tcttgccctc acatgcccat gtattttttg      180
ctccataatt tatctattgc cgatatctgc ttctactcca tcacagagcc caagggtctg      240
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ctcttccacc ttattggagg ggtggatgca ttttctctat cagtgatggc attggatcaa      360
tatgtggcca tttccaagtc cctgcactat gcgaccatca tgagtagaga ccgttgcatt      420
gggctcacag tggctgcctg gttggggggc tttgtccact ccattgtgca gattaccctg      480
ttgtctccac tccctttctg tggaccaaatt gttcttgaca ctttctactg tgatgttccc      540
caggttctca aactcgccca tacagacatt ttcatacttg agctgttgat gattttccaac      600
aatggactgc tcaccacact gtgggtttttc ctgctcctgg tgtcctacat ggtcatatta      660
tcattactca agtctcagggc aggatagggc aggaggaaag tcactctccac ctgcacctcc      720
cacatcactg tggtgacctt gcattttgtg ccctgcactc atgtctatgc ccggcctttc      780
actgccctcc ccacggataa ggccatctct gtcaccttca ctgtcatctc ccctctgctc      840
aacccttgat ctacactctg agaaaccatg agatgaagtc aaccatgaag agactgaaga      900
ctctgacctt ctgataggaa atagaccagt gcttccctcc ttctc      945

```

<210> 854

<211> 962

<212> DNA

<213> Unknown (H38g704 nucleotide)

<220>

<223> Synthetic construct

<400> 854

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cacacagagc cacggaatct cacagggtgc tgaaaagtgc tcctgggact ctctctgaga      60
ggatccagaa ctgcagccca tcctcgctgg gctgtccctg tccatgtatc tggtcacggc      120
gctgaggaac gtgctcatca tcctggctgt cagctctgac tcccacctcc acacccccat      180
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caagatgact gtggacatgc agtcgcatag cagagtcatc tcttatgtga gctgcctgac      300
acagatatct ttcttggtcc tttttgcatg tatggaagac atgctcctgt gatggcctat      360
gacagagttg tggccatctg tcacccctcg cactatccag tcatcatgaa tcctcacctt      420
cgtgtcttct tagttttgct gtcctttttc cttagcttgt tggattccca gctgcacagt      480
tggatttgtt tacaattcac cttattcaag aatgtggaaa actctagttt tgtctgtgac      540
ccctctcaac ttctcaacct tgccctgttct gacagcgtca tcaatagcat attcatatat      600
ttcagataga ctatgtttgg ttttcttccc atttcaggga tcctttttat ttactataaa      660
attgtccctt ccattctaag gatgtcatca tcagatggga agtataaagc cttctccacc      720
tatggctctc aactggcagc tctttgctga ttttatggaa caggcattgg catgtacctg      780
acttcagctg tggcactacc ccccaggaat ggtgtcgtgg catcagtgat gtaggctgtg      840
gtcaccccca tgctgaactt tttcatctac agcctgagaa acagggacat acaaagtgcc      900
ctgaggaggc tgcgcagcag aacagtcgaa tctcatgata tgttccatcc tttttcttgt      960
gt

```

<210> 855

<211> 952

<212> DNA

<213> Unknown (H38g705 nucleotide)

<220>

<223> Synthetic construct

<400> 855

```

aagcagcagg aaaatgggac ctgtctgggtg acagaattcc tgatgatggg attctccaac      60
ctccacacc tgaggaacac actcttcacc ctgttcttcc ttacctacct ggtcaccttc      120
ggtggcaacy tcaccatcat caccatcacc catgcggata ggccccgcca cactcccatg      180
taccacttcc tgggtggtgt gtccctctcg gagacctgct atacacgctg gtcaccatcc      240
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tcagatgttt ttcttctctg gtctgggagt cagccactgc ttcttcttta cctgatggg      360
ttatgaccgc tatgtggcca tctgccacc cctgcgtac tctatgggtc tgagaccac      420
cgtttgcttc tgccctgggag cctgggtttt ctgctctggg ttctcgggtg ccttgatcga      480

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gaccagcatg atctttctcat cgcccttttg cggcggagac cacgtggagc acttcttctg	540
tgacatcgcc ccggtgctga agctcagctg cgccaagagt gccagcaagg cgctgggcat	600
ctttttcctg agcgtcctgg tgggtgctgat gtccttcgtc ccgatacctct tctcctatgc	660
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cacctgtgtg gcccacgtca ccgtggctgt agtacatttt gactgcgcct ccatcatcta	780
cttgcgctccg gagtccgggg ccaaccccgga ccaggaccgc ttgggtggctg tgttctacac	840
ggtgggtgatg ccactgctga accctgtggg gtgcactctg tggacaagagg aggtgagagt	900
ggctctgagg aggaccctgg cgtggagccg tggggttttt aaataagaat ct	952

<210> 856

<211> 339

<212> DNA

<213> Unknown (H38g706 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1) ... (339)

<223> n = A,T,C or G

<400> 856

ctgctggacc acttcatctg tgagctgccg gcgttgctca agctggcctg cggaggcgac	60
ggagacacta ccgagaacca gatgttcgcc gccgcgtgg tcactcctgct gctgccgttt	120
gccgtcatcc tggcctccta cgggtgccgtg gcccgagctg tctgttgcat gcggttcage	180
ggaggccgga gggagggcgg tgggcacgtg ttgggtccca cctgacagcc gtctgcctgt	240
tctacggctc ggccatctac acctacctgc agcccgcgca gcgctacaac cagcacgggn	300
ncagnttcgt atcgctcttc tacacccgtg gtcacaccc	339

<210> 857

<211> 939

<212> DNA

<213> Unknown (H38g707 nucleotide)

<220>

<223> Synthetic construct

<400> 857

atggatcaga gaaattacac cagagtgaag gaatttacct tcctgggaat tactcagtc	60
cgagaactga gccaggtctt atttaccttc ctgttttttg tgtacatgac aactctaagt	120
ggaaacttcc tcactcatggg tacagttacc tgtgaatctc accttcatac gcccatgtac	180
ttcctgctcc gcaacctgtc tattcttgac atctgctttt cctccatcac agtccctaag	240
gtcctgatag atcttctatc agagacaaaa acctctctct tcagtggctg tgtcactcaa	300
atgttcttct tccaccttct ggggggagca gacgtttttt ctctctctgt gatggcggtt	360
gaccgtata tagccatctc caagcccctg cactatatga ccatcatgag tagggggcga	420
tgcacaggcc tcactcgtggg ctctctgggt ggggggcttg tccactccat agcgcagatt	480
tctctattgc tccactccc tgtctgtgga cccaatgttc ttgacacttt ctactgcgat	540
gtcccccagg tcctcaaaact tgctgcact gacaccttca ctctggagct cctgatgatt	600
tcaaataatg ggtagtcag ttggtttgta ttcttcttct tcctcatatc ttacacgggc	660
atcttgatga tgcctgaggtc tcacactggg gaaggcagga ggaaagccat ctccacctgc	720
acctcccaca tcacctgggt gacctgcat ttctgtccct gcacttatgt ctatgcccg	780
cccttctactg ccctcccac agacactgcc atctctgtca ccttcaactgt catctccct	840
ttgctcaatc ctataattta cacgtgagg aatcaggaaa tgaagttggc catgaggaaa	900
ctgaagagac ggctaggaca atcagaaagg attttaatt	939

<210> 858

<211> 486

<212> DNA

<213> Unknown (H38g708 nucleotide)

<220>

<223> Synthetic construct

<400> 858

gtagccatat	gtaatccctt	gctttatcca	gtgatgatgt	ccaacaaact	cagcgctcag	60
ttgctaagta	tttcatatgt	aattgggttc	ctgcacccct	tggttcatgt	gagtttacta	120
ttgcgactaa	ctttctgcag	gtttaacata	atacattatt	tctactgtga	aattttacaa	180
ctgttcaaaa	tttcatgcaa	tgggtccatct	attaacgcac	taataatatt	tatttttgggt	240
gctttttatc	aaatacccac	tttaatgact	atcataatct	cttataactcg	tgtgctcttt	300
gatattctga	aaaaaaaagtc	tgaaaagggc	agaagcaaag	ccttctccac	atgcggcgcc	360
catctgcttt	ctgtctcatt	gtactacgga	actctgatct	tcatgtatgt	gcgtcctgca	420
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<210> 859

<211> 774

<212> DNA

<213> Unknown (H38g709 nucleotide)

<220>

<223> Synthetic construct

<400> 859

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gcccagctgt	gcgcacgcgt	ggctctgggt	tcggccgaat	gcgtccctct	ggcgggtgatg	180
gctctggacc	gcgcggccgc	agtgtgccgc	ccgctgcgct	atgcgggggt	cgtctccccg	240
cgcctatgtc	gcacgctggc	cagcgcctcc	tggctaagcg	gcctcaccac	ctcggttgcg	300
caaaccgcgc	tcctggctga	gcggccgctg	tgcgcgcccc	gcctgctgga	ccacttcac	360
tgtgagctgc	cggcgttgct	caagctggcc	tgcggaggcg	acggagacac	taccgagaac	420
cagatgttgc	ccgccegcgt	ggtcatcctg	ctgctgccgt	ttgccgtcat	cctggcctcc	480
tacgggtgccg	tggcccgagc	tgtctgttgc	atgcggttca	gcggaggccg	gaggaggcg	540
gtgggcacgt	gtgggtccca	cctgacagcc	gtctgcctgt	tctacggctc	ggccatctac	600
acctacctgc	agcccgcgca	gcgctacaac	caggcacggg	gcaagtctgt	atcgctcttc	660
tacaccgtgg	tcacacctgc	tctcaaccgc	ctcatctaca	ccctcaggaa	taagaaagtg	720
aagggggcag	cgaggaggct	gctgcggagt	ctggggagag	gccaggctgg	gcag	774

<210> 860

<211> 948

<212> DNA

<213> Unknown (H38g710 nucleotide)

<220>

<223> Synthetic construct

<400> 860

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ggcaacctgc	tcacatggc	caccgtctgg	agcgagcgca	gcctccacac	gcccattgtac	180
ctcttctgt	gcgcctctc	cgtctccgag	atctcttaca	ccgtggccat	catcccgcgc	240
atgctggccg	acctgctgtc	cacccagcgc	tccatcgctc	tcttggcctg	tgccagtcag	300
atgttctctc	ccttcagctt	cggttcacac	cactccttcc	tgtccaccgt	catgggttac	360
gaccgctacg	tggccatctg	ccacccccctg	cgtacaaacg	tgtcatgag	cccgcggggc	420
tgcgcctgcc	tgggtgggtg	ctcttgggtc	ggtggcttgg	tcatggggat	ggtgggtgacc	480
tcggccattt	tcacacctgc	cttctgtgga	cacaaggaga	tccaccattt	tgtttgccat	540
gtgccacctc	tgttgaagtt	ggcctgtgga	gacgatgtgc	tgggtgggtg	caaaggcgtg	600
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gtcctcacac	ccttctctcag	ccccatcacc	ttcagcctca	ggaacaagga	gctgaaggctc	900
gccatgaaga	agaccttctt	cagtaaactc	taccagaaaa	aaaatgta		948

<210> 861
 <211> 674
 <212> DNA
 <213> Unknown (H38g711 nucleotide)

<220>
 <223> Synthetic construct

<400> 861
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 gaagcatgga agagaggcat gctcctgagt gtgatggcat atgaccgggt ttagccatc 180
 tgtcaccctc tatatcggtc agccatcttg aaccctgtat tctgtggctt cctagatttg 240
 ttgtctttgt ttttttttgt ttgtttgttt tgtttttctc agtcttctag actccagct 300
 gcacaacttg attgccttac aaatgacctg ctccaaggat gtggaaattc ctaatttctt 360
 ctgggaacct tctcactcc cccatcttgc atgttgtgac accttcacca ggaacatcaa 420
 catgtatttc cctgctgccg tatttgggtt tcttcccatc tcagggaacct tttctcttac 480
 tgtaaaattc tttcctccat tctgagggtt tcatcatcag gtgggaagta taaaccttct 540
 ccacctgtgg gtctcacctg tcagttgttt gctgatttta tgggaacaggc gttggagggt 600
 acctcggttc agatgtgtca tcttccccga gaaagrgtgc agtggcctca gtgatgtaca 660
 ygggtggtcac cccc 674

<210> 862
 <211> 653
 <212> DNA
 <213> Unknown (H38g712 nucleotide)

<220>
 <223> Synthetic construct

<400> 862
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 gaggcagga agagagacat gctcctgagt gtgatggcct atgaccgggt ttagccatc 180
 tgtcaccctc tatgtcattc agccatcacg aaccctgtgt tctgtggctt tctagttttg 240
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 aggacctgct tcaaggatgt ggaaattcct aatttcttct gtgaccttc tcaattcccc 360
 gtcttgcatg ttgtggcacc ttcaccaata acataatcat gtatttccct gctgccatat 420
 ttggttttct tcccatctcg gggaccttt tctcttacga taaaattggt tctccattc 480
 tgagggtttc atcatcaggt gggaagcata aggccttctc caccaggggg tctcactgt 540
 cagttgtttg ctgattttat ggaacaggcg ttggagagta cctcggttca gatgtgtcat 600
 cttccccgag aaagggtgca gtggcctcag tgatgtacac ggtggtcacc ccc 653

<210> 863
 <211> 648
 <212> DNA
 <213> Unknown (H38g713 nucleotide)

<220>
 <223> Synthetic construct

<400> 863
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 gaagacaagg tcatctctta caatgcagt gtgctcaaa tgtatatctt ttagctttt 120
 gccactgtgg aaaattacct cttggcctca atggcctatg accgctatgc agcagtgtgc 180
 aaaccctac attacaccac aacctgaca acaactgtgt gtgctcgtct ggccataggc 240
 tcctacctct gtggtttctt gaatgcctcc atccacactg gggacacatt tagtctctct 300
 ttctgtaagt ccaatgaagt ccatcacttt ttctgtgata ttccagcagt catggttctc 360
 tcttgctctg atagacatat tagcgagctt gttcttattt atgtgtgtgag cttcaatctc 420
 tttatagctc tcttggttat cttgatattc tacacattca ttttatcac catcctaaag 480

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atgcactcag cttcagtata ccagaagcct ttgtccacct gtgcctctca tttcattgca      540
gtcggcatct tctatgggac tattatcttc atgtacttac aaccagctc cagtactcc      600
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<210> 864

<211> 645

<212> DNA

<213> Unknown (H38g714 nucleotide)

<220>

<223> Synthetic construct

<400> 864

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attgttgaca tatectatgc ttccaactat gtccccaaga tgctgacgaa tcttatgaac      60
caggaaagca ccatctcctt ttttccatgc ataatgcaga cattcttgta tttggctttt      120
gtcacgtag agtgtctgat tttgggtggt atgtcctatg atcgctatgc ggacatctgc      180
caccctttac gttacaatat cctcatgagc tggagagtgt gcactgtcct ggctgtggct      240
tcctgggtgt tcagcttctt cctggctctg gtccctttag ttctcctcct gaggctgccc      300
ttctgcgggc ctcatgaaat caaccacttc tgtgaaatcc tgtctgtcct caagttggcc      360
tgtgttgaca cctgggtcaa ccaggtgggc atctttgcag cctgcgtgtt catcctgggtg      420
gggccactct gcctgggtgt ggtctcctac ttgcgcaccc tggccgccat cttgaggatc      480
cagtctgggg agggccgcag aaaggccttc tccacctgct cctcccacct ttgcgtgggtg      540
ggactcttct ttggcagcgc cattgtcacg tacatggccc ccaagtcccg ccatectgag      600
gagcagcaga aagttctttc cctgttttac agccttttca atcca      645

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<210> 865

<211> 486

<212> DNA

<213> Unknown (H38g715 nucleotide)

<220>

<223> Synthetic construct

<400> 865

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gtggccatct gtaaaccctt tcattatgtg gtcacatga acaacagggt gtgtacctta      60
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ctccagctcg aattctgtga ctccaatgcc attgatcatt ttagctgtga tgcaggctct      180
ctcctaaaga tctcatgtct agatacatgg gtaatagaac agatgggtat acttatggct      240
gtatttgcac tcattatcac cccagtttgt gtgattctgt cctacttgta catagtcaga      300
acaattctga agttcccttc tgttcagcaa aggaaaaagg ccttttctac ctgttcatcc      360
cacatgattg tggtttccat tgcctatgga agctgcatct tcatctatat caagccctct      420
gcaaaagatg aggtggccat aaataaagga gtttcagttc ttactacttc tgtcgcaccc      480
ttgttg      486

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<210> 866

<211> 670

<212> DNA

<213> Unknown (H38g716 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(670)

<223> n = A,T,C or G

<400> 866

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ggaggcatgg aagagagaca tgctcctgag cgtgatggcc tacgaccagt ttgtagccat      180
ctgtcaccct ccatatcggt cagccatctt gaaccctgtt ttctgtggct tccaagattt      240

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gttgctccttg	tntttttttt	tttttttttt	tttttctca	ggctttttaga	ctcccagctg	300
cataacttga	ttgccttaca	aatgacctgc	ttcaaggatg	tggaaatttc	taatgtcttc	360
tgggaacctt	ctcaactctc	ccatcttgca	tgttggtgaca	ccttcaccag	gaacatcagt	420
atttccttgc	tgccatattt	ggttttcttc	ccatcttggg	gaccttttcc	tcttactgta	480
aaattgtttc	ctccattctg	agggtttcat	catcagggtg	gaagtataaa	ccttctccac	540
ctgtgggtct	cacctgtcag	ttgtttgctg	attttatgga	acagggtgtg	gagggtacct	600
cagttcagat	gtgtcatctt	ccctgagaaa	ggctgcagtg	gcctcagtga	tgtacaagat	660
ggtcaccccc						670

<210> 867

<211> 654

<212> DNA

<213> Unknown (H38g717 nucleotide)

<220>

<223> Synthetic construct

<400> 867

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cacagcagag	tcatctccta	tgcaggctgc	ctgactcaga	tgtctctctt	tgtgtttttt	120
ggaggcatgg	aagaaagaca	tgtctctgag	tgtgagggcc	tatgaccggt	ttgtagccat	180
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gtgttttttt	tttttctcag	tcttttagac	tcccagctgc	acaatttgat	tgccttacia	300
atgacctgca	tcaaggatgt	ggaaattcct	aatttcttct	gtgaccttcc	tcaactcccc	360
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tttggttttc	ttcccatctc	ggggaccctt	ttctcttact	ctaaaattgt	ttcctccatt	480
ctgagggttt	catcatcagg	tgggaagtat	aaagccttct	ccacctgtgg	gtctcacctg	540
tcagttgttt	gctgagttta	tgggaacaggc	gttgagggtt	acctcagttc	agatgtgtca	600
tcttccctga	gaaaggctgc	agtggcctca	gtgatgtaca	cggtggtcac	cccc	654

<210> 868

<211> 882

<212> DNA

<213> Unknown (H38g718 nucleotide)

<220>

<223> Synthetic construct

<400> 868

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ctagacatcc	tctccactac	agtcaactgtc	cccaagacgc	tgcccctggt	cttgcttggg	180
gaccaacttc	tcagcttccc	tgcctgtctc	ctacagatgt	acctgttcca	cagcttctcc	240
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ccactgcaat	accctgttct	catgaaccca	cagaccaatg	ctgtcttggc	aaccggtgcc	360
tggtcactg	ccctcctcct	gcccattcca	cgagtagtac	agacctccca	gatggcattt	420
gacagcattg	ctgacatcta	ccactgtctc	tgtgatcatc	tggctgtggg	ccaggcctcc	480
tgtcttgata	ccacccccag	accttcatgg	gtttctgcat	cgccatgggt	gtgtccttcc	540
tcccccttct	cctgggtgctt	ctctcctatg	cccacatctt	gacctcgggt	cttcgcatta	600
actcccaaga	aggacgtccc	aaagccttct	ccacctgcag	ctcccatctc	ccggtagtgg	660
gcacctacta	ctcatccatt	gccatagcct	atgtggccta	cagcgctgac	ctgcccctcg	720
acttccacgt	catgggcaat	gttgtacatg	tcttcttctt	cctcttcttc	ttcttcttcc	780
tcttctctct	cttctctctc	ctctctgtct	tctcttctct	cttcttctcc	ttctcttctc	840
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<210> 869

<211> 934

<212> DNA

<213> Unknown (H38g719 nucleotide)

<220>

<223> Synthetic construct

<400> 869

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ggaaacctcc	tcatcatggt	cactgttacc	tgtgaatctc	gccttcacac	gcccattgat	180
tttttgctcc	ataattttatc	tattgccgat	atctgcttct	cttccatcac	agtgcccaag	240
gttctgggtg	accttctgtc	tgaaagaaag	accatctcct	tcaatcattg	cttcactcag	300
atgtttctat	tccaccttat	tggaggggtg	gatgtatttt	ctctttcggg	gatggcattg	360
gatcgatatg	tggccatctc	caagcccctg	cactatgcga	ctatcatgag	tagagaccaa	420
tgcattgggc	tcacagtggc	tgcctgggtg	gggggctttg	tccactccat	cgtgcagatt	480
tcctgttg	tcccactccc	tttctgcgga	cccaatgttc	ttgacacttt	ctactgtgat	540
gtccaccggg	tectcaaact	ggcccataca	gacattttca	tacttgaact	actaatgatt	600
tccaacaatg	gactgtctac	cacactgtgg	tttttcctgc	tcctgggtgc	ctacatagtc	660
atattatcat	tacccaagtc	tcaggcagga	gagggcagga	ggaaagccat	ctccacctgc	720
acctcccaca	tcactgtggt	gacctgcat	ttctgtgccc	tgcattctatg	tctatgcccg	780
gcccttcaact	gccctccccca	tgataaggc	catctctgtc	accttcaactg	tcattctcccc	840
tctgtctaac	cccttgatct	acactctgag	gaaccatgag	atgaagtcag	ccatgaggag	900
actgaagaga	agacttgtgc	cttctgatag	aaaa			934

<210> 870

<211> 898

<212> DNA

<213> Unknown (H38g720 nucleotide)

<220>

<223> Synthetic construct

<400> 870

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ttgaggcaga	aaatagtgtt	tgtaatcttc	ttattttct	atatgggaac	tgtgggtggg	120
aatatgctca	ttattgtgac	catcaagtcc	agccggacac	taggaagccc	catgtacttc	180
tttctatttt	atttgcctt	tgcagattct	tgcttttcaa	cttccacagc	ccctagatta	240
attgtggatg	ctctctctga	aaagaaaatt	ataacctaca	atgagtgcac	gacacaagtc	300
tttgactac	atttatttgg	ctgcatggag	atctttgtcc	tcattctcat	ggctgttgat	360
cgctatgtgg	ccatctgtaa	gcccttgcgt	tacccaacca	tcattgagcca	gcaggctctgc	420
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ctggccttaa	gattgccttt	ctgtggaccc	tatttgattg	atcattattg	ctgtgatttg	540
cagcccttgt	tgaaacttgc	ctgcatggac	acttacatga	tcaacctgct	gttgggtgct	600
aacagtgggg	caatttgcctc	aagtagtttc	atgattttga	taatttcata	tattgtcatc	660
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ccgaccactt	tccccatgga	caagatgggtg	gcagtatttt	atactatttg	aacacccttt	840
ctcaatccac	tcattctacac	atctgaggaa	tgcagaagtg	aaaaatgcca	tgagaaag	898

<210> 871

<211> 943

<212> DNA

<213> Unknown (H38g721 nucleotide)

<220>

<223> Synthetic construct

<400> 871

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caagaccaga	gtttgggtctt	gtttcttttt	ttatgtcttg	tgtacatgac	gactctgctg	120
ggaaacctcc	tcatcatggt	caccgtgacc	tgtgagtctc	gccttcacac	ccccatgtac	180
ttctgtctcc	gcaatctagc	catccttgac	atctgcttct	cttccacaac	tgctcctaaa	240
gtcttgctgg	accttctgtc	aaagaaaaag	accatatact	atacaagctg	catgacacag	300
atatttctct	tccacctcct	tggtggggca	gacatttttt	ctctctctgt	gatggcggtt	360
gactgtctaca	tggccatctc	caagcccctg	cactatgtga	ccatcatgag	tagagggcaa	420

tgcactgccc	tcattctctgc	ctcttggatg	gggggctttg	tccactccat	cgtgcagatc	480
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gcccttcaact	gccctcccca	cagaaaaggc	catctctgtc	accttcaactg	tcattctcccc	840
tctgctgaac	cctttgatct	acactctgag	gaaccaggaa	atgaagtcag	ccatgagaag	900
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<210> 872

<211> 942

<212> DNA

<213> Unknown (H38g722 nucleotide)

<220>

<223> Synthetic construct

<400> 872

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ccccacctcc	aactgatgct	cttctgtctg	ttctgtctga	tgtacctgtt	cacgtgtctg	120
ggcaacctgc	tcattcatggc	caccgtctgg	agcgagcgca	gcctccacac	gcccattgtac	180
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ggcttgggat	gtatcatggc	actgctgggc	tgttttctcc	tcactcctct	ctcctatgcc	660
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acctgtgcct	ctcaccttat	tgtgggtcatt	gtgcactatg	gctttgcctc	tgctatctac	780
ctcaagccca	aagggtcccca	ctctcaggag	ggtgacaccc	tgatggccac	cacctacgca	840
gtcctcacgc	ccttctcag	ccccatcatc	ttcagcctca	ggaacaaaga	actgaaggtt	900
gccatgaaga	ggaccttcct	cagcacactc	tattcctcag	gc		942

<210> 873

<211> 948

<212> DNA

<213> Unknown (H38g723 nucleotide)

<220>

<223> Synthetic construct

<400> 873

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ccccagcagc	tcctgctgtg	cttgttctctg	ctgtacctcc	tgatgttctt	gttcacattg	120
cttggaacac	ttcttatcat	ggccacagtt	tggattgaac	gcagactcca	cacacccatg	180
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cgcattgtgg	ctgatctgtc	cttcacctat	cgttccatca	cctttgtggc	ttgtgccatt	300
cagatgttct	tctccttcat	gtttggcttc	actcactcct	tccttctcat	ggtcatgggc	360
tatgatcact	acgtgacctt	ctgccaccca	ctgcattaca	acatgcta	gagtcctcgt	420
ggctgtgccc	atcttgtggc	ctggacctgg	gctgggtggc	cggtcattgg	gatgatgggt	480
acaatgatgg	tttttcaact	cactttctgt	gggtctaatg	tgatccacca	ttttctctgt	540
catgtgcttt	ccctcttgaa	gttggcctgt	gggagcaaga	catcatctgt	catcatgggt	600
gtgatgctgg	tgtgtgtcac	agccctgata	ggctgtttgt	tcctcatcat	cctctccttt	660
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tccacttgtg	tatccacctt	cactgtgggtg	gtcatgcact	atagttttgc	ctcccttatt	780
tacctcaaac	ccaaggccct	ccattctatg	tacagtgtatg	ccttgatggc	caccacctat	840
actgtcttca	cccccttctt	cagcccaatc	atcttctcagtc	taaggacaaa	ggagctgaag	900
aatgccataa	ataaaaactt	ttgcagaagg	ttctgccttc	taagctcc		948

<210> 874
 <211> 484
 <212> DNA
 <213> Unknown (H38g724 nucleotide)

<220>
 <223> Synthetic construct

<400> 874
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 tggacttcga gagggtggc ccttcttggg cctgcctctt gtcttcctct ttgtgaccat 120
 catctctgcc aatgccctgg tcatccacac agtggttgcc cggcaaaatc tgcacagcc 180
 tacgtgtatg ctcatcactg tgctcctggc tgtcaatatt cgtgctgcca cagccgtgat 240
 gcctaaaatg ctggagggct ttgtatatta tgctaacccc atatcgctgc atggccgcct 300
 ggcctagggtg ttctttatct acttcaccct cctcctggac tacaacttcc tctggccctg 360
 gccctggact gggtactttg ccactctgcca cccactctgc ttttctgacc tgatgacctc 420
 ccagctgctg ggactgctgg ccattcttgc ctttgaacaa agccctggga gtgaccccg 480
 cccct 484

<210> 875
 <211> 595
 <212> DNA
 <213> Unknown (H38g725 nucleotide)

<220>
 <223> Synthetic construct

<400> 875
 gtagccatct ggcaccctc tctgttttca aactgaatga cttccagct ggctgggatt 60
 gctggccatt cttgccttga cacagagctg gggagtgaca gtgccttttg tagtactaac 120
 tgcaaaagcc gatttctgcc ggacagcagt gattcgacac ttcacctgtg agtgcatgac 180
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 tttggctact gtaatctctg atatggccct gctggggacc tctacaccc acatcatcta 300
 tgctgccttc cggatctctt cttggggagc ccaagccaag gccttacaca cgtgtggctc 360
 ccacctactg gtcacacctc ccatctacgt ctctggtctt tccacttcca tcaccttctg 420
 agtagccaag actgtgtccc agaattgcca gaattactc agtgccatat acttgctgct 480
 tccaggagcc ttgaatcctg tcatttatgg ggtgaggact agggagatcc agcaacatgt 540
 agaaaagatg ctctgtgaaa aggaaacagc ccagaaggct ggggagaagc caaag 595

<210> 876
 <211> 944
 <212> DNA
 <213> Unknown (H38g726 nucleotide)

<220>
 <223> Synthetic construct

<400> 876
 ttcagtcaga acttgctgat ctctgggtct gggctcctttg tcttctctggg gatgccggga 60
 ctggaggctc tgcctgctg gctctctgtg cctgtgtgcc tgctctacat ggcagctttg 120
 gtagggaatg ccttctagt ggggctgggt ggtcgtgac aaggcactct gggcaccat 180
 gtaccagctg ctgtggcttc tggcagctgc tgattttgtt ctggccacat ccacagtgcc 240
 caaagctctg gctgtacttt ggggcttgct tagtgagata tcatttggag gctgcttggc 300
 tcaactcttt gttgcccctg tgtcaatcat tgccacattg ctgagtcctc agtgctgctg 360
 tccacggccg tagactgcca gcctttgcgc tatggggcgt tgctggccca gtttgtggta 420
 ggtctagtgg ctctgactac catgaccctg gatgtctgtg tcatgtacac cctgtgatcc 480
 tgttcaagaa actgccttac tgtggacagt gggccctgcc ccacacctac tgcgaacaca 540
 tgggtgtggc ttgctggcca tgtggagata cgtgccccat catcaggat ggactggcca 600
 ccacactgct ctccccagcc ctggacctag ggctcatagg tgcttcctat gccctcattt 660
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ggacctatgc tagcatcatt ggtctcttct acacacctgc cctcttctcc ttccttgctc	780
actgttttgg gtgtcacaca gtgccaacc atattcacat cctactggct aacctctacg	840
cagtgggtgt cccagcttcc aatcctgtgg tctatggagt gcagactcag cagagctcag	900
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<210> 877

<211> 939

<212> DNA

<213> Unknown (H38g727 nucleotide)

<220>

<223> Synthetic construct

<400> 877

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gcttggttac aaatgcccct ttttgtgggc ctgttaatat catacacaat caccatattt	120
ggcaatgtgt ccatcatgat ggtgtgcatt ctggatccca aacttcatac tcccatgtat	180
ttctttctca ctaatctctc catcttagat ctctgtata ccacaactac agtccctcat	240
atgttggtta atattggttg caacaaaaag accatcagct atgctggctg tgtggccac	300
ctcatcatct tcctggccct aggtgctaca gagtgtctcc ttctggctgt tatgtcctt	360
gacagatatg tggctgtttg cagacccctc cactatgtag tcatcatgaa ttattggttc	420
tgccaaagga tggcagcctt ctcatggctc attgggttctg gcaactcagt gctgcagtct	480
tccttgactc ttaacatgcc acgtgtgggt caccaggaag tggaccactt tttctgtgag	540
gtgcctgcac ttctcaagtt gtcattgtgt gacacaaagc ctattgaggc tgagctcttc	600
ttcttttagt tactaattct tctaattcca gtgacattga tctcatctc ctatggcttc	660
atagctcaag cagtattaaa aatcagggtc gcagaaggac ggcaaaaagc atttgggaca	720
tgtgggtccc acatgattgt ggtgtccctc ttttatggaa cagccattta tatgtatctt	780
caaccacctt catccacctc taaggactgg ggaaagatgg tttccctctt ctatggaatc	840
atcacatcca tgttgaactc cctcatctac agccttagaa ataaagatat gaaggaggcc	900
ttcaagaggc tgatgccaaag aatctttttc tgtaagaaa	939

<210> 878

<211> 968

<212> DNA

<213> Unknown (H38g728 nucleotide)

<220>

<223> Synthetic construct

<400> 878

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ctggagtggg tctgcatctg gatgggaatt ctctccttta ccagttacct tgtctccctt	120
gcagggaatg tcatccttct ctaccttacc actgtggaac acaacctcca taaacctatg	180
ttttccttcc tctctatacc ggcctctgca aacctcatat tatgcattac atatttcccc	240
aaaacatttg ggatattcta gctgaaagct cagaaaataa tatttccttg atgttcacc	300
agggtttttt ttttgggtct acttcacttt agctttttt ctggacttgg ccatcttgtt	360
gggtctggca ttgatcatt acatgacctt tggtttctt ctgagataca ccagtggctt	420
gacacctcaa cacttggcaa gattgtgggt agcattgatt gaaggtttaa taacattttg	480
cccattgatt tcctggggaa gcatttgccc ttctgcagaa cacacattaa ttctaacaca	540
tactgtgagc acatagggtg ggccctgctt tcctatgctg atatctccat caatatctgg	600
tatgacttta ctatattggt aatgactatt atctcagatc tgatcctcac tgatatttcc	660
tacacctca ccttctatgc tgttttccac ctcccatcca gtgatgccct tctgaaggcc	720
ctaagcacct cggttctca tgtcagtgtc attctcatgt tgtacacacc aacctgtctt	780
tctgccctta ctcatcactt tggccagagt atctcttgca ctttttacct tatgtttgtg	840
ggcctctata gggcaatccc tcctgtactc aattccataa ttatggagta aaaacaaagc	900
agattggaaa caaggtcata cttttattct ttcttaaagg gatgcagtga tatgaggatg	960
agaatatg	968

<210> 879

<211> 1011

<212> DNA

<213> Unknown (H38g729 nucleotide)

<220>

<223> Synthetic construct

<400> 879

atgaaaaaaa	atgcaagttt	tgaagacttc	tttattctac	ttggattttc	taactggcct	60
catctggaag	tagttctctt	tgtgggtatc	ttgatcttct	acttgataac	actgatagga	120
aacctgttca	tcatcatcct	gtcataacctg	gactcccac	tccacactcc	catgtacttc	180
ttcctttcaa	atctctcatt	tctggatctc	tgctacacca	ccagctctat	ccctcagttg	240
ctggtgaatc	tctggggccc	ggaaaagacc	atctcttatg	ctgggtgtac	agttcâactt	300
tactttgttc	tcgcaactgg	aaccgcagag	tgtgtcctac	tgggtggtgat	gtcctatgat	360
cgttatgcag	ctgtgtgtag	acctttgcat	tacactgtcc	tcatgcaccc	tcgtttctgc	420
cgcttgttgg	ctgcggcttc	ttgggtaagt	ggttttacaa	cctcagcact	tcattcctcc	480
tttactttct	ggataccctt	atgtagacat	cgcctagtgg	atcacttctt	ctgtgaagct	540
ccagcacttc	tgcgattatc	atgtgttgat	acctaggcaa	atgagctgac	cctcatggtc	600
atgagctcca	tttttgttct	catacctctc	atcctcatcc	tcacttccta	tgggtgccatt	660
gcccgggctg	tactgagcat	gcaatcaacc	actgggcttc	agaaagtgtc	taggacatgt	720
ggagcccac	ttatggttgt	atctctcttt	ttcattccag	tcatgtgcat	gtatctccag	780
ccaccatcag	aaaattctca	agatcaaggc	aagtccattg	ccctctttta	cactgttgtc	840
acacctagtc	ttaacctctt	aatctacact	ttcagaaaca	aggatgtaag	aggggcagtg	900
aagagactaa	tgggggtggga	atgggggatg	tgacagggaa	atcatgttgg	ctgttgtttt	960
tcctagggtc	ttatccattt	tgaaaggttg	tttccctgct	tctttgtgat	t	1011

<210> 880

<211> 956

<212> DNA

<213> Unknown (H38g730 nucleotide)

<220>

<223> Synthetic construct

<400> 880

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ggacttgagc	agtaccacgt	ctggatcagc	atcccatctt	gcttaatacta	tctcatggct	120
gtcgtggcca	agagtatcct	tctctacctc	attgtggtag	agcacagtct	tcatgcaccc	180
atgttctttt	tcctttccat	gctggccatt	actgatctca	tattgtccac	cacatgtgtc	240
cccaaaacac	ttagcatctt	ctggtttggg	cccaaaacag	tttccctggc	tgtctcacc	300
aattattctt	tctgcactat	agcttttgtg	tggactcagc	tatactgctg	gccatggcat	360
ttgaccgcta	tatggccatt	tgtccaccct	tgagatacac	tactattctg	actcccaaaa	420
ccattgtcaa	aattgctgtg	ggaatatgtt	tccgaagttt	ctgtgttttt	gtcccgtgtg	480
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tttgtgttcc	catcatgacg	gtgatgacag	acgtgatect	cattgtctgtc	tcctacaccc	660
tcattgctctg	tgggtgtctt	tgcctccctt	cccaagatgc	ccgtcagaag	gcccttttgt	720
cctgtgggtc	ccatgtctgt	gttatccctca	tattctatac	accagcatte	ttctccatcc	780
ttgcccacg	ctttgggcat	aatgtccctc	atacctttca	tattatgttt	gccaaccttt	840
atgtaatcat	tccacctgct	ctcaacccta	ttgtctacag	aataaagacc	aagcaaattcc	900
agaacagaat	cctttttgtc	tttcccaagg	gggccagtg	ataggtgcct	gagctc	956

<210> 881

<211> 933

<212> DNA

<213> Unknown (H38g731 nucleotide)

<220>

<223> Synthetic construct

<400> 881

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tctaattggc	ctcatctgga	agtagttatc	tttgtgggtg	tcttgatctt	ctacttgatg	120

acactgatag	gaaacctggt	catcatcatc	ctgtcatacc	tggactceca	tctgcacaca	180
ccaatgtact	tcttcctttc	aaacctctca	tttctggatc	tctgtacac	caccagctct	240
atccctcagt	tgctgggtcaa	tctctggggc	cgggaaaaga	ccatctctta	tgctgggtgc	300
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atgtcctatg	accgttatgc	agctgtgtgt	agacctttgc	attacactgt	cctcatgcac	420
cctcgtttct	gccacctgct	ggctgtggct	tcttgggtaa	gtgggttttac	caactcagca	480
cttcattcct	ccttcacctt	ctgggtacct	ctgtgtggac	accgccaagt	agatcacttt	540
ttctgtgaag	ttccagcact	tctgcgatta	tctgtgtgtg	atacccatgt	caatgagctg	600
accctcatga	tcacaagctc	catatttgtt	ctcatacctc	tcattcctcat	tctcacttct	660
tatggtgcc	tctgccgagc	tgtactgagg	atgcagtcaa	ccactgggct	tcagaaagtg	720
tttgaacat	gtggagctca	tcttatggct	gtatctctct	ttttcattcc	ggccatgtgc	780
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tatactgttg	tcacacctag	tcttaacctt	ctaattctaca	ccctcagaaa	caaagttgta	900
agaggggcag	tgaagagact	aatggggtgg	gaa			933

<210> 882

<211> 264

<212> DNA

<213> Unknown (H38g732 nucleotide)

<220>

<223> Synthetic construct

<400> 882

tttattcatg	ccctctcagt	cattgaatcc	atcattgtgc	tggccatggc	ctttgagcgt	60
tatgtggcca	tatgccaccc	actgtgccat	gctgaagtgc	tcaacagtac	agtaacagcc	120
catattggca	tctagctgg	ggtagggga	tccctctttt	tttccccact	ggctctgctg	180
ataaagacgc	tgggcttatg	ccactcctat	gtgctctcgc	actcctatct	gctccaccag	240
gatgtagcga	acttgtccta	tgcg				264

<210> 883

<211> 477

<212> DNA

<213> Unknown (H38g733 nucleotide)

<220>

<223> Synthetic construct

<400> 883

gttgccatct	gtaacccttt	gcgctacctt	acagtcatga	acccccagct	atgccttttg	60
ttggttcttg	cctgctgggtg	tgggggtttt	atccactcta	tcatgcagg	catactagtc	120
atccagctgc	ctttctgtgg	gcccaatgaa	ctggacaact	tctactgtga	tgctctacaa	180
atcatcaagc	tggcctgcat	ggacacctat	gtggtagagg	tgctgggtgat	agccaacagt	240
ggtctgctgt	ctcttgtctg	cttcttggtc	ttactattct	cttatgctat	catcctgac	300
acctgagaa	cacgcttctg	ccagggccag	aacaaggctc	tctctacctg	tgcttctcac	360
ctgacagtgg	tcagcctgat	cttcgtgcc	tgcgtattca	tctatttgag	gcctttctgc	420
agcttctctg	tggataagat	attctccttg	ttttacacag	tgattacacc	tatggtg	477

<210> 884

<211> 948

<212> DNA

<213> Unknown (H38g734 nucleotide)

<220>

<223> Synthetic construct

<400> 884

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gtgtcaggaa	atggctctct	tgtctgtgtg	gtggcagtg	agcacagtct	tcataaacct	180
atgtaccttt	tcctctccat	gctggcattt	tgggatctga	ttctatccac	atctgcagta	240

cccaaagcct	tgagcatttt	ctgggttgat	gatgtggaca	tctcctttgg	tggtgtgtgc	300
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gctttcgacc	gctatgtggc	catctgctac	ccattgaggt	atagcaccat	acttagccac	420
agtgttattg	gcaaaattgg	gggtgtcgtg	gtgttcagga	gttttgcaac	tgtcttctcc	480
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tgtgaacaca	tggggctggc	aaagctaggt	tgttctgaaa	tcaccatcaa	tatttggtat	600
ggaatctctg	taccactact	cagtgttacg	ttagatatgg	tgacaatagt	catctcctag	660
gggctcatag	ttcaagcagt	cttcaggctg	ccctcccttg	gtgcttggat	gaaagcactc	720
agcacctgtg	gttcccatgg	cagtgtcatc	ctcatgttct	gccttccagg	aattttcact	780
gtcattgttc	agcgcttttg	ctgaaaattt	cccaagtatg	tccacatcct	gctggccaat	840
ctctatgttc	ttgttcccc	catgatgaac	ccaattatct	atggagtaaa	gactaaacag	900
attcagaaag	gggttgcctt	tgtgttttct	ccaaaaggaa	aattgttgc		948

<210> 885

<211> 1087

<212> DNA

<213> Unknown (H38g735 nucleotide)

<220>

<223> Synthetic construct

<400> 885

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ccttggctag	agcttccctc	gttcactagt	cttcttataa	tgtaccctat	agccgtgatg	120
ggaaacatca	caatcattct	catgtccagg	ttagactctc	gtcttcatag	ccccatgtac	180
tttttcccca	ccaacctctc	ctttttggac	atgtgttata	ccacaagcat	tgtccctcag	240
atgctgttta	acctgggaag	ctctaagaag	accatcagct	atatgggggtg	tgcggttcag	300
ctttattttc	ttcacataat	gggggggaaca	gaatgtttgc	ttttggctat	tatgtccttt	360
gatcgctatg	tggtccatctg	cagacctctt	cactacaccc	tcacatgaa	tcagcgcgtc	420
tgtatcccta	gtttccaccg	tgtggctaag	tggaataatc	tatgctgtct	cagaggccac	480
tgccacatta	caattgccac	tgtgtgctct	aataaactgg	accacttggg	gtgtgagatt	540
cctgttctga	taaagattgc	ctgtgggtgaa	aagggttcta	acgagctcac	actctctgtg	600
gtatgcattt	ttatgttagc	tgtcccaacta	tgtttaattc	ttgcttccta	tgctagtatt	660
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tcctcccatc	ttattgtagt	tttcttattt	tatggcccag	ccatcagcat	gtaccttcag	780
ccccctctct	ccatctcaag	ggatcaaccc	aagtctcatg	ccctcttcta	tggagtgggtg	840
actccctcac	tcaacctctt	tatctacacc	ctgcggaata	agaatgtaaa	gggggcatta	900
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attgaacagt	tagagttagt	tgctatgggt	ttatctaaca	aattcttgtc	tcataatcaa	1020
atatcgcttt	acatgttctt	gcaaaatatg	ttatgtctcc	gagactcttt	gtaaacatgt	1080
tcagcaa						1087

<210> 886

<211> 498

<212> DNA

<213> Unknown (H38g736 nucleotide)

<220>

<223> Synthetic construct

<400> 886

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tatgtggcca	tctgccaccc	actgcgccat	gctgcagtgc	tcaacaatac	agtaacagcc	120
cagattggca	tcgtggctgt	ggtccgcgga	tccctctttt	ttttcccact	gcctctgctg	180
atcaagcggc	tggtcttctg	ccactccaat	gtgctctcgc	actcctattg	tgtccaccag	240
gatgtactga	agttggccta	tgcagacact	ttgcccattg	tggtatatgg	tcttactgcc	300
attctgctgg	ccatgggcgt	ggacgcaatg	ttcatctcct	tgtcctattt	tctgataata	360
cgaacgggtc	tgcaactgcc	ttccaagtca	tagcgggcca	aggcctttgg	aacctgtgta	420
gtacacattg	gtgtgggtact	cggcttgtat	gtgccactta	ttggcacttc	aagtgggtcac	480
cggtttggga	acaaactt					498

<210> 887
 <211> 936
 <212> DNA
 <213> Unknown (H38g737 nucleotide)

<220>

<223> Synthetic construct

<400> 887

atgatgatta	aaaaaaaaatgc	aagttcggaa	gacttcttta	ttctacttgg	atthttcta	60
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acaggaaacc	tggtcatcat	catcctgtca	tacgtggact	cccatctcca	cacaccaatg	180
tactttcttc	tttcaaacct	ctcatttctg	gatctctgcc	acaccaccag	ctctatccct	240
cagttgctgg	tgaatctccg	gggcccggaa	aagaccatct	cgtatgctgg	ttgcatgggt	300
caactttact	ttgttcttgc	actgggaatc	gcagagtgtg	tcctactggg	ggatgatgtc	360
tatgatcggt	atgtagctgt	gtgtagacct	ttgcattaca	ctgtctcat	gcacctctgt	420
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gccattgccc	gggctgtact	gagcatgcaa	tcaaccactg	ggcttcagaa	agtgtttagg	720
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ctccagccac	catcagaaaa	ttctcctgat	cagggcaagt	tcattgcect	cttttatact	840
gttgctcacac	cgagtcttaa	tcctctaata	tacactctca	gaaacaagca	tgtaaaaggg	900
gcagcgaaga	gactattggg	gtgggagtgg	gggaag			936

<210> 888

<211> 453

<212> DNA

<213> Unknown (H38g738 nucleotide)

<220>

<223> Synthetic construct

<400> 888

cggccgctgt	gcgcgccccg	cctgctggac	cacttcatct	gtgagctgcc	ggcgttgctc	60
aagctggcct	gcggaggcga	cggagacact	accgagaacc	agatgttcgc	cgcccgctg	120
gtcatcctgc	tgccgggggt	tgccgtcatc	ctggcctcct	acggtgccgt	ggcccgagct	180
gtctgttgca	tgcggttcaa	cggaggccgg	aggaggccgg	tgggcacgtg	tgggtcccac	240
ctgacagccg	ctcgctgtgt	ctacggctcg	gccatctaca	cctacctgca	gcccgcgcag	300
cgctacaacc	aggcacgggg	caagtctgta	tcgctcttct	acaccgtggg	cacacctgct	360
cttaaccgcg	tcctctacac	cctcaggaat	aagaaaatga	aaggggcacc	gaggaggctg	420
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<210> 889

<211> 1014

<212> DNA

<213> Unknown (H38g739 nucleotide)

<220>

<223> Synthetic construct

<400> 889

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ctgttcatca	tcactctgac	gtacctggac	tcctcatctc	atactccctt	gtatttcttc	180
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gtcagtctct	gggggtgtgga	aaagaccatt	tcttatgctg	gttgcatggg	tcaactttac	300
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tatgcagctg	tgtgtagacc	tttgatttac	actgtcctca	tgactctctg	tttctgccac	420
ttgttggctg	tggcttcttg	ggtaagtggg	tttacaaccc	cagcacttca	ttctccttc	480

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accttctggg tacctctgtg tggacaccgc caaatagatc actttttctg tgaagttccg      540
gcacttttat gattatcatt tgtcaatacc cgtgaaaata aactgaccct catgatcaca      600
agctccatth ttgttctgct acttctcacc ctcattttca ctcctatgg tgctattgcc      660
caggctgtac tgaggatgca gtcaaccact gggcttcaga aagtatttgg aacatgtgga      720
gctcatcata tggttgtatc tctctttttc attccggcca tgtgcatgta tctccagcca      780
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cctagtctta accctctaata ctacaccctc agaaacaaag atgtaagagg ggtagtgaag      900
agactaaggg ggtgggagtg agcctgtgtt tgtgtgatat taacaatata atggagtctt      960
tcctcacaat gattcatcca tctgttcatt tatcaacatc tctttttatc actc      1014

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<210> 890

<211> 656

<212> DNA

<213> Unknown (H38g740 nucleotide)

<220>

<223> Synthetic construct

<400> 890

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ttgcctgaca tcggttttcac ctccaccacg gtccccaaga tgattgtgga catccaatct      60
cacagcagag tcatctccta tgcaggctgc ctgactcaga tgtctctctt tgccattttt      120
ggaggcatgg aagacagaca tactcctgag tgtgatggcc tatgaccagt ttgtagccaa      180
atgtcaccct ctatatcatt cagccatcat gaacccgtgt tctgtggctt tctacttttg      240
ttgtcttttt tttttccctc agtcttttag atgccagct gtacaatttg attgccttac      300
aaatgacctg cttcaaggat gtggaaattc ctaatttctt ctgtgacct tctcaactcc      360
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tatttggttt tcttcccatc tcggggacac ttttctctta cgataaaaatt gtttctcca      480
ttctgagggt ttcacgtgca ggtgggaggt ataaagccct ctccacctgt gggctcaccg      540
tgtcagttgt ttgctgagtt tatggaacag gcgttgagg gtacctcagt tcggatgtgt      600
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```

<210> 891

<211> 971

<212> DNA

<213> Unknown (H38g741 nucleotide)

<220>

<223> Synthetic construct

<400> 891

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atgattataa tttgcaatga cagccacagt gatttcatcc ttctgggctt ctctaacaag      60
ccacatttgg agaagatact ttttggatca tttttatttt ttattttttg actcttgcag      120
gaaatatggg catagtctct gtgtccttga aggatccaaa actccacatc cctatgtatt      180
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tggtgattaa cttctggggc ccagaaaaga ccatcagcta cattggctgt gccattcaac      300
tctatgtttt tttgtggctt gggggccacg aatatgtcct tcttgttgtc atggctgtgg      360
attgttatgt agcagtgtgt catccactgc aaaataccat gatcatgcac ccaaaacttt      420
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tcgccagtgt tgtcctcctg gtgatgccct tgatcattat ctttctctct tctgggtgta      660
ttgctaaggc tgttgtaga attaatgcaa ctgcaggaca gaagaaagca tttggcacct      720
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taacccaac tcttaatccc ctcatctaca ctctaaggaa caaggaggta aaggagcac      900
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ttacctttgc t

```

<210> 892

<211> 651

<212> DNA

<213> Unknown (H38g742 nucleotide)

<220>

<223> Synthetic construct

<400> 892

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tatgtataga	tgacatgctc	ctgactgtga	tggcctataa	ctgatttggtg	gccatctgtc	180
accccttgca	ctaccacgtc	atcatgaatc	ctcacctctg	tgtcttctta	gttttggtgt	240
cctttttcct	tagcctgttg	gattcccagc	tgcacagctg	gattgtgtta	cacaaatcac	300
cttcttcaag	aatgtggaaa	tctataattt	ttttctgtg	acccatctca	acttctcaac	360
cttgctgtt	ctgacagcat	catcaataac	atattatgta	ttttagatat	ccctatat	420
ggttttcttc	ccatttcagg	gattcctttg	tcttactata	aaattgtctc	ctccattcca	480
agaattccat	cgtcagatgg	gaagtataaa	gccttctcca	cctgtggctc	tcacctggca	540
gttggttgc	tattttatgg	aacagggctt	gtagggtacc	tcagttcagc	tgtgttacca	600
tccccagga	agagtatggt	ggcttcagtg	atgtacactg	tggtcacccc	c	651

<210> 893

<211> 373

<212> DNA

<213> Unknown (H38g743 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(373)

<223> n = A,T,C or G

<400> 893

ttcctccttt	aggccaactt	acagcgcaga	ggagcgcttt	ctcctgctgg	gtttctccga	60
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gacgggcaat	tcgggcgctg	gtgctgcttg	gcnngnngg	acccacgcct	gcanaacnac	180
gatgtatgna	ctacttcctc	tgccacctgg	ccttggtaga	cgcgggcttc	actactagcg	240
tggtgcccgc	gctgctggcc	aacctgcgcg	gaccagcgct	gctntgncgc	gcagccactg	300
cacggcccga	gctgtgcgca	tcgctggctc	tgggttcggc	cgaatgcgct	ctctggcggt	360
gatggctctg	gan					373

<210> 894

<211> 648

<212> DNA

<213> Unknown (H38g744 nucleotide)

<220>

<223> Synthetic construct

<400> 894

atattagaaa	tttcgttcac	aaccgtcagt	ataccaagt	ttctgggtaa	cattatttca	60
ggagataaaa	ccatttcctt	taataattgc	atagttcagt	tatttttctt	cattctcttg	120
ggagtcacag	agttttacct	tctggctgcc	atgtcctatg	accgctatgt	ggccatctgc	180
aagcctctgc	attacttgag	tatcatgaat	cgaagagtct	gcacactgct	tgtttttact	240
tcttggtgtg	tttcattctt	aatcatattc	ccagcactca	tgttgctttt	aaagcttgat	300
tactgtaggt	ctaatttat	tgaccatttt	acctgtgatt	attttccact	gctgcaactt	360
gcttgttcag	acacaaaatt	cttagagggt	atgggatttt	cttggtgtgc	gtttactcta	420
atgttcactt	tggcattaat	atttctgtcc	tacatataca	ttatcagaac	aattttgaga	480
attccttcta	ctagtcagag	gacaaaggcc	ttttccacat	gttcttccca	catgggtggt	540
atctccatct	cttatggcag	ctgcattttt	atgtacatta	aaccctcagc	aaaagataga	600
gtgtccttga	gcaagggagt	ggcaatacta	aacacctcag	tagcccc		648

<210> 895

<211> 659

<212> DNA

<213> Unknown (H38g745 nucleotide)

<220>

<223> Synthetic construct

<400> 895

tttcttgaca	tcggtttcac	ctccaccaca	gtccccaaga	tgattgtgga	catccagtct	60
cacagcagag	tcattctccta	tgcaggctgc	ctgactcaga	tgtctctctt	tgccattttt	120
ggaggcatgg	aagagagaca	tgctcctgag	tgtgatggcc	tatgaccggg	ttgtagccat	180
ctgtcaccct	ctatatcgct	cagccatctt	gaaccctgtg	ttctgtggct	tcctagattt	240
gttgcctttt	ttttttttcc	ctcagtcttt	tagactccca	gctgcacaac	ttgattgcct	300
tacaaatgac	ctgcttcaag	gatgtggaaa	ttcctaattt	cttctgtgac	ccttctcaac	360
tccccatct	tgcatgttgt	gacaccttca	ccaataacat	aatcatgtat	ttccctgctg	420
ccatatttgg	ttttcttcag	atctcgggga	ccctttttct	ttactataaa	attgtttcct	480
ccattctgag	ggtttcatca	tcagggtggga	actataaagc	cttctccacc	tgtgggtctc	540
acctgtcagt	tgtttgctga	ttttatggaa	caggcggttg	agggtaccct	agttcagatg	600
tgtcatcttc	cctgagaaaag	gctgcagtg	cctcagtgat	gtacatgggtg	gtcacaccc	659

<210> 896

<211> 804

<212> DNA

<213> Unknown (H38g746 nucleotide)

<220>

<223> Synthetic construct

<400> 896

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gtcctctcgt	ttcttgatat	ttgttactct	tctgtgggtca	cacctaaagt	cttgggtcaac	120
ttcctgggtc	ctgacaagtc	catctctttt	gagggtctgtg	tggtccagct	cgccttcttt	180
gtagtgcatt	tgacagctga	gagcttccctg	ctggcctcca	tggtccatga	ccgcttccca	240
gccatctgtc	aacccctcca	ttatggttct	atcatgacca	gggggacctg	tctccagctg	300
gtagctgtgt	cctatgcatt	tggtggagcc	aactccgcta	tccagactgg	aaatgtcttt	360
gccctgcctt	tctgtgggce	caaccagcta	acacactact	actgtgacat	accacccctt	420
ctccacctgg	cttgtgccaa	cacagccaca	gcaagagtgg	tcctctatgt	cttttctgct	480
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tctactaaca	ataccaatgg	ccaagtagtg	tccgtctctt	acaccatcat	aattcccatg	720
ctcaatccct	tcattctatag	cctccgcaac	aaggagggtga	agggcgctct	gcagaggaag	780
cttcagggtca	acattctttcc	cggc				804

<210> 897

<211> 949

<212> DNA

<213> Unknown (H38g747 nucleotide)

<220>

<223> Synthetic construct

<400> 897

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ctagaggatc	aacagtgtgt	ctttgcaactg	tttctgtcca	tgtacctggg	caccgttctg	120
gggaacctgc	tcattcatcct	ggccatcagc	tctgactccc	acctccacac	ccccaggtac	180
ttcttctctt	ccaatctgtc	cctggctgac	atcggttttca	cctccaccgc	agtccccaag	240
atgctgggtga	acatccagggt	gcagagcaat	gccatcagct	atgcagactg	catcgcccag	300
atgtatgttt	ttcatgggtt	ttggaggcat	ggacacattt	ctcctcaccg	tgatggccta	360
tgaccgggtat	gtggccatct	gtcacccctt	gtactactgt	gtcaccagga	acctctgcct	420
ctgtggcctg	ctgggttcttg	tgtcctgggt	cctcagcttg	tcatactccc	tgatccagag	480

tctgttggtg	ctgcggggtgt	ccttctgcac	cagttgagtc	attcagcact	tttactgtga	540
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cgtgggtggcc	ggccttctgg	actttgtgccc	cttctcaggg	atccttttct	cctacaccca	660
aattgtctcc	tacatcctga	gaatctcate	cacagatggg	aaacacaaag	ccttttctac	720
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ggtcaccccc	atgctgaacc	ccttcactta	ttgcttgctg	aacagggaca	tcaagaggac	900
cctagaaaca	ctgcttgagg	gaatgctgta	tgctcaatga	cggggacat		949

<210> 898

<211> 927

<212> DNA

<213> Unknown (H38g748 nucleotide)

<220>

<223> Synthetic construct

<400> 898

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ctacagatcc	ccctctttat	cttggtcacc	ttcatctacc	tcctcactct	gtgtgggaac	120
ctggggatga	tgttgctgat	cctgatggac	tcttgctctc	acacccccat	gtactttttc	180
ctcagtaacc	tgtctctggt	ggactttgga	tactcctcag	ctgtcactcc	caagggtcatg	240
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atcaccatct	tgaagatgca	ttcagctaa	ggacacccaaa	aagcattgtc	cacctgtgccc	720
tctcattcca	ctgcagtctc	cgtcttctat	gggacagtaa	tcttcatcta	cttgcagccc	780
agctccagcc	actccatgga	cacagacaaa	atggcatctg	tgttctatgc	tatgatcatc	840
cccattgctga	accctgtggt	ctacagcctg	aggaacagag	aagtcagaaa	tgcattcaag	900
aaagtgttga	gaaggcaaaa	atttctta				927

<210> 899

<211> 938

<212> DNA

<213> Unknown (H38g749 nucleotide)

<220>

<223> Synthetic construct

<400> 899

atgcacacca	tgggtggagaa	ccacacccaa	gtcacctggt	tccgcctgct	gggacttaca	60
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gttatgggca	acctgggaat	gatcactctg	atccatgcag	acccacagct	ccacaccccc	180
atgtattttct	tcctgagcgt	cctatccttc	atagactcct	cgtttttccac	agtggacacc	240
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ctgtgggtcat	cgcaggctg	aacctctga	tctacagcct	gaggaataaa	gatgtaaaat	900
atgctttgaa	gaggagatgc	ctgtgcaagc	tgtcttca			938

<210> 900
 <211> 942
 <212> DNA
 <213> Unknown (H38g750 nucleotide)

<220>
 <223> Synthetic construct

<400> 900
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 ctgcagggtc cctcttttat aacgttcccc ttcatctata ttatcactct ggttggaâac 120
 ctgggaatta ttgtattgat attctgggat tcctgtctcc acaatcccat gtactttttt 180
 ctcaagtaact tgtctctagt ggacttttgc tactcttcag ctgtcactcc catcgatcatg 240
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 gtgagcttca atatctttat agctctcctg gttatcttga tctctacac attcattttt 660
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 tctcatttca ttgcagtcgg catcttctat gggactatta tcttcattga cttacaaccc 780
 agctccagtc actccatgga cacagacaaa atggcacctg tgttctatac aatgggtcatc 840
 cccatgctga accctctggt ctatagtctg aggaacaagg aagtgaagag tgcattcaag 900
 aaagtgtgtg agaaggcaaa attgtctgta ggtgggtcag tt 942

<210> 901
 <211> 936
 <212> DNA
 <213> Unknown (H38g751 nucleotide)

<220>
 <223> Synthetic construct

<400> 901
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 caactacata tctggctgtc catccctctc tgcattcatgt acatcgctgc cctggaaggc 120
 aatggcatcc taatttgtgt catcctctcc caggcaatcc tgcattgagcc catgtacata 180
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 aagatcgta ctgccaccct gagccgcagc ttcatcatta tgtttccatc catctttctc 480
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 caagcagtc tccgcctcct ttctcaagat gcccgctcca aggcctgag tacctgtgga 720
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 aggtttgggt ggagaagcat cccatgctat gtccatattc tcctggccag cctctacgtt 840
 gtcattctc ctatgctcaa tcccgttatt tatggagtga ggactaagcc aatactggaa 900
 ggggctaagc agatgttttc aaatcttgcc aaagga 936

<210> 902
 <211> 994
 <212> DNA
 <213> Unknown (H38g752 nucleotide)

<220>
 <223> Synthetic construct

<400> 902

agcattcttt	tcctttat	ctcattgctg	caggcatcct	ctgattttct	aataacattg	60
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ctacaagtc	ccctccttat	catgttcact	ctcatatacc	ttgtcaatgt	ggttggaaac	180
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ttttttgcag	cctttgccac	tgtggaaaat	ttcctcttgg	cctcaatggc	ctatgaccgc	420
tatgatgcag	tgtgcaaacc	cctacattac	accaccacca	tgacaacaag	tgtgtgtgca	480
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agtcattggc	ctgtcttgct	gtgatagaca	tgtgaatgag	ctagtcttca	tttatgtagc	660
cagtttcaat	atcttttctg	ccatcctagt	tatcttgatc	tcctacctat	tcataatttat	720
caccatccta	aagatgcact	cagcttcagg	ataccagaag	gctttgtcca	cctgtgcctc	780
ccacctcact	gcagtcac	tcttctatgg	gactattatc	ttcatgtact	tacagcccag	840
ctctgggtcac	tccatggaca	cagacaaact	ggcatctgtg	ttctatacta	tgatcatccc	900
catgctgaac	cccctggctc	atagcctgag	gaacaacgaa	gtgaagagcg	cattcaagaa	960
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<210> 903

<211> 954

<212> DNA

<213> Unknown (H38g753 nucleotide)

<220>

<223> Synthetic construct

<400> 903

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gcactgggtg	gaaatgctgc	cctcactcctg	gtcattgcc	tggacaatgc	tcttcatgca	180
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gtgcccaga	tgctggccat	tttgtggctc	catgctgggt	agatttctct	tggtggatgc	300
ctggcccaga	tgttttgtgt	ccattctatc	tatgctctgg	agtcctcgat	tctacttgcc	360
atggcctttg	ataggtatgt	ggctatctgt	aaccatttaa	ggtacacaac	cattctcaac	420
catgctgtca	taggcagaat	tggtttgtgt	gggtatttcc	gtagtgtggc	tattgtctcc	480
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tatgggctaa	ctgtggctct	gctggccatg	ggactggatt	ccattctcat	tgccatttcc	660
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tcttctctca	cccaccgctt	tggtcaccac	gaagtcccca	agcatgtgca	catctttctg	840
gctaattctc	atgtgctgg	gcctcctgta	ctcaatccta	ttctctatgg	agctagaacc	900
aaggagattc	ggagtcgact	tctaaaactg	cttcacctgg	ggaagacttc	aata	954

<210> 904

<211> 989

<212> DNA

<213> Unknown (H38g754 nucleotide)

<220>

<223> Synthetic construct

<400> 904

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cttgggaatc	tgctcatcat	cctggccaca	atctcagact	cccacctcca	caccccatgt	180
acttcttctc	ctccaacctg	tcctttgcgg	acatctgttt	catctctact	acaatcccaa	240
agatgctcgt	aaacatccag	acacagagca	gagtcatcac	ttatgcaggc	tgcatcacc	300
agatgtgctt	ttttgtactc	ttagaagcac	tggacagctt	actcctgacc	gtgatggcct	360
atgaccagtt	tgtggccatc	tgtaaccccc	tgcactacat	ggatcatcatg	agccctgggt	420
tctgtggact	gctggttctg	gcatacctgga	tcatacatgag	ccctgggtc	tgtggactgc	480

tggttctggc	atcctggatt	atcagtgatc	tggattcctc	attacatagc	ttgatgggtgc	540
tgctactgcc	cttctgcaca	gatttccaaa	ttccacattt	tgtctatgaa	cttaatcagg	600
tcattccgct	tgcgggttct	gatacctttc	ttaatgacat	ggcgatgtat	tttgtagtag	660
ggccactggg	tggagttccc	ctcgtctgga	tctgtacttt	gtactgtaag	atagttttct	720
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tgctgaaccc	cttcactctgc	agtctgagga	ataaagacat	aaagagagct	ctgaatcaat	960
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<210> 905

<211> 932

<212> DNA

<213> Unknown (H38g755 nucleotide)

<220>

<223> Synthetic construct

<400> 905

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gccccagaac	tacaggtcca	cctctttgtc	ttatttaact	tcattctacct	cttcactctg	120
agtgggaacc	tggggatgat	gctgctgac	ctgctggact	ctcgtctcca	cacttccatg	180
tactttttcc	tcagtaacct	gtctctgggtg	gacttttgtc	actcagaaac	tgctactcca	240
aagatgatgg	ctgggttgct	gatagctcac	aaggctcatc	cctacaatgt	atgtgctgct	300
cagatgttct	tttttgcagt	ctttgctact	gtggaaagtt	acttcttgac	ttcagtggcc	360
tatgattgct	acagagtaat	gtgtaaacc	ctacattaca	ccaccaccat	gacaacaaat	420
gtgtgtgctt	ctctggccat	acatgcatgt	cttaggttta	ctgactgctg	ctgttgacat	480
tggagacatt	ttatgtccaa	tgagatccat	cactttttct	gtgatattct	ggcagtcatt	540
actctgactt	gctctaataa	acatattaat	gagttgatcc	ttgttccctac	ttcaagctat	600
atttttttacc	ctcctagtta	tcttgatttc	ctgcttggtt	gtatttgtat	ttgtcaccat	660
tttaaagatg	ctctctttta	gtatacaaga	aggttttatc	tacctatggt	tctcacctca	720
ctgcagttcc	tttattttat	gagactgtcc	tcattcacata	tgtgcagcca	agttctatca	780
tttcatgaac	acagaaaaaa	ttgtatctgt	gtttcatatt	atggttatcc	ccatgctaatt	840
ccctgtgggt	tatagcctga	gaaacaacga	ggccaagagt	gcattcaaga	ctgtttgttg	900
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<210> 906

<211> 945

<212> DNA

<213> Unknown (H38g756 nucleotide)

<220>

<223> Synthetic construct

<400> 906

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gagatgaagg	gtctggagca	ctggctggct	gcccttctgc	tgctgctttg	tgctatttcc	120
ttcctgggca	acatccctcat	cctctttatc	ataaagggaag	agcagagctt	gcaccagcca	180
atgtactact	tectgtctct	tttttctggt	aatgacctgg	gtgtgtcctt	ttctacattg	240
cccactgtac	tggctgctgt	gtgttttcat	gccccagaga	caacttttga	tgctgtcctg	300
gcccagacgt	tcttcatcca	cttttctctc	tggacagagt	ttggcatcct	actggccatg	360
agttttgacc	actatgtggc	catctgtaac	ccgctgcgct	atgccacagt	gctcactgat	420
gtccgtgtgg	cccacaatgg	catatccatt	gtcatccgca	gcttctgcat	ggtattccca	480
cttcccttcc	tectgaagag	actgccttcc	tgtaaggcca	gtgtgggtact	ggcccatcc	540
tactgtctgc	atgcagacct	gattcggctg	ccctgtggag	acactaccat	caacagcatg	600
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tatgtgtctca	ttctacattc	tgtgtgccca	ttgcctccag	gggtgagagg	cttaagacac	720
tcgaacacat	gtgtgtcaca	tatctatgca	gtgtgtatct	tctatgtgcc	tatgggtagt	780
gtgtccatgg	ttcatcgatt	tgggagggcat	gctcctgaaat	atgtgcacaa	gttcatgtct	840
ctttgtacct	gccaatgtct	taccgcaatt	atctattcca	tcaagactaa	ggagattcgc	900
aggagactac	acaagatggt	attgggagct	aagttctgat	cgaag		945

<210> 907
 <211> 989
 <212> DNA
 <213> Unknown (H38g757 nucleotide)

<220>
 <223> Synthetic construct

<400> 907
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 cccagactgc aacgatttcg atttctcttt ggagtgttct tatccatgta cctcatcatt 120
 gtatttggaa acttgcttat catcctgggt atcattttat gctccacct ccacacctcc 180
 atgtacttct ttctctccaa cctgtccttt gtagacatct gttttgcctc caccagggtc 240
 ccaaagatgc tggatgaatat ccaggcacag agcaaagtca tcacctctgc aggetgcatc 300
 acccagatgt actttttcat acattttgta ggattggaca gcttcctcct gactgtgatg 360
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 caactctgtg gattgcttgt tctggatcc tggatcacia gtgtcttgca ttccttatta 480
 catagcttaa tggatgtgca gttgtcctta tgcagagagt tggaaatccc ccactttttc 540
 tgtgaactta atcagggtcat ccaccttgcc tgttctgaca cctttcttaa tgacatgggtg 600
 atgtatctgg cagctgtgct gctgggtggg gggatgtctc gctgggatcc tttactctta 660
 ctctaagaca gtttctccca tatgtgcaat ctcacagct caaggggaagt ataaggcatt 720
 ttccacctgt ccactctacc tctcagttgt ctccttgttt tactgtacaa gcctaggagt 780
 gtaccttagc tgggtgcat cccacaactc acactcaggt gcaatagcct cagtgatgta 840
 cactgtgtgc acccccatgc tgaaccctt catctacagc ctgaggaata aggacataaa 900
 gagggctctg aagaattctt tgggagggaa actagaaaag ggccagttgt cctagggctg 960
 aagctatata catgattgca aggtcaaaa

<210> 908
 <211> 960
 <212> DNA
 <213> Unknown (H38g758 nucleotide)

<220>
 <223> Synthetic construct

<400> 908
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 ggaaacctgc tcatcatcct gaccatcagt tcagactccc acctccacac ccccatgtac 180
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 atattttttt tcattgcatt tggatgcctg gacaatttgc tcctgacctat gacggcctat 360
 gaccgcttgc tggccatctg ttacccctg cactacacgg tcatcatgaa ccccggtc 420
 tgtggactgc tggttctggg gtccctgtgc atcagtgtca tgggttcctt gcttgagacc 480
 ttgaccattt tgaggctgtc ctccctgcaca aatatggaaa ttccgcactt tttttgtgat 540
 ccttcgaag tcctgaagct ggccgtgtct gacaccttca tcaataacat cgtgatgtgt 600
 tttgtgacca ttgtcctggg tgtttttcct ctctgtggaa tcctattctc ttattctcag 660
 attttctcct cgtcctaag agtatcatct gccagaggcc agcacaagc ctttaccacc 720
 tgtgggtccc acctctcagt ggtcagcttg ttctatggca ctggccttgg ggtctatctc 780
 agttctgcag ttacaccacc ttctaggaca agtctggcag cctcgggtgat gcacaccatg 840
 gtcaccccca tgcgaaccc cttcatctac agcctgagga acaaggacat gaaggggtca 900
 ctggggagac tcctcctcag ggcaacgtct ctcaaagagg ggaccattgc taagctctca 960

<210> 909
 <211> 981
 <212> DNA
 <213> Unknown (H38g759 nucleotide)

<220>
 <223> Synthetic construct

<400> 909

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gatccagcac	tgcagctggg	cgctactggg	ctgtgcctgt	gtgcctgggc	acgggtgctgt	120
ggaacctgct	cagcatcctg	gccgtcagcc	ctgactccca	cctccacacc	cccatgcact	180
tcttcctctg	caacctgtcc	ttgcctgaca	tcgggtttcac	ctccaccacg	gtccccaaga	240
tgatcgtgga	catccaatct	cacagcagag	tcatctccta	tgcaggctgc	ctgactcaga	300
tgtctctctc	tgccattttt	ggaggcatgg	aagagagaca	tgctcctgag	tgtgatggcc	360
tatgaccagt	ttgtagccat	ctgtcaccct	ctgtatcatt	cagccatcat	gaaccctgtg	420
ttctgtggct	tcctgggtttt	gttgtctttt	tttttctcag	tcttttagac	tccagctgc	480
aaaacttgat	cgccttaca	atcacctgct	tcaaggatgt	ggaaattcct	aattttctct	540
gtgacccttc	tcaactcccc	catcttgcat	gttgtgacac	cttcaccaat	aacattatca	600
tgtatttccc	tgctgccata	tttgggtttc	ttcccatctc	ggggaccctt	ttctcttact	660
ataaaaattgt	ttcctccatt	ctgagggttt	catcatcagg	tgggagctat	aaagccttcg	720
ccacctgtgg	atctcacctg	tcagttgttt	gctgatttta	tggaaacaggc	gttggagggt	780
acctcagttc	agatgtgtcg	tctccctga	gaaagcgtgc	agtggcctca	gtgatgtaca	840
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gtgtcctgtg	gcagccgtgc	agccgcacgg	cagcacagtc	tcattctcaat	atcttatctg	960
ttccattcct	tttgaggat	g				981

<210> 910

<211> 628

<212> DNA

<213> Unknown (H38g760 nucleotide)

<220>

<223> Synthetic construct

<400> 910

tcagtgaagt	acttgaatga	aagtttccca	gaggatttca	ttctcatggg	ctttgtcaaa	60
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ttgggaaata	gtgctattat	tctggctctc	caactagatt	cccaacttca	tagtcctatg	180
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caaattgctgt	tcaatttagg	gggcccaca	agaacatcac	ttaaattaggc	tgtatggccc	300
aggcctatgt	atttcaactg	ctagcctgta	ttgaatgtgt	ccttcttggc	atcgtggcct	360
tagactgcta	tgtggctgtc	tgtaaagctc	caaggtagac	tataatcata	gaccataagg	420
tctgcctgca	cctgtccagc	actgcttggc	taattggctc	ggccaattca	ctgctgcagt	480
caacaatcac	aattcagttg	cccctgtaga	ggtgtatagc	tcagatcttc	ctttagttag	540
agtctgtcac	ctaacagtct	ctaactgtaa	caacctttga	gatctgctac	agcattctat	600
ctgaggccaa	cttcatgctg	gggagctc				628

<210> 911

<211> 945

<212> DNA

<213> Unknown (H38g761 nucleotide)

<220>

<223> Synthetic construct

<400> 911

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ccagagcatc	agaccctcct	cttcacaatg	ttcctctcca	catacctggg	caccatcatt	120
ggaaatgccc	tcattatcct	ggccatcacc	acggactctc	acctccacac	acccatgtac	180
ttctttctct	tcaacctctc	actcgttgac	acctatttat	cctccaccac	cgtccccaag	240
atgctagcga	acatccaggc	tcagagcaga	gccatcccct	ttgtgggctg	cctcaccag	300
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gaccgcttcg	tggccattgt	ccacccacag	cgttacttgg	ttctcatgtg	ctccctgtc	420
tgtgggctgc	tgtggggagc	atcatggatg	atcaccacac	tccagtctct	catacacacc	480
tgcctcatgg	ctcaactgac	cttctgcgcc	ggctctgaaa	tctccactt	cttctgtgac	540
ctcatgcccc	tgtgaagct	ctccggctca	gacacgcaca	ccaacgagct	ggtgatcttt	600
gcttttggca	ttgtcgtggg	caccagccca	ttctcctgca	tccttctctc	gtacatccgc	660

atcttcttga	cagtccttta	gatcccttct	actcggggca	agtggaaagc	cttctccacc	720
tgtggcttac	acctcaactgt	ggtgtcactg	tcctatggga	ccatctttgc	tgtgtactta	780
cagccacat	ccccagctc	ctcccagaag	gacaaggcag	ccgcccta	gtgtgggggtg	840
ttcatcccca	tgtcaaccc	ctttatctac	agcatagga	acaaggatat	gaaggcagcc	900
ctggggaagc	tcacggcaa	agtggcgcgc	ccctgtccta	ggcca		945

<210> 912

<211> 949

<212> DNA

<213> Unknown (H38g762 nucleotide)

<220>

<223> Synthetic construct

<400> 912

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acagacgccc	acccgctgct	gttctctgctc	tgccttggca	tctatctgct	caacgccctg	120
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tacttcttgg	gtcacctgag	ctctgtggac	gtctgtctta	ccaccgtcac	ggtccccagg	240
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cgcctgctgc	tgcctactca	gcccgtctacg	accgcctggc	cagcggtggtc	tacgctgtca	840
tcacgcccag	cttgaaccct	ttcatcaaca	gccttcgcaa	caaagagggtc	aagggcgccc	900
tgaaaagggg	gctcagatgg	agggctgcac	cccaagaggc	gtgagggca		949

<210> 913

<211> 936

<212> DNA

<213> Unknown (H38g763 nucleotide)

<220>

<223> Synthetic construct

<400> 913

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ggaaacatcc	tcattgtgtt	ttctgtgacc	actgaccctc	acttacactc	ccccatgtac	180
tttctactgg	ccagtctctc	cttcattgac	ttaggagcct	gctctgtcac	ttctcccaag	240
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atcttcttca	tccacgtcat	tggtggtgtg	gagatggtgc	tgctcatagc	catggccttt	360
gacagatatg	tggccctatg	taagccccctc	cactatctga	ccattatgag	cccaagaatg	420
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atcctgttta	ctgtttggaa	acattcctca	ggtggttcat	ccaaggccct	ttccactctt	720
tcagctcaca	gcacagtggg	ccttttgttc	tttgggtccac	ccatgtttgt	gtatacacgg	780
ccacacccta	attcacagat	ggacaagttt	ctggctatatt	ttgatgcagt	tctcactcct	840
tttctgaatc	cagttgtcta	tacattcagg	aataaggaga	tgaaggcagc	aataaagaga	900
gtatgcaaac	agctagtgtat	ttacaagagg	atctca			936

<210> 914

<211> 954

<212> DNA

<213> Unknown (H38g764 nucleotide)

<220>

<223> Synthetic construct

<400> 914

atgtggcaga	agaatcagac	ctctctggca	gacttcatcc	ttgaggggct	cttcgatgac	60
tccettaccc	accttttcc	tttctccttg	accatgggtg	tcttccctat	tgcggtgagt	120
ggcaacaccc	tcaccattct	cctcatctgc	attgatcccc	agcttcatac	accaatgtat	180
ttcctgctca	gccagctctc	cctcatggat	ctgatgcatg	tctccacaac	catcctgaag	240
atggctacca	actacctatc	tggcaagaaa	tctatctcct	ttgtgggctg	tgcaatccag	300
cacttctct	atgtgtgtct	aggtgggtgct	gaatgttttc	tcttagctgt	catgtcctat	360
gaccgctatg	ttgccatctg	tcatccactg	cgctatgctg	tgctcatgaa	caagaagggtg	420
ggactgatga	tggctgtcat	gtcatgggtg	ggggcatccg	tgaactccct	aattcacatg	480
gcgatcttga	tgcacttccc	tttctgtggg	cctcggaaag	tctaccactt	ctactgtgag	540
ttcccagctg	ttgtgaagt	ggtatgtggc	gacatcactg	tgtatgagac	cacagtgtac	600
atcagcagca	ttctcctcct	cctccccatc	ttcctgattt	ctacatccta	tgtcttcac	660
cttcaaagt	tcattcagat	gcgctcatct	gggagcaaga	gaaatgcctt	tgccacttgt	720
ggctcccacc	tcacgggtgt	ttctcttttg	tttgggtgct	gcactttctc	ctacatgaga	780
cccaggtccc	agtgcactct	attgcagaac	aaagttgggt	ctgtgttcta	cagcatcatt	840
acgcccacat	tgaattctct	gatttatact	ctccggaata	aagatgtagc	taaggctctg	900
agaagagtgc	tgaggagaga	tgttatcacc	cagtgcattc	aacgactgca	attg	954

<210> 915

<211> 309

<212> DNA

<213> Unknown (H38g765 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(309)

<223> n = A,T,C or G

<400> 915

acgctgtgcg	ccacagcctn	gctgggccac	ttcatctgtg	agctgccggc	gttgcctcaag	60
ctggcccgcg	gagcatcgga	gacactaccg	agaaccagat	gttcgcccgc	cgcgtgggtca	120
tctgtgtgct	gccgtttgcc	gtcatcctgg	cctcctacgg	tgccgtggcc	gagctgtctg	180
ttgtatgcgg	ttcagcggag	gccggagagg	gcggtgggca	cggtgtgggtc	ccactgacag	240
ccgtctgcct	gttctacggc	tcggcatcta	cacctacctg	cagcccgcgc	agctaacaac	300
caggcacgg						309

<210> 916

<211> 313

<212> DNA

<213> Unknown (H38g766 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(313)

<223> n = A,T,C or G

<400> 916

attcatgccc	tctcagccat	tgaatccacc	atcctgctgg	ccatggcctt	tnaccgttat	60
gtggccatct	gccaccact	gcgccatgct	gcagtgtctca	acaatacagt	aacagcccag	120
attggcatcg	tggctgtggt	cgcgggatac	ctcttttttt	tcccactgcc	tctgtgtgatc	180
aagcggctgg	ccttctgcca	ctccaatgtc	ctctgcact	cctattgtgt	ccaccaggat	240
gtaatgaagt	tggcctatgc	aagacanttt	gcccgaatgtg	gtatatggtc	ttaactgncc	300

attttggttg gtc

313

<210> 917

<211> 960

<212> DNA

<213> Unknown (H38g767 nucleotide)

<220>

<223> Synthetic construct

<400> 917

atggaaacag	gaaatcaaac	acatgcccaa	gaattttctcc	tcctgggatt	ttcagcaacg	60
tcagagattc	agttcattct	ctttgggctg	ttcctctcca	tgtacctagt	cactttcacc	120
gggaacctgc	tcatcatcct	ggccatatgc	tcagactccc	acctccacac	ccccatgtac	180
ttcttctct	ccaacctgtc	ttttgctgac	ctctgtttta	cctccacgac	tgtcccaaag	240
atgttactga	atatactgac	acagaacaaa	ttcataacat	atgcaggctg	tctcagtcag	300
atTTTTTTTT	tcacttcatt	tggatgcctg	gacaatttac	tcttgaccgt	gatggcctat	360
gaccgcttcg	tggcgcgtcg	tcacccctg	cactatacgg	tcatcatgaa	ccccagctc	420
tgtggactgc	tggttctggg	gtcctgggtc	atcagtgta	tgggttcct	gctcgagacc	480
ttgactgttt	tgaggctgtc	cttctgcacc	aaaatggaaa	ttccacactt	tttttgtgat	540
ctacttgaag	tcctgaagct	cgcctgttct	gacaccttca	ttaataacgt	ggtgatatac	600
tttgcaactg	gcgtcctggg	tgtgatttcc	ttcactggaa	tatttttctc	ttactataaa	660
attgttttct	ctatactgag	gatttcctca	gctgggagaa	agcacaaagc	gttttccacc	720
tgtggttccc	acctctcagt	ggtcaccttg	ttctatggca	cgggcttttg	ggtctatctc	780
agttctgcag	ccacaccatc	ttctaggaca	agtctggtgg	cctcagtgat	gtacaccatg	840
gtcaccccca	tgctgaacct	cttcattctac	agcctgagga	acacggacat	gaagagggcc	900
ctggggagac	tcctcagtag	ggcaacattt	tttaatggtg	acatcactgc	aggactttca	960

<210> 918

<211> 937

<212> DNA

<213> Unknown (H38g768 nucleotide)

<220>

<223> Synthetic construct

<400> 918

atgggggaca	accaatcacg	ggtcacagaa	ttcatcctgg	ttggattcca	gctcagtggtg	60
gagatggaag	tgctcctctt	ctggatcttc	tccctgttat	atctcttcag	cctgctggca	120
aatggcatga	ttttggggct	catctgtctg	gatcccagac	tgcgcacccc	catgtacttc	180
ttcctgtcac	acttggccgt	cattgacata	tactatgctt	ccagcaattt	gctcaacatg	240
ctggaaaacc	tagtgaaaca	caaaaaaac	tatctcgttc	atctcttgca	ttatgcagat	300
ggctttgtat	ttgacttttg	ctgctgcagt	gtgcatgatt	ttgggtggtga	tgtcctatga	360
cagatttgtg	gcgatctgcc	atccccctgca	ttacactgtc	atcatgaact	ggagagtgtg	420
cacagtactg	gctattactt	cctgggcatg	tggattttcc	ctggccctca	taaatcta	480
tctccttcta	aggctgccct	tctgtgggcc	ccaggagggtg	aaccacttct	tcggtgaaat	540
tctgtctgtc	ctcaaaactgg	cctgtgcaga	cacctggatt	aatgaaattt	ttgtctttgc	600
tgggtggtgtg	tttgtcttag	tcggggccct	ttccttgatg	ctgatctcct	acatgcgcac	660
cctcttggcc	atcctgaaga	tccagtcaaa	ggaggggccgc	aaaaaagcct	tttccacctg	720
ctcctcccac	ctctgtgtgg	ttgggcttta	ctttggcatg	gccatggtgg	tttacctggt	780
cccagacaac	agtcaacgac	agaagcagca	gaaaattctc	accctgtttt	acagcctttt	840
caaccatttg	ctgaaccccc	tcatctacag	cctgcggaat	gctcaagtga	agggtgcctt	900
atacagagca	ctgcagaaaa	agaggaccat	gtgaatg			937

<210> 919

<211> 957

<212> DNA

<213> Unknown (H38g769 nucleotide)

<220>

<223> Synthetic construct

<400> 919

atggaaccag	gaaatgatac	acaaatttca	gaattttcttc	ttctgggatt	ttcacaagaa	60
cctggactgc	aacccttctt	ctttgggctg	ttcctgtcca	tgtacctggt	caactgtgtc	120
gggaacctgc	tcatcatcct	ggccacaatc	tcagactccc	acctccacac	ccccatgtac	180
ttcttctctt	ccaacctgtc	ctttgctgac	atctgtgtta	cttccaccac	cattccaaaa	240
atgctgatga	acatccagac	acagaacaaa	gtcatcacct	acatagcctg	cctcatgcag	300
atgtattttt	tcatactctt	tgctggattt	gaaaacttcc	tcctgtccgt	gatggcctat	360
gaccggtttg	tggccatctg	tcaccccctg	cactacatgg	tcattatgaa	ccctcacctc	420
tgtggactgc	tggttctagc	atcctggacc	atgagtgttc	tgtattcctt	gtacaaaaac	480
ttaatggtag	tacggctgtc	cttctgcaca	gccttagaaa	tcctccactt	tttctgtgaa	540
cttaatcagg	tcatccaact	tgcttgttct	gatagctttc	ttaatcacat	ggtgatatat	600
tttacagttg	cgctgctggg	tggaggctcc	ctgactggga	tcctttactc	ttactctaag	660
ataatttctt	ccatacatgc	aatctcatca	gtcaggggga	agtacaaggc	atcttccacc	720
tgtgcatctc	acctctcagt	tgtctcctta	ttttatgggt	caatcctagg	ggtgtacctt	780
agttctgtct	ccaccgcgaa	ctcacactca	agtgaacag	cctcagtgat	gtacactgtg	840
gtcaccccca	tgctgaacct	ctttatctat	agtctgagga	ataaagacat	aaagagggtc	900
ctgggaatac	atctgttgtg	gggaacaatg	aaagggaat	ttttcaagaa	gtgccca	957

<210> 920

<211> 222

<212> DNA

<213> Unknown (H38g770 nucleotide)

<220>

<223> Synthetic construct

<400> 920

ggagacacta	cagagaacca	gatgttcgcc	gcccgcgtgg	tcatectgct	gctgccgtat	60
gacgtcatac	tggcctccta	aggtgccgtg	gcccagagctg	tctgttgcac	gcggttcagc	120
ggaggaccga	ggagggcgct	gggcacgtgt	gggtcccacc	cgacagccgt	ctggctgttc	180
taaggctcgg	gcaataaac	ctatctgcaa	gccgcgcagc	ta		222

<210> 921

<211> 927

<212> DNA

<213> Unknown (H38g771 nucleotide)

<220>

<223> Synthetic construct

<400> 921

atgaaatcat	ggaacaatac	aataatttta	gaattttcttc	tcctgggaat	ttcagaggaa	60
ccagaattgc	aggccttctt	ctttgggctg	ttcctgtcca	tgtacctggt	caactgtgtc	120
gggaacctgc	tcatcatcct	ggccacaatc	tcagactccc	acctccacac	ccccatgtac	180
ttcttctctt	ccaacctgtc	cttcgtaggc	atctgttttg	tctctaccac	tgtcccgaag	240
atgctgggtga	acatccagac	acacaacaaa	gtcatcacct	atgcaggctg	catcacccag	300
atgtgctttt	tcttactctt	tgtaggattg	gataacttcc	ttctgaccgt	gatggcctat	360
gaccggtttg	tggccatctg	tcacccctctg	cactacatgg	tcattatgaa	ccctcaactc	420
tgtggactgc	tggttctggc	atcctggatc	atgagtgttc	tgaattccat	gttacaaagc	480
ttaatgggtg	tggcactgcc	cttttgtaca	cacatggaaa	tccttcattt	tttctgtgaa	540
attaatcagg	tggctccacct	tgcctgttct	gacacctttc	ttaatgacat	agtgtgtgat	600
ttcgcagtag	cgctgctggg	cggtgggtccc	ctcactggga	tcctgtactc	ttactctaag	660
atagtttctt	ccatacgtgc	aatctcatca	gtcaggggga	agtataaggc	atcttccacc	720
tgtgcatctc	acctctcagt	tgtctcctta	ttttatggta	catgcttagg	ggtgtacctt	780
agttctgtct	ccaccacaaa	ttcacacaca	ggtgtgtcag	cctcagtgat	gtacactgtg	840
gtcaccccca	tgctgaacct	cttcatctac	agtctgagga	ataaacacat	aaagggtgct	900
atgaaaacat	tcttcagagg	aaagcaa				927

<210> 922

<211> 246

<212> DNA

<213> Unknown (H38g772 nucleotide)

<220>

<223> Synthetic construct

<400> 922

atgggtcacag agttcctccc actgggattt ctcctggggc caaggattca gatgctcctc	60
cttgggctct tctccctggt ctatgtcttc accccgctgg ggaatgggac catccccggg	120
ctcatctcac tggactccag actccacacc cccatgtact tcttcctctc acacctggcc	180
gtcgtcaaca tcgcctatgc ctgcaacaca gtgccccaga tgctggtgaa cctcctgcat	240
ccagcc	246

<210> 923

<211> 648

<212> DNA

<213> Unknown (H38g773 nucleotide)

<220>

<223> Synthetic construct

<400> 923

ctcatggacc tcaagctcat ctgcaccacc gtacccaaga tggccttcaa ctacctgtct	60
ggcagcaagt ccattttctat ggctggttgt gtcacacaaa ttttcttcta tatatcactg	120
tctggctctg aatgttttct tttggctggt atggcttatg accgctatat tgctatttgc	180
cacctcttaa gatataccaa tctcatgaat cctaaaattt gtggacttat ggctaccttc	240
tcttggtacc tgggctctac agatggaatc attgatgctg tagccacatt ttccttctcc	300
ttttgtgggt ctcgggaaat agcccacttc ttctgtgaat tcccttccct actaatcttc	360
tcatgcaatg acacatcaat atttgaagag gttattttca tctgctgtat agtaatgctt	420
gttttccctg ttgcaatcat cattgcttcc tatgctcgag ttattctggc tgcattcac	480
atgggatctg gagagggtcg ttgcaaagct ttcacgacct gttcctctca cctcatggtg	540
gtgggaatgt actatggagc agctttgttc atgtacatac ggcccacatc tgatcactcc	600
ccaacgcagg acaagatggt gtctgtattc tacaccatcc tcaactccc	648

<210> 924

<211> 916

<212> DNA

<213> Unknown (H38g774 nucleotide)

<220>

<223> Synthetic construct

<400> 924

atgaaaccag ggaatgatac acgaatttca gaattttctc ttctaggact ttcagcagaa	60
ccagaattgc agcccttctt ctttgggctg ttctgtgcca tgtacctggg caccgtgtc	120
gggaacctgc tcatcatcct ggccacaatc tcagactccc acctccacac ccccatgtac	180
ttcttctctt ccaacctgtc ctttgcagat atcagttttg tgtctaccac tgtcccgaag	240
atgctggtga atatccagac gcagagcaga gtcatcacct atgcaggctg catcaccag	300
atgtgctttt tctactatt tgcagtgttg gacagccttc tctagctgtg gatggcctat	360
gatcggtttg tggccatctg tcatcctctg tactacacaa tcatcatgaa cctcagttc	420
tatagactgg attcttagtg tctgaattc tctgttataa agcttaatgg tgttgccact	480
gcccttctat acagacatag caatccccca ctttttctgt gaacttaatc agataatctg	540
cattgcctgt tctgacacct ttcttaatga catcatgata tattgtgcaa ctgtgtgtct	600
gggcgggtgt cccctcactg gaatccttta ctcttactct aagatagttt cctccatag	660
tgcaatctca tcagctcagg ggaagtacaa ggcattttcc acctgtgcat ctcacctctc	720
agttgtctcc ttgttttatg gtacaagcct aggaatgtac cttagtcttg ctgcaaccca	780
caactcacc tcaagtgcac cagcctcagt gatgtacact gtggtcacc ccatgctgaa	840
cccctttatc tacagtctga ggaataaaga cctaaaggat gctctgaaac gcttcttcag	900
aaggaagcaa taaaag	916

<210> 925

<211> 360
 <212> DNA
 <213> Unknown (H38g775 nucleotide)

<220>
 <223> Synthetic construct

<400> 925
 ttttcctct caccctggc ggttggtgac attgcctacg cctgcaacac ggtgccccgg 60
 atgctgggtga acctcctgca tccagccaag cccatctcct ttgcggggccg catgatgcag 120
 acctttctgt tttccacttt tgcgtgcaca gaatgtttcc tctggtggt gaagtccaat 180
 gatttgtaacg tggccatctg ccacccctcc cgatatttgg ccatcatgac ctggagagtc 240
 tgcacacccc tcgcggtgac ttctgggacc actggagtcc ttttatcctt gattcatctt 300
 gtgttacttc tacctttacc cttctgtagg cccagaaaaa tttatcactt tttttgtgaa 360

<210> 926
 <211> 643
 <212> DNA
 <213> Unknown (H38g776 nucleotide)

<220>
 <223> Synthetic construct

<400> 926
 ttgcctgaca tcggtttcac ctccaccacg gtccccaaga tgattgtgga atccaatctc 60
 acagcagagt catctcctat gcaggctgcc tgactcagat gtctctcttt gccatttttg 120
 gaggcagatga agagagacat gctcccgagt gtgatggcct atgaccgggt tgtagccatc 180
 tgtcacccctc tatatcattc agccatcatg aaccggtgtt tctgtggctt cctagttttg 240
 ctgtcttttt tttctttctt tttctcagct gcacaacttg attgccttac aaatgacctg 300
 cttcaagaat gtgggaattc ctaatttcct ctgtgacctc tctcaactcc cccatctcac 360
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 tcttcccatc tcgggggacc tttctcttta ccatgtaatt gtttcctcca ttctgagggt 480
 ttcacatca ggtgggaagt ataaagcctt ctccacctat ggggtctacc tgcagatgt 540
 ttcttgattt tatggaacag gcgttgagg gtacctcagt tcagatgtgt catcttcccc 600
 gagaaagact gcagtggcct cagtgatgta cgcagtgggtc acc 643

<210> 927
 <211> 498
 <212> DNA
 <213> Unknown (H38g777 nucleotide)

<220>
 <223> Synthetic construct

<400> 927
 gtgaaaaatc agacaatggt cacagagttc cttctatttg gatttttctt gagcccaagg 60
 atacacatgc tctcttttgg gctctttctac ctgttctatg tcttcaccct gctgggggaat 120
 gggaccatcc tgggggtcat ttcactggac tccatactcc acaccccat gtacttcttc 180
 ctataacacc tgtccgtcgt caacatcgcc tatgcctgca acacagtgcc ccagatgctg 240
 gtgaacctcc tgcattcagc caagcccat tactttgctg gctgcatgac atataccttt 300
 ctctttttga gatttgacac tactgaatgc ctctgttgg tgctgatgtc ctacgattgg 360
 tacgtggcca tcttgacacc tctccgat atcatcatta tgacctgtaa agtcttcac 420
 atctctgcca tcaatttcat gtacatgtgg ttcctttctg tcttggtcca tgtaagcctc 480
 atactaagac tgcctttt 498

<210> 928
 <211> 276
 <212> DNA
 <213> Unknown (H38g778 nucleotide)

<220>

<223> Synthetic construct

<400> 928

caaattgagct	tgttttgaat	ctttgcctct	ggctgaatgc	aatttggtta	aactcgcaact	60
ggcctataga	cccctgttac	tgccatctgt	gcacccaccc	gttctaccac	attgaccatg	120
tctaagaggc	cattatcttt	ttcttggtag	caggatgcta	ccttggtggg	ttagttaaga	180
tggtcactgt	gacaacttcc	atcacacaac	tatcgctttg	tcaaccatgt	gtccacctgc	240
cttctctgtg	acattccctc	attttgtage	tattcg			276

<210> 929

<211> 645

<212> DNA

<213> Unknown (H38g779 nucleotide)

<220>

<223> Synthetic construct

<400> 929

ttctctgac	tctgcttttc	ctctgtcaca	atacctaaat	tgcttcagaa	catgcagagc	60
caagtaccaa	cgatataccta	tgcagattgc	ctgacacagc	tgtacttctt	tatggttttt	120
ggagatatgg	agagcttcct	tcttggtggtc	atggcctatg	accgctatgt	ggccatctgc	180
tttccctttgc	attataaccag	catcatgagc	accaaatttt	gtgctttact	agtgtacta	240
ctgtggatgc	tgacaataac	ccatgccttg	ctgcataccc	tactcatggc	tagattgtct	300
ttttgtgaga	agaatgtcat	tcttcacttt	ttctgtgata	tttctgctct	tctgaagtgt	360
tcctgtctcag	acacttatgt	taatgagttg	atgatattta	tcatgggagg	gatcatcagt	420
attattccat	ttctactcat	tgttatgtct	tatgtaagga	tttttttctc	cattctcaag	480
gttccatctt	ctcaggacat	ccacaaggtc	ttctctacct	gtggttccca	tctgtctgtg	540
gtgaccttgt	tttatgggac	aattattggt	ctctacttat	gtccatcagg	caataattct	600
actgtgaatg	agatttccat	ggccatgatg	tacacagtgg	tggct		645

<210> 930

<211> 657

<212> DNA

<213> Unknown (H38g780 nucleotide)

<220>

<223> Synthetic construct

<400> 930

agcaacctat	ccttcactga	cctctaattt	tcctctgtca	caatgcccaa	gttgctgcag	60
aacatgcaga	gccaagttcc	ttcaatcccc	tatgcaggct	gcctgacaca	aatgtacttc	120
cttttgtttt	ttggagatct	tgagagcttc	ctccttggtg	ccatggccta	tgaccgctat	180
gtagccatct	gcttccctct	tcattacacc	agcatcatga	gccccaggct	ctgtgtgagt	240
cttgtgctgc	tgctctgggt	gctgaccatg	tcccatccca	tgtctgcacac	tttgcctcta	300
actagggttg	ctttctgtga	aaacaatgtg	atccccatt	ttttctgtga	tctgtctgcc	360
ctgctgaagc	tggcctgctc	tgatattcac	attaatgaat	tggatgatt	gatcatagga	420
gggcttggtg	ttatacttcc	atctctactc	atcacagtgt	cttatgcacg	catcatctcc	480
tccattctca	aggctccctc	aactcaaggc	atccacaagg	tcttctccac	ttgtgggtct	540
cacctgtctg	tgggtgctact	gttctatggg	acaattattg	gcctctactt	atgtccatct	600
gctaataact	ctactctaaa	ggacactgtc	atgtctatga	tgtacaccgt	ggtaact	657

<210> 931

<211> 942

<212> DNA

<213> Unknown (H38g781 nucleotide)

<220>

<223> Synthetic construct

<400> 931

atggagaaca	acacagaggt	gactgaattc	atccttggtg	gggttaactga	tgaccagaa	60
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ctgcagatcc	cactcttcat	agtcttccct	ttcatctacc	tcatactctt	ggttggaac	120
ctggggatga	ttgaattgat	tctactggac	tctgtctcc	acaccccat	gtacttcttc	180
ctcagtaacc	tctccctggg	ggactttggg	tattcctcag	ctgtcactcc	caaggtgatg	240
gtggggtttc	tcacaggaga	caaattcata	ttatataatg	cttgtgccac	acaattcttc	300
ttctttgtag	cctttatcac	tgcagaaagt	ttcctcctgg	catcaatggc	ctatgaccgc	360
tatgcagcat	tgtgtaaacc	cctgcattac	accaccacca	tgacaacaaa	tgtatgtgct	420
tgccctggcca	taggctccta	catctgtggg	ttcctgaatg	catccattca	tactgggaac	480
actttcaggc	tctccttctg	tagatccaat	gtagttgaac	actttttctg	tgatgctcct	540
cctctcttga	ctctctcatg	ttcagacaac	tacatcagtg	agatgggtat	tttttttgtg	600
gtgggattca	atgacctctt	ttctatcctg	gtaatcttga	tctcctactt	atttatatct	660
atcaccatca	tgaagatgcg	ctcacctgaa	ggacgccaga	aggccttttc	tacttgtgct	720
tcccacctta	ctgcagtttc	catcttttat	gggacaggaa	tctttatgta	cttacgacct	780
aactccagcc	atttcatggg	cacagacaaa	atggcatctg	tgttctatgc	catagtcatt	840
cccattgtga	atccactggg	ctacagcctg	aggaacaaag	aggttaagag	tgccctttaa	900
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<210> 932

<211> 562

<212> DNA

<213> Unknown (H38g782 nucleotide)

<220>

<223> Synthetic construct

<400> 932

gcaacaaagg	agctgtgttt	tcttggggta	tatattccca	aaggcgatgc	ctgctggaaa	60
tgactcctct	gggcctgcat	ttactcttgc	taggttgaca	agttgtctcc	atgggtggga	120
acctggcctt	gattgctcta	attggctgaa	attcatacct	tcccaccccc	aagctctgtt	180
ttctttcacc	cagtccttcc	ctgatctcta	ttgtcctggt	tgcaccccca	gaatgctcat	240
gacttttcta	tcaaagaaaa	acatcttcta	tgtaggtgac	atgactcagc	tgtagcagct	300
ttctttcttc	tttattgtcc	tactctatta	aataccacgt	gttagtggtc	atagcctgtg	360
gttgccttagt	ggccatctac	aatccatcat	tgcatgaggt	caccatgtct	cctcaggtga	420
gagagagaga	gagagtggat	ttgctggaac	cactcccaca	cagggcacat	acttaggccg	480
aacttggtga	atattgatgt	catcaatcat	catcttatga	cagcctcttg	gtcctctaag	540
ttctttgtac	cagcacctgt	gc				562

<210> 933

<211> 933

<212> DNA

<213> Unknown (H38g783 nucleotide)

<220>

<223> Synthetic construct

<400> 933

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gcctggaacc	tctccctcat	tgttttaata	aggatggatt	cccacctcca	tacacccatg	180
tatttcttcc	tcagtaacct	gtccttcata	gatgtctgct	atatcagctc	cacagtcccc	240
aagatgctct	ccaacctctt	acaggaacag	caaactatca	cttttggttg	ttgtattatt	300
cagtaactta	tcttttcaac	gatgggactg	agttagtctt	gtctcatgac	agccatggct	360
tatgatcggt	atgctgccat	ttgtaacccc	ctgctctatt	catccatcat	gtcaccacc	420
ctctgtgttt	ggatgggtact	gggagcctac	atgactggcc	tcactgcttc	tttattccaa	480
attgggtgctt	tgcttcaact	ccacttctgt	gggtctaatg	tcatacagaca	tttcttctgt	540
gacatgcccc	aactgttaat	cttgctcctg	actgacactt	tctttgtaca	ggcatgact	600
gctatattaa	ccatgttctt	tgggatagca	agtgccttag	ttatcatgat	atcctatggc	660
tatattggca	tctccatcat	gaagatcact	tcagctaaag	gcaggccaaa	ggcattcaac	720
acctgtgctt	ctcatctaac	agctgtttcc	ctcttctata	catcaggaat	ctttgtctat	780
ttgaggtcca	gctctggagg	ttcttcaagc	tttagacagt	ttgcatctgt	tttctacact	840
gtggtcattc	ccatgttaaa	tcccttgatt	tacagtttga	ggaacaaaga	aattaaagat	900
gccttaaaga	ggttgcaaaa	gagaaagtgc	tgc			933

<210> 934
 <211> 935
 <212> DNA
 <213> Unknown (H38g784 nucleotide)

<220>
 <223> Synthetic construct

<400> 934
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 tcctggaaca taaacctcat cacccttate aggacgactc ccatctgcat acacctatgt 180
 actttttcct tagtaatctg tcgtttctgg acatctgcta tgtttccact atagcccca 240
 agatgctctc agacttcttc aagaagcata aattcatctc ctttatgggg tgcagtatgc 300
 agtacttttt cttctctagc ctaggtctaa ctgagtgtg tcttctggga gccatggctt 360
 atgatcgata tgctgccatt tgcaaccctc tgctctacag ggccatcatg ttcccccacc 420
 tctgctgca gatggtggca ggatcttgta taactggatt cttaggctca tttatccaac 480
 tctgtgcctt gcttcagctc catttctgtg ggccaaatgt catcaaccat ttcttctgtg 540
 atctgcccc gctgctgatt ctatcctgtt ctgacacctt tttctttcaa gtcatgacct 600
 ctgttctcac agtgatcttt ggactcacgt ctgtcttagt tatcatgata tcttatgggt 660
 atatcattgc caccattctg aagatcacct cagctgaagg cagagccaaa tctttcaaca 720
 cttgtgcttc tcaccttaca gcagtgatec ttttctttgg ctcagggtatc tttgtttata 780
 tgtatcctaa tgctggtgat tccctgagcc aaaacaagtt ggcatcagtc ttatacacag 840
 ttacaatccc catgttaaat ccagtgatct acagcctgag gaacaaggaa atcaaagatg 900
 ctctaaacag atggaagaag agaattcttct cctgg 935

<210> 935
 <211> 1330
 <212> DNA
 <213> Unknown (H38g785 nucleotide)

<220>
 <223> Synthetic construct

<400> 935
 atgactgtgg aaaggagtag catgacaatt acaaagttca ttctcttggg attctctgaa 60
 tattcaaaga ccaactattt tctcttttca gtattcctag ggatataacct cctgaccatg 120
 tcctgaaacg tgagtctcat cgcccttate aggacggact cccatctaca tgcacctgtg 180
 tactttttcc ttagtaatcc gtcttttctg gacatctgct gtgtttccac tatagcccc 240
 aagatgccct cagacttttt caagaagcat aaattcattt cctttatggg gtgcaccatg 300
 cagtacttct ctagecctgaa tgtgactgag tgctgtcttc ttacagccat ggcttatgat 360
 taatatgctg ccatttgtga tctctgtctc tacacagcca tcatgtcacc tgctctctgt 420
 atgccaatgg tggcaggatc ttgtacaact ggatactttg tctcatttat ccaactctgt 480
 gccttgcttc tgctccattt ctgtgagtca aatagcagcc atttcttttg tgacctgccc 540
 caactgctga ttctatcctg ttctcatact gttttttttt tctcaagtca tgaccactat 600
 gctcacagta acctttatac tcacctctat cttggttatc atgataactt atgggttatat 660
 cattgccaac attcatctct tttatgggat gcaccatgta atacttcttc tctagcctgg 720
 gtctgactga gtgctgtctt ctggaagcta tggcttataa ttgatatgct gccatttgtg 780
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 gctatgacac ctttttctgt caagtcatga catccatgct tacagtggta ttggagta 1020
 catctgtctt agttatcatg atattttatg gctatgtcat tgctaccatt ctgaagatca 1080
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 tctcttctat tgctcaagaa tctttgtcta tatgtgctct cactctgatg cttctctgag 1200
 tagaaacaag gtggattcta ttgtatacac tgtggtgatc cccaggttga atccattgat 1260
 ctacagcctg agtgacaagt aaatcaaaga tgccctaaag agatggacga agagaatatt 1320
 ctctggcct 1330

<210> 936

<211> 930
 <212> DNA
 <213> Unknown (H38g786 nucleotide)

<220>
 <223> Synthetic construct

<400> 936
 atgggggaaa atcagacaat ggtcacagag ttctctctac tgggatttct cctggggccca 60
 aggattcaga tgctctctct tgggctcttc tccctgttct atatcttcac cctgctgggg 120
 aacggggcca tcctggggct catctcactg gactccagac tccacacccc catgtacttc 180
 ttctctctac acctggctgt cgtcgacatc gcctacaccc gcaacacggg gccccagatg 240
 ctggcgaacc tcctgcatcc agccaagccc atctcctttg ctggctgcat gacgcagacc 300
 tttctctgtt tgagtttttg acacagcgaa tgtctctctg tgggtgctgat gtccctacgat 360
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 atcacccctg ccgtcaactc ctggacgtgt ggctccctcc tggctctggc ccatgtgggt 480
 ctcatcctaa gactgccctt ctctgggctt catgaaatca accacttctt ctgtgaaatc 540
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 gcctgcgtgt tcttctctgt gggggccacc agcctgggtg ttgtctctca ctgcacatc 660
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 tcctccacc tctgcgtggg gggactcttc tttggcagtg ccatcatcat gtacatggcc 780
 cccaagtccc gccatcctga ggagcagcaa aaggctcttt ttctatttta cagttttttc 840
 aacccaacac ttaacccctt gatttacagc ctgaggaacg gagaggtcaa gggtgccctg 900
 aggagagcac tgggcaagga aagtcattcc 930

<210> 937
 <211> 942
 <212> DNA
 <213> Unknown (H38g787 nucleotide)

<220>
 <223> Synthetic construct

<400> 937
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 cctgagctcc aggggcagct ctttgtgggt ttcttggtta tttatctggt gaccctgata 120
 ggaaatgccca ttattatagt catcgtctcc ctgaccaga gcctccacgt tcccatgtac 180
 ctgtttctcc tgaacttata tgtggtggac ctgagtttca gtgcagttat tatgcctgaa 240
 atgctgggtg tcctctctac tgaaaaaact acaatttctt ttgggggctg ttttgcacag 300
 atgtatttca tccttctttt tgggtggggt gaatgttttc ttctgggagc aatggcttat 360
 gaccgatttg ctgcaatttg ccatcctctc aactaccaa tgattatgaa taaaggagtt 420
 tttatgaaat taattatatt ttcatgggcc ttaggtttta tgtaggtac tgttcaaaca 480
 tcatgggtat ctagttttcc ctttgtggg cttaatgaaa ttaaccatat atcttgtgaa 540
 accccagcag tgtagaact tgcagtgcga gacacgtttt tgtttgaaat ctatgcattc 600
 acaggcacct ttttgattat tttggttctt ttcttgttga tactctgtc ttacattcga 660
 gttctgtttg ccactctgaa gatgccatca accactggga gacaaaaggc cttttccacc 720
 tgtgccgctc acctcacatc tgtgacctta ttctatggca cagccagtat gacttattta 780
 caacccaaat ctggctactc accggaaacc aagaaagtga tgtcattgtc ttactcattt 840
 ctgacaccac tgctgaatct gcttatctac agtttgcgaa atagttagat gaagagggtc 900
 ttgatgaaat tatggcgaag gcgagtgggt ttacacacaa tc 942

<210> 938
 <211> 993
 <212> DNA
 <213> Unknown (H38g788 nucleotide)

<220>
 <223> Synthetic construct

<400> 938
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ctcatctcac	tggactccag	actccacacc	cccattgtact	tcttctcttc	acacctggcc	180
gtcgtcaaca	tcgcctatgc	ctgcaacaca	gtgcccaga	tgctgggtgaa	cctcctgcat	240
ccagccaagc	ccatctcctt	tgttggtgct	atgacataga	cctttctctt	tttgagtttt	300
gcacatactg	aatgcctcct	gttggtgctg	atgtcctacg	atcgggtacgt	ggccatctgc	360
cacctctctc	gatatttcat	catcatgacc	tggaaagtct	gcatcactct	ggccatcact	420
tcctggacat	gtggctccct	cctggctatg	gtccatgtga	gcctcatcct	aagactgccc	480
ttttgtgggc	ctcgtgaaat	caaccacttc	ttctgtgaaa	tcctgtctgt	cctcaggctg	540
gcctgtgctg	atacctgggt	caaccagggt	gtcatctttg	cagcctgcat	gttcatcctg	600
gtgggaccac	tctgcctggt	gctggctctc	tactcacaca	tcctggcggc	catcctgagg	660
atccagtctg	gggagggccg	cagaaaggcc	ttctccacct	gtcctcccca	cctctgcgta	720
gtgggactct	tctttggcag	cgcacccgtc	atgtacatgg	cccctaagtc	ccgccatcct	780
gaggagcagc	agaaggctct	ttttctatct	tacagttctt	tcaacccgat	gctaaacccc	840
ctgatttaca	acctgaggaa	tgtagaggtc	aagggtgccc	tgaggagagc	actgtgcaag	900
gaaagtcatt	cctaagaggt	gtgacatttg	aactgccagc	ctcagttgtc	acgtggactc	960
ttgatgcccc	attattgcct	caatccagaa	aag			993

<210> 939

<211> 930

<212> DNA

<213> Unknown (H38g789 nucleotide)

<220>

<223> Synthetic construct

<400> 939

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aggattcaga	tgctcctctt	tgggctcttc	tcctgtttct	acgtcttcac	cctgctgggg	120
aacgggacca	tactggggct	catctcactg	gactccagac	tgacacgccc	catgtacttc	180
ttcctctcac	acctggcggt	cgtcgacatc	gcctacgcct	gcaacacggt	gccccggatg	240
ctggtgaacc	tccgtcatcc	agccaagccc	atctcctttg	cgggccgcat	gatgcagacc	300
tttctgtttt	ccacttttgc	tgtcacagaa	tgtctcctcc	tggtgggtgat	gtcctatgat	360
ctgtacgtgg	ccatctgcca	ccccctccga	tatttggtcca	tcatgacctg	gagagtctgc	420
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cccagatatg	ggaaccccaa	ggagcagaag	aaatatctcc	cgctgtttca	cagcctcttt	840
aatcccatgc	tcaatcccct	tatctgtagt	cttaggaact	cagaagtga	gaatactttg	900
aagagagtgc	tgggagtaga	aagggttta				930

<210> 940

<211> 942

<212> DNA

<213> Unknown (H38g790 nucleotide)

<220>

<223> Synthetic construct

<400> 940

atgaaaagac	aaaatcaaag	ctgtgtgggt	gaattcatcc	tcctgggctt	ttctaacttt	60
cctgagctcc	agggtgcagct	ctttgggggt	ttcctagtta	tttatgtggt	gacctgatg	120
ggaaatgcc	tcattacagt	catcatctcc	ttaaaccaga	gcctccacgt	tcccatgtac	180
ctgttctctc	tgaacctatc	tgtgggtggag	gtgagtttca	gtgcagtc	tacgcctgaa	240
atgctgggtg	tgctctctac	tgagaaaact	atgatttctt	ttgtgggctg	ttttgcacag	300
atgtatttca	tccttctttt	tgggtgggact	gaatgttttc	tcctgggagc	gatggcttat	360
gaccgatttg	ctgcaatttg	ccatcctctg	aactaccag	tgattatgaa	cagaggggtt	420
tttatgaaat	tgctaatatt	ctcatggatc	tcagggatca	tggtgggtac	tgtcagacc	480
acttgggtat	ttagttttcc	attttgtggc	cccaatgaaa	ttaatcatct	cttctgtgag	540

actcccccg	tactagagct	tgtgtgtgca	gacacettct	tatttgaaat	ctatgccttc	600
acaggcacca	ttttgattgt	tatggttcct	ttcttgttga	tcctcttgte	ttacattcga	660
gttctgtttg	ccatcctgaa	gatgccatca	actactggga	gacaaaaggc	cttttccacc	720
tgtgcctctc	acctcacatc	tgtgacctg	ttctatggca	cagccaatat	gacttattta	780
caacccaaat	ctggctactc	acccgaaacc	aagaaactga	tctcattggc	ttacacgttg	840
cttaccctc	tgctcaatcc	gctcatctat	agcttacgaa	acagtgagat	gaagaggact	900
ttgataaaac	tatggcgaag	aaaagtgatt	ttacacacat	tc		942

<210> 941

<211> 936

<212> DNA

<213> Unknown (H38g791 nucleotide)

<220>

<223> Synthetic construct

<400> 941

atgagtgcaa	acacctccat	ggtgactgag	tttcttcttc	tcggcttctc	ccacctggcc	60
gacctccagg	gcttgcctct	ctctgtcttt	ctcactatct	acctgctgac	cgtggcaggc	120
aatttctctca	ttgtgggtgct	ggctctccact	gatgctgccc	tccagtcctcc	tatgtacttc	180
ttctctgcgca	ccctctcggc	cttgagatt	ggctatacgt	ctgtcacggg	ccccctgcta	240
cttcaccacc	tccttactgg	cgggcgccac	atctctcgct	ctggatgtgc	tctccagatg	300
ttcttcttcc	tcttcttttg	cgccacggag	tgctgcctcc	tggcagccat	ggcctatgac	360
cgctatgcag	ccatctgtga	acccctccgc	taccactgc	tgctgagcca	ccgggtgtgt	420
ctacagctag	ctgggtcggc	gtgggcctgt	gggtgctgg	tggggtggg	ccacacct	480
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cagcctgtcc	tgcagctggt	atgtggagac	acctcgctta	atgaactgca	gattatcctg	600
gcaacagccc	tcctcatcct	ctgccccttt	ggcctcatcc	tgggctccta	cgggcgtatc	660
ctcgttacca	tcttccggat	cccctctgtt	gcgggcggcc	gcaaggcctt	ctccacctgc	720
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cctaaggcca	gctacgatcc	ggccactgac	cctctggtgt	ccctcttcta	tgctgtggtc	840
acccccatcc	tcaaccccat	catctacagc	ctgcgggaaca	cagaggtaaa	agctgcctta	900
aagagaacca	tccagaaaac	ggtgcctatg	gagatt			936

<210> 942

<211> 828

<212> DNA

<213> Unknown (H38g792 nucleotide)

<220>

<223> Synthetic construct

<400> 942

atgtacctgg	tcactgtgct	cggaacctg	ctcatcatcc	tggccgcaat	ctcagactcc	60
tgctccacca	cccccatgta	cttctttctc	tccaacctgt	ccttcgtaga	tatctgtttt	120
gcctccacca	tggtcccaaa	gatgttggtg	aacatccaga	cacagagcaa	agtcattacc	180
tatgcagggt	gcatcaccca	gatgtgcttt	tttgactct	ttatagtgtt	ggacagctta	240
ctcctgaccg	tgatggccta	tgaccagttt	gtggccatct	gtcaccctcc	gcactacacg	300
gtcatcatga	gccctcagct	ctgtggactg	ctgggtctgg	tgctcctggat	catgagtgtc	360
ctaaactcca	tgttacaaaag	cttagtgaca	ttgcagttgt	ccttctgcac	agacttggaa	420
atccctcact	ttttctgtga	acttaatgag	atgatccacc	ttgcctgttc	tgacaccttt	480
gtgaacaaca	tggatgatga	ttttgcagct	gtgctgtctg	acgggtgggtc	tctcgttggg	540
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aagtacaagg	cactttccac	ctgtgcactc	cacctctcag	ttgtctccat	attttatggt	660
acggggctag	gggtgtacct	tagctctact	atgacccaaa	acttacactc	aactgctgtc	720
gcctcgggtga	tgtacactgt	ggtcaccccc	atgctcaacc	ccttcattta	cagtctgagg	780
aataaagaca	taaaagggggc	tctgacacaa	ttcttcagag	ggaaacaa		828

<210> 943

<211> 950

<212> DNA

<213> Unknown (H38g793 nucleotide)

<220>

<223> Synthetic construct

<400> 943

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tgcccagaac	tgcataattct	gtccttcctt	ggggtcagcc	tgggttatgg	tttgatcacc	120
actgggaaca	ttctcattgt	ggtgtccatt	cacacagaaa	cctgtctatg	cacatccatg	180
tactatttcc	tgggcagcct	ttctgggatt	gaaatatgct	acactgcagt	ggtgggtgccc	240
catatcctgg	ccaacaccct	acagtcagag	aagacatcac	tctcctgggc	tgtgccaccc	300
agatggcttt	cttcattgca	ctgggcagtg	ctgattgctt	cctcttggct	gccatggcct	360
atgaccgcta	tgtggccatt	tgccaccctg	tgcagtaccc	tctcctcatg	acattgactc	420
tttgtgtcca	cttgggtgtg	gcatcagtea	tcagtggtct	gttcctgtcc	ttacaactgg	480
tggccttcat	cttctctctg	ccattctgcc	aggctcaggg	cattgagcac	ttcttttgtg	540
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tgtgccccag	ctccagctac	aaccccaagc	aagatcgggt	catctcactg	gtgtacacat	840
tgggaacccc	actgctcaac	ccacttatct	atgccctgag	gaacagttag	atgaaagggg	900
ccgtaggggag	agttcttacc	aggaactgcc	tttcccagaa	cagctaggaa		950

<210> 944

<211> 927

<212> DNA

<213> Unknown (H38g794 nucleotide)

<220>

<223> Synthetic construct

<400> 944

atggaaccag	agaatgacac	agggatttca	gaatttggtc	ttctgggact	ttctgaggaa	60
ccagaattgc	agcccttctt	ctttgggctg	tttctgtcca	tgtacctggg	cactgtgctc	120
gggaatctgc	tcatactcct	ggccacaatc	tcagactccc	acctccacac	ccccatgtac	180
ttcttctctt	ccaacctgtc	ctttgcagac	atctgtttca	tctccactac	aatcccaaag	240
atgctcatta	acatccagac	acagagcaga	gtcatcacct	atgcaggctg	catcacccag	300
atgtgctttt	ttgtactttt	tggagggtta	gacagcttac	tcctggctgt	gatggcctat	360
gatcggtttg	tggccatctg	tcactctctg	cactacacag	tcatactgaa	ccctcggctc	420
tgtggactcc	tggttctggc	atcctggatg	attgctgccc	tgaattcctt	gtcacaaagc	480
ttaatgggat	tgtggctgtc	cttctgcaca	gacttggaaa	tccccactt	tttctgtgaa	540
cttaatcagg	tcataccact	tgcctgttct	gacacctttc	ttaatgacat	ggggatgtat	600
tttgcagcag	ggctgctggc	tgggtgtccc	cttgtgggga	tcctttgtct	ttactctaag	660
atagtttctt	ccatacgtgc	aatctcatca	gtcaggggga	agtacaaggc	attttccacc	720
tgtgcatcac	acctctcagt	tgtctcttta	ttttgttgta	cgggcctagg	tgtgtacctt	780
acttctgctg	caaccacaaa	ctcacacaca	agtgaacag	cctcagtgat	gtacactgtg	840
gccacccccca	tgctgaaccc	ctttatctac	agtctgagga	ataaagacat	aaagagggct	900
ctgaaaatgt	ccttcagagg	aaagcaa				927

<210> 945

<211> 942

<212> DNA

<213> Unknown (H38g795 nucleotide)

<220>

<223> Synthetic construct

<400> 945

atggagaata	atacagaggt	gagtgaattc	atcctgcttg	gtctaaccaa	tgccccagaa	60
ctacaggttc	ccctctttat	catgtttacc	ctcatctacc	tcatactct	gactgggaac	120
ctgggggatga	tcataattaat	cctgctggac	tctcatctcc	acactcccat	gtactttttt	180

ctcagtaacc	tgtctcttgc	aggcattggt	tactcctcag	ctgtcactcc	aaaggtttta	240
actgggttgc	ttatagaaga	caaagccatc	tcctacagtg	cctgtgctgc	tcagatgttc	300
ttttgtgcag	tctttgccac	tgtggaaaat	tacctcttgt	cctcaatggc	ctatgaccgc	360
tacgcagcag	tgtgtaaccc	cctacattat	accaccacca	tgacaacacg	tgtgtgtgct	420
tgtctggcta	taggctgtta	tgtcattggt	tttctgaatg	cttctatcca	aattggagat	480
acatttcgcc	tctctttctg	catgtccaat	gtgattcatc	actttttctg	tgacaaacca	540
gcagtcatta	ctctgacctg	ctctgagaaa	cacattagtg	agttgattct	tgttcttata	600
tcaagtttta	atgtcttttt	tgcacttctt	gttaccttga	tttcctatct	gttcatattg	660
atcaccattc	ttaagaggca	cacaggtaag	ggataccaga	agcctttatc	tacctgtggt	720
tctcacctca	ttgccatttt	cttattttat	ataactgtca	tcattcatgta	catagacca	780
agttccagtc	attccatgga	cacagacaaa	attgcatctg	tgttctacac	tatgatcatc	840
cccattgctca	gtcctatagt	ctataccctg	aggaacaaag	acgtgaagaa	tgcattcatg	900
aaggttggtg	agaaggcaaa	atattctcta	gattcagttc	tt		942

<210> 946

<211> 946

<212> DNA

<213> Unknown (H38g796 nucleotide)

<220>

<223> Synthetic construct

<400> 946

atgtaaaata	actcaaagtt	tactgatttc	atcctggtag	gtctaaccac	tgccacagaa	60
cttcagatcc	ccctctttat	cttggtcctc	ctcatccacc	tcctcattct	gactaggaac	120
ctggagatca	tactgttgat	cctgctggac	tcttgtctcc	aattcccatg	tactttttcc	180
tcagtaacct	gtctctgctt	ggatacttaa	ctgtcactcc	caggggtcacg	gctagcaggg	240
ctaggttact	tagagggtag	gaggctaagt	tcctcgtaca	atgcttgtgc	tgctcagatg	300
ttcttttttg	tagccttggc	cacagtggaa	aatatcgctg	ttgacatcaa	tgccctatga	360
ccactatata	gcagtgtgca	aacccttaca	ctacactacc	accacgatag	ccagtgtatg	420
tgctcatctg	gtcataggct	cctatgtctg	tggttttcta	aatgcctccc	tcgcattgg	480
ggacatattc	agtctctctt	tctgtaagtc	caatcttgtc	catcaccttt	tctgtgatgt	540
tccaccagtc	atggctgtgt	cttgcctctg	ttaacacatt	agcaagaaga	ttctggtttt	600
tatgtcaagc	ttcaatgtct	ttttggctct	tctagttatc	ttgacctcct	acctgttcat	660
attcatcacc	atcttgaaga	tgcactcagc	tcagggacac	ttaaaagctt	tgtccacctg	720
tgccctcacc	ctcattgcag	tctccatctt	ctatggaaact	actatcttta	tgcacttaca	780
gcctagctcc	agccattcca	tggacacaga	tgaattggca	tccttgttct	atgctgtggt	840
catctccatg	ctgaaccttg	tgttctacag	cctgaggagc	aaagaagtca	agaatgcatt	900
caaaaaggcg	gttgagaagg	caaaattttt	cttagaactg	tgattt		946

<210> 947

<211> 942

<212> DNA

<213> Unknown (H38g797 nucleotide)

<220>

<223> Synthetic construct

<400> 947

atggacaaca	gcaactggac	cagtgtgtcc	cattttgttc	tcttgggcat	ttccacccac	60
ccagaagagc	aaatcccact	cttcttgggt	ttctcactca	tgtaacgcaat	caatattttct	120
ggcaacttgg	ccatcatcac	actgattctc	tctgtctcac	gcctccacat	ccccatgtac	180
atcttctctca	gtaacttggc	cttgacagac	atctgtctca	cctccaccac	ggcccccaag	240
atgctgcaga	ttattttctc	ccctacaaaag	gtaatttctc	acacaggctg	tttagcccaa	300
acttattttct	tcattttgctt	cgccgtcatg	gaaaacttca	tcctgggtgt	gatggcctat	360
gacagggtaca	ttgccatctg	ccaccctttc	cactacacta	tgatcctgac	tagaatgctg	420
tgtgtgaaga	tggtgggtcat	gtgccatgct	ctctcccacc	ttcatgccat	gctgcatacc	480
ttctctatgg	gccaactaat	cttctgtgca	gataacagaa	tcctccactt	cttctgtgac	540
ctctacgctc	tgatgaagat	ctcctgcacc	agcacctacc	tcaacacctc	tatgattcac	600
acagaagggtg	ctgttgtaat	cagtggagct	ctggccttca	ttactgcctc	ctatgcctgc	660
atcctctctg	tggtcctccg	gatccccctca	gccaagggca	gggtggaaaac	cttttctacc	720

tgcggctccc	acctcactgt	ggtggccata	ttctatggca	ccctcagttg	ggtctacttc	780
cgggcccttt	ccagctatcc	agtgaccaag	ggtcgcatta	taacagtcgt	gtacacagtg	840
gtgactccca	tgctgaaccc	cttcactctac	agcctgagga	atggggatgt	caagggaggc	900
ttcatgaaat	ggatgagcag	aatgcagact	ttttcttcta	ga		942

<210> 948

<211> 948

<212> DNA

<213> Unknown (H38g798 nucleotide)

<220>

<223> Synthetic construct

<400> 948

atgggttaacc	aaagctcccc	catgggcttc	ctccttcttg	gcttctctga	acaccagca	60
ctggaaagga	ctctctttgt	ggttgtcttc	acttcctacc	tcttgaccct	ggtgggcaac	120
acactcatca	tctgctgtc	tgtactgtac	cccaggctcc	actctccaat	gtactttttc	180
ctctctgacc	tctccttctt	ggacctctgc	tttaccacaa	gttgtgtccc	ccagatgctg	240
gtcaacctct	ggggcccaaa	gaagaccatc	agcttcctgg	gatgctctgt	ccagctcttc	300
atcttctctg	ccctggggac	cactgagtgc	atcctcctga	cagtgatggc	ctttgaccga	360
tacgtggctg	tctgccagcc	cctccactat	gccaccatca	tccacccccc	cctgtgctgg	420
cagctggcat	ctgtggcctg	ggttatgagt	ctgggtccaat	cgatagtcca	gacaccatcc	480
accctccact	tgcccttctg	tccccaccag	cagatagatg	actttttatg	tgagggtcca	540
tctctgattc	gactctcctg	tggagatacc	tcctacaatg	aaatccagtt	ggctgtgtcc	600
agtgtcatct	tcgtggttgt	gcctctcagc	ctcatccttg	cctcttatgg	agccactgcc	660
caggcagtg	tgaggattaa	ctctgccaca	gcatggagaa	aggcctttgg	gacctgtccc	720
tcccatctca	ctgtggtcac	cctcttctac	agctcagtea	ttgctgtcta	cctccagccc	780
aaaaatccgt	atgcccagg	gaggggcaag	ttctttggtc	tcttctatgc	agtgggcact	840
ccttcactta	accctctcgt	atacaccctg	aggaacaagg	agataaagcg	agcactcagg	900
aggttactag	ggaaggaaag	agactccagg	gaaagctgga	gagctgct		948

<210> 949

<211> 971

<212> DNA

<213> Unknown (H38g799 nucleotide)

<220>

<223> Synthetic construct

<400> 949

cacacagagc	cacggaatct	cacagggtgc	tgagaattcc	tcctcctggg	actctcagag	60
gatccagaac	tgcagccggg	cctcgctttg	ctgtccctgt	ccctgtccat	gtatatgggc	120
acgggtgctga	ggaacctgct	cagcatectg	gctgtcagct	ctgactcccc	gctccacacc	180
cccattgtgct	tcttctcttc	caaactgtgc	tgagctgaca	tcggtttcac	cttgggccatg	240
gttcccaaga	tgattgtgaa	catgcagtcg	catagcagag	tcattctcta	tgagggtctg	300
ctgacacgga	tgtcttttct	tgctcttttt	gcatgtatgg	aagacatgct	cctgactgtg	360
atggcctatg	actgctttgt	agccatctgt	cgccctctgc	actaccaggt	catcgtgaat	420
cctcacctct	gtgtcttctt	cgtcttgggt	tcctttttcc	ttagcccgtt	ggattcccag	480
ctgcacagtt	ggattgtgtt	actattcacc	atcatcaaga	atgtggaaat	cactaatttt	540
gtctgtgaac	cctctcaact	tctcaacctt	gcttgttctg	acagcgtcat	caataacata	600
ttcataatatt	tcgatagtac	tatgtttggg	tttcttccca	tttcagggat	cctttttgtct	660
tactataaaa	ttgtcccttc	cattctaagg	atgtcatcgt	cagatgggaa	gtataaaggc	720
ttctccacct	gtggctctta	cctggcagtt	gtttgtgat	ttgatggaac	aggcattggc	780
atgtacctga	cttcagctgt	gtcaccaccc	cccagggaatg	gtgtggtggc	gtcagtgatg	840
tatgtctgtg	tcacccccat	gctgaacctt	ttcatctaca	gcctaggaaa	gagggatata	900
caaagtgtcc	tgcggaggct	gtgcagcaga	acagtcgaat	ctcatgatat	gttccatcct	960
ttttcttctg	t					971

<210> 950

<211> 474

<212> DNA

<213> Unknown (H38g800 nucleotide)

<220>

<223> Synthetic construct

<400> 950

atggaaccag	agaatggtac	gaggatttta	ggattttcttc	ttctgggact	ttcagaggaa	60
ccagaattgc	agcccgttat	gtttggactc	tctctctcca	tgtatctgac	aactgtgttt	120
ggaaacctgc	tcatcatcct	ggccatctgc	tctgggtccc	acctccacac	ccccatgtac	180
ttcttctctc	ctaacctgtc	ctttgtagac	atctgtgtta	cctccaccac	agtcccaaag	240
acactgtcaa	acatccggac	acagagtaaa	gtcatcacct	atgcagggtg	catcacccag	300
atgtactttt	ttgtactctt	tatagtgttg	gacagcttac	tcttgaccgt	gatggcctat	360
gaccagtttg	tggccatctg	tcaccccctg	cactacacgg	tcatcgtgaa	ccctcggctc	420
tgtggactgc	tggttcttgg	gtcctggatc	atgagtgcc	tgaattcctt	gata	474

<210> 951

<211> 954

<212> DNA

<213> Unknown (H38g801 nucleotide)

<220>

<223> Synthetic construct

<400> 951

atgatgagct	ttgcccctaa	tgettccacac	tctccggttt	ttttgtctct	tgggtttctcg	60
agagctaaca	tctcctacac	tctcctcttc	ttcctgttcc	tggctattta	cctgaccacc	120
atactgggga	atgtgacact	ggtgctgctc	atctcctggg	actccagact	gcactcacc	180
atgtattatc	tgtctcgttg	cctctctgtg	atagacatgg	ggctatccac	agttacactg	240
ccccagttgc	tggcccattt	ggtctctcat	tacccaacca	ttcctgtctg	ccgtgtcttg	300
gctcagttct	ttttcttcta	tgcatttggg	gttacagata	cacttgtcat	tgtgtctatg	360
gctctggatc	gctatgtggc	catctgtgac	cccctgcact	atgctttggg	aatgaatcac	420
caacgggtgtg	cctgcttact	agccttgagc	tgggtgggtg	ccatactgca	caccatgttg	480
cgtgtgggac	tcgtcctgcc	tctttgctgg	actggggatg	ctgggggcaa	cgtaaaccct	540
cctcacttct	tttgtgacca	ccggccactt	ctgcgagcct	cctgttctga	catacattct	600
aatgagctgg	ccatattctt	tgagggtggc	ttccttatgc	tgggcccctg	tgccctcatt	660
gtactctctt	atgtccgaat	tggggccgct	attctacgtt	tgccttcagc	tgtgtgtcgc	720
cgccgagcag	tctccacctg	tggatcccac	ctcaccatgg	tgggttctct	ctacggcacc	780
atcattttgtg	tctacttcca	gcctcccttc	cagaactctc	agtatcagga	catgggtgct	840
tcagtaatgt	atactgccat	tacacctttg	gccaaacctat	ttgtgtatag	cctccacaat	900
aaggatgtca	agggtgcact	ctgcaggctg	cttgaatggg	tgaaggtaga	cccc	954

<210> 952

<211> 921

<212> DNA

<213> Unknown (H38g802 nucleotide)

<220>

<223> Synthetic construct

<400> 952

atgctgaata	caacctcagt	caccgaattt	ctcctcttgg	gagtgcacaga	cattcaagaa	60
ctgcagcctt	ttctcttcgt	ggttttcttc	accatctact	tcatcagtgt	gactgggaat	120
ggagccgttc	tgatgattgt	catctccgat	cctagactcc	attcccttat	gtatttcttc	180
ctgggaaacc	tgtcctacct	ggatatctgt	tactctacgg	tgacactgcc	aaaaatgctg	240
cagaactttc	tctctacaca	caaagcaatt	tctttcttgg	gatgcataag	ccagcttcat	300
ttcttccact	tcctgggcag	cacggagtcc	atgttggttcg	ccgtgatggc	atttgacctc	360
tctgtggcta	tctgcaagcc	acttcgtctc	actgtcatca	tgaacctca	gctctgtacc	420
cagatggcca	tcacaatctg	ggtcattggg	tttttccatg	ccctgctgca	ctccgtaatg	480
acttctcgct	tgaacttctg	tggttccaac	cgtatccatc	attttctctg	tgatattaag	540
ccattgctaa	agctggcctg	tgggaacact	gagcttaatc	agtggctact	cagtactgtc	600
acggggacaa	ttgccatggg	ccccttcttt	ctgacacttc	tctcctattt	ctacattatc	660

acttatctct	tcttcaagac	ccgttcttgt	agcatgctct	gtaaagcact	gtccacttgt	720
gcctcccact	tcatggtagt	tattcttttc	tatgcacctg	ttctttttcac	ctatatccat	780
cctgcgttag	agagcttcat	ggaccaggac	cggattgttg	ccatcatgta	cactgtgggc	840
actcctgtac	taaaccact	gatctatact	ttgaggaaca	aggaagtga	gggggccttg	900
ggtagagtga	tcagaaggct	t				921

<210> 953

<211> 959

<212> DNA

<213> Unknown (H38g803 nucleotide)

<220>

<223> Synthetic construct

<400> 953

cagccacgga	atctcacaga	tgtctgagaa	ttcctcctca	tgggactctc	agaggatcca	60
gaactgcagc	ccgtcctcgc	tgggctgtcc	ctgtccatgt	atctggtcac	ggtgctgagg	120
aacctgctca	gcacctggc	tgtcagctct	gactcccacc	tccacacccc	catgtacttc	180
ttcctctcca	acctgtgctg	ggctgacatc	ggtttcacct	cggccacggt	tcccaagata	240
attgtggaca	tgcagtcgca	tagcagagtc	atctcttatg	tgggctgcct	gacacggatg	300
tcttttttgg	tcctttttgc	atgtatagaa	gacatgcttc	tgactgtgat	ggcctatgac	360
tgtttttag	ccatctgtcg	ccctctacac	taccacagtc	tcgtgaatgc	tcacctccgt	420
gtcttcttag	ttttggtgtc	ctttttcctt	agcctgttgg	attcccagct	gcacagttag	480
attgtgttac	aattcacctt	cttcaagaat	gtggaaatct	ctaattttgt	ctgtgagcca	540
tctcaacttc	tcaagcttgc	ctgttctgac	agcatcatca	atagcatatt	catatatctc	600
gatagtacta	tgtttggttt	tcttccatt	tcagggatcc	ttttgtctta	ctgtaaaatt	660
gttccctcca	ttctaaggat	ttcaacatca	gatgggaaat	ataaagcctt	ctccacctgt	720
ggctctcacc	tggcacttgt	ttgcttattt	tatggagcag	gcattggcgt	gtacctgact	780
tcagctgtgt	caccaccccc	caggaatggt	gtggtggtgt	cagtgatgta	cactgtgggc	840
accccatgc	tgaaccctt	catctacagc	ctgagaaaca	gggacattca	aagcaccctg	900
cggaggctgc	tcagcagaac	agtcgaatct	catgatctgt	tccatccttt	ttcttgtgt	959

<210> 954

<211> 984

<212> DNA

<213> Unknown (H38g804 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(984)

<223> n = A,T,C or G

<400> 954

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ccagatctcc	agtccctctt	gttcttctctg	tttctagtaa	tctatgtggg	cactctgttg	120
ggaaacttgg	gcttggtaac	tctaattggg	ctgaactcac	accttcatac	ccccatgtac	180
ttcttctctt	ttaacttgct	cttcatagat	ctctgttatt	cttctgtgtt	tatacccaaa	240
atgctaata	actttatttc	agagaagaat	attatgtcct	tcaaggggtg	catgacccaa	300
ctttcctttt	nctgattttt	ttgggtcattt	ctgaagggtta	tgtgctgacg	tcaatggcgt	360
atgatecgtg	tggccatctg	taccccaactt	ctgtatcaca	ttgccatgtc	tcctacagtg	420
tgtccagcc	ttagttttgg	ttcctatttg	atgccttttt	ctgggtgccat	ggcccacact	480
ggatgcatgc	tgagactgac	tttctgtgat	gcgaacacca	tcgatcacta	cttctgtgac	540
atcctccctc	tgtccagct	ctcctgcacc	agcacctaca	tcaatgagct	ggtgggtttc	600
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aaccatctt	ctgctgggtc	catggataag	agaaaattat	cttctgtctt	ttatacaaat	840
gtggttccca	tgttgaaacc	cttaatctac	agcctgagga	acaaagatgt	taaatttgcc	900
ctaagaaaag	ccctgagtag	taggaaactt	tgataagtaa	tagtatgtgt	ctgtgtgtat	960

agtcacaaga cagggatatt ctgt

984

<210> 955

<211> 930

<212> DNA

<213> Unknown (H38g805 nucleotide)

<220>

<223> Synthetic construct

<400> 955

atgggaagaa	ataacctaac	aagaccctct	gaattcatcc	tccttggact	ctcctctcga	60
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ggaaacctgc	ttatcaccct	ggccatccgc	tcagacactc	gtctccagac	gcccatgtac	180
ttctttctaa	gcacccctgc	ttttgttgac	atttgctatg	tgacagtcac	tatccctaag	240
atgctgggtga	acttcttata	agagacaaag	accatctctt	acagtgaagt	tctgaccagg	300
atgtactttt	tcttagcctt	tggaaacaca	gacagttacc	tgctagcagc	catggccatt	360
gaccgctatg	tggccatag	taatcccttc	cactacatca	ccattatgag	tcacagatgc	420
tgtgtcctgc	ttctgggttc	ctccttctgc	attccacatt	ttcactccct	cctgcacatt	480
cttctgacta	atcagctcat	cttctgtgcc	tcaaagtgtc	tccatcactt	tttctgcgat	540
gatcaaccag	tgctaaaatt	gtcctgttcc	tcccatcttg	tcaaagaaat	cacagtaatt	600
acagaaggct	tggctgtcat	aatgaccccg	ttttcatgca	tcacatcttc	ttatttaaga	660
atcctcatca	ctgttctgaa	gattccttca	gctgctggaa	agcgtaaagc	attttctacc	720
tgtggctctc	atctcacagt	ggtgaccctg	ttttatggaa	gcattagcta	tctctatttt	780
cagccctctg	ccaactatac	tgtcaaggat	caaatagcaa	caattatcta	caccgtactg	840
actcctatgc	taaatccatt	tatctatagt	ctgaggaaca	aagacatgaa	gcagggtttg	900
gcaaagttga	tgcacaggat	gaaatgtcag				930

<210> 956

<211> 945

<212> DNA

<213> Unknown (H38g806 nucleotide)

<220>

<223> Synthetic construct

<400> 956

atggaaattg	tctccacagg	aaacgaaact	attactgaat	ttgtcctcct	tggtttctat	60
gacatccctg	aactgcattt	cttggttttt	attgtattca	ctgctgtcta	tgtcttcac	120
atcataggga	atatgctgat	tattgtagca	gtgggttagc	cccagaggct	ccacaaacct	180
atgtatattt	tcttggcgaa	tctgtccttc	ctggatattc	tctacacctc	cgcagtgatg	240
caaaaaatgc	tggagggtct	cctgcaagaa	gcaactatct	ctgtggctgg	ttgcttgctc	300
cagttcttta	tcttcggctc	tctagccaca	gctgaatgct	tactgctggc	tgtcatggca	360
tatgaccgct	acctggcaat	ttgctaccca	ctccactacc	cactcctgat	ggggcccaga	420
cggtacatgg	ggctgggtgg	cacaacctgg	ctctctggat	ttgtggtaga	tggactggtt	480
gtggccctgg	tggcccagct	gaggttctgt	ggccccaacc	acattgacca	gttttactgt	540
gactttatgc	ttttcgtggg	cctggcttgc	tggatccca	gagtggctca	ggtgacaact	600
ctcattctgt	ctgtgttctg	cctcactatt	ccttttggac	tgattctgac	atcttatgcc	660
agaattgtgg	tggcagtgtc	gagagtccct	gctggggcaa	gcaggagaag	ggctttctcc	720
acatgctcct	cccactagc	tgtagtgacc	acattctatg	gaacgctcat	gatcttttat	780
gttgacacct	ctgctgtcca	ttcccagctc	ctctccaagg	tcttctccct	gctctacact	840
gtggtcaccc	ctctcttcaa	tctgtgatc	tataccatga	ggaacaagga	ggtgcatcag	900
gcacttcgga	agattctctg	tatcaaacaa	actgaaacac	ttgat		945

<210> 957

<211> 565

<212> DNA

<213> Unknown (H38g807 nucleotide)

<220>

<223> Synthetic construct

<400> 957

cactggaaaa	ttttaagaag	aaacagcaag	atgatacatg	aaattatata	gaccttatgc	60
caaatacctt	actcagagga	caaaacttgt	tacatacaga	tacaaagctt	gtttgtact	120
gacttgga	tcccaaactt	tttctgtgaa	cttaattagg	tggccacct	tgctgttct	180
gacacctt	tcaaagacat	agtgaggtat	tgtacaacta	tgctgtgag	tgggtgtccc	240
attgctggta	tttttttact	ctttctctaa	gatcatttca	tccatatgtg	caatcccatc	300
agctcagggg	aagcataaag	catttccac	ctgcgtgtct	cacctctcaa	atatgtcctt	360
attttattgt	aggagcacag	gattgtacct	tagttttgct	gtaaccaca	actcatgctc	420
taatgaact	gcctcagtga	ggcacactgt	ggttaaaccc	ttactaaacg	ttttcatctt	480
aaagtcaagt	aataaagaca	taaaatgagc	tctgaaagta	ttcttcagag	gaaagcaatg	540
gaagcatcat	ttttcaaaaa	gtgca				565

<210> 958

<211> 939

<212> DNA

<213> Unknown (H38g808 nucleotide)

<220>

<223> Synthetic construct

<400> 958

atggaaaaaa	gaaatctaac	agttgtcagg	gaattcgtcc	ttctgggact	tcctagctca	60
gcagagcagc	agcacctcct	gtctgtgctc	tttctctgta	tgtatttagc	caccaccttg	120
gggaacatgc	tcatacttgc	gacgattggc	tttgactctc	acctccattc	ccctatgtac	180
ttcttccctta	gtaacttggc	ctttgttgac	atctgcttta	cgctcgactac	agtcccccaa	240
atggtagtga	atatcttgac	tggcaccaag	actatctctt	ttgcaggctg	cctcaccacag	300
ctcttcttct	tcgtttcttt	tgtgaatatg	gacagcctcc	ttctgtgtgt	gatggcgat	360
gatagatatg	tggcgatttg	ccaccctta	cattacaccg	ccagaatgaa	cctgtgcctt	420
tgtgtccagc	tagtggctgg	actgtggcct	gttacttacc	tccacgccct	cctgcatact	480
gtcctaatag	cacagctgtc	cttctgtgcc	tccaatatca	tccatcattt	cctctgtgat	540
ctcaatcctc	tectgcagct	ctctgtctct	gacgtctcct	tcaatgtaat	gatcattttt	600
gcagtaggcg	atctattggc	tctcacgccc	cttgtctgta	tctcgtatc	ttatggactt	660
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agcccttcat	ccccccatat	gcctgagagc	gacactctgt	caaccatcat	gtattcaatg	840
gtggctccga	tgctgaatcc	tttcatctat	accctaagga	acaggggat	gaagagggga	900
cttcagaaaa	tgcttctcaa	gtgcacagtc	tttcagcag			939

<210> 959

<211> 936

<212> DNA

<213> Unknown (H38g809 nucleotide)

<220>

<223> Synthetic construct

<400> 959

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cctgagcagc	agcagatcct	gttttggtatg	ttcctgtcca	tgtacctggt	cacggtggtg	120
ggaaatgtgc	tcatactcct	ggccatcagc	tctgattccc	gcctgcacac	ccccgtgtac	180
ttcttccctgg	ccaacctctc	cttcaactgac	ctcttctttg	tcaccaaacac	aatccccaa	240
atgctgggtga	acctccagtc	ccataacaaa	gccatctcct	atgcagggtg	tctgacgcag	300
ctctacttcc	tgggtctcctt	ggtggccctg	gacaacctca	tcctggctgt	gatggcatat	360
gaccgctatg	tggccatctg	ctgccccctc	cactacacca	cagccatgag	ccctaagctc	420
tgtatcttac	tcctttcctt	gtgttggtgc	ctatccgtcc	tctatggcct	catacacacc	480
ctcctcatga	ccagagtgc	cttctgtggg	tcacgaaaaa	tccactacat	cttctgtgag	540
atgtatgtat	tgtctgaggat	ggcatgttcc	aacattcaga	ttaatcacac	agtgtgtatt	600
gccacaggct	gcttcatctt	cctcattccc	tttggattcg	tgatcatttc	ctatgtgctg	660
attatcagag	ccatcctcag	aataccctca	gtctctaaga	aatacaaagc	cttctccacc	720
tgtgcctccc	atgtgggtgc	agtctccctc	ttctatggga	cactttgtat	ggtataccta	780

aagccccctcc	atacctactc	tgtgaaggac	tcagtagcca	cagtgatgta	tgctgtggtg	840
acacccatga	tgaatccctt	catctacagc	ctgaggaaca	aggacatgca	tggggctctg	900
ggaagactcc	tagataaaca	ctttaagagg	ctgaca			936

<210> 960

<211> 951

<212> DNA

<213> Unknown (H38g810 nucleotide)

<220>

<223> Synthetic construct

<400> 960

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tctgaagacc	agaggccact	ctttgcccct	tttcttatca	tatacctggg	cactttgatg	120
ggaaatctgc	tcatcatctt	ggctatccac	tctgatccct	gacttcaaaa	ccctatgtat	180
tttttcttaa	gcatcttgtc	ctttgctgat	atgtgctaca	caacagtcac	agtcccaaa	240
atgctcgtga	acttcttata	agagaaaaag	accatttctc	atgctgaatg	tctggcacag	300
atgtatttct	tcctgggttt	tggaacata	gatagttatc	tcctggcggc	tatggccatc	360
aaccgctgtg	tagccatttg	taacccattc	cattatgtca	ctgttatgaa	ccgcagatgc	420
tgtgtgttgc	tactagcatt	ccccatcaat	ttctcttatt	tccactctct	cctacatgtc	480
ctcctgggtg	atcggtcac	cttttgtaca	tcaaatgtta	tccatcattt	tttttgtgat	540
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acagaagggc	tggtctctgt	gatggctcca	tttgtctgta	tcatcatctc	ttatctaaga	660
attctcatcg	ctgttctcaa	gattccctca	gcagctggaa	aacacaaagc	cttctccacc	720
tgagctccc	atctcactgt	ggtagttctg	ttttatggga	gtattagcta	tgctctattg	780
cagcctttgt	ccagctatac	tgtcaaggac	cgaatagcaa	caatcaacta	cactgtgttg	840
acatcagtg	tgaacccatt	tatctacagt	ttaagaaaca	aagacatgaa	acggggctta	900
cagaaattga	taaacaagat	taagtctcaa	atgagtaggt	tctctacaaa	g	951

<210> 961

<211> 926

<212> DNA

<213> Unknown (H38g811 nucleotide)

<220>

<223> Synthetic construct

<400> 961

atgctgaata	caacctcagt	cactgaattt	ctccttttgg	gagtgcacaga	cattcaagaa	60
ctgcagcctt	ttctcttctg	tgttttcctt	accatctact	tcatcagtg	ggctgggaat	120
ggagccattc	tgatgattgt	catctctgat	cctagactcc	attccccat	gtattttctt	180
ctgggaaacc	tgctctgctt	ggacatctgc	tactccagcg	taacactgcc	aaaaatgctg	240
cagaacttcc	tctctgcaca	caaagcaatt	tctttcttgg	gatgcataag	ccaactccat	300
ttcttccact	tcctgggcag	cacagaggcc	atgttgttgg	ccgtgatggc	atttgaccgc	360
tttgtggcta	tttgcaagcc	acttcgctac	actgtcatta	tgaacccctc	gctctgtacc	420
cagatggcca	tcacaatctg	gatgattgg	tttttccatg	ccctgctgca	ctccctaatt	480
acctctcgct	tgaacttctg	tggttctaac	cgtatctatc	acttcttctg	tgatgtgaag	540
ccattgctaa	agctgagctt	aatcagtggc	tgctcagtac	tgctcacagg	acaatcgcca	600
tgggcccctt	ctttctcaca	ttactctcct	atttctacat	tatcacccat	ctcttcttca	660
agactcatte	ttttagcatg	ctccgcaaag	cactgtccac	ttgtgctccc	cacttcatgg	720
tagttattct	tttgtatgca	cctgttctct	tcacctatat	tcatcatgcc	tcagggaact	780
ccatggacca	ggaccggatc	actgccatca	tgtatactgt	ggctactcca	gtactaaacc	840
cactgatcta	cactttgagg	aacaaggaag	tgaaaggggc	ctttaataga	gcaatgaaaa	900
ggtggctttg	gcctaaagaa	atcttg				926

<210> 962

<211> 983

<212> DNA

<213> Unknown (H38g812 nucleotide)

<220>

<223> Synthetic construct

<400> 962

tcagtggacc	aagtaaata	ctctctggta	acagaatttg	tattacttgg	acttgcacaa	60
tccttggaaa	tgcagttttt	cctttttctc	ttcttctctt	tattctatgt	gggaattatc	120
ctgggaaacc	tcttcattgt	gttcacagtg	atctttgatc	ctcacttaca	ctcccccatg	180
tatattctgc	tggccaacct	atcgctcatt	gacttgagcc	tttcatctac	cacagttcct	240
aggttgatct	acgatctttt	tactgattgt	aaagtatttt	ccttccataa	ttgtatgata	300
caaaagttct	ttatccatgt	tacgggagga	gttgaaatgg	tgctgctgat	agtcattgaa	360
tatgataggt	acactgcat	ctgcaagcct	ctccactatc	caactattat	gaatcccaaa	420
atgtgcatgt	ttttggtagc	agcagcttgg	gtcattgggg	tgattcatgc	tatgtctcag	480
tttgtttttg	tcataaatta	accttctgtg	gccctaataa	tgtggggagc	ttttattgtg	540
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ctgccaacag	tggattcata	tcgatgggca	ccttcttttt	cttaattgta	tcatacattt	660
ttattctggg	cactgtccaa	cgacattcct	caaattgattt	atccaaagca	ttcttcactt	720
cgtaggctca	catcaccgta	gtggttttgt	tttttgctcc	atgcatgttt	ctctacgtgt	780
ggcctttccc	tactaagtca	ttggataaat	tttttgccat	catgaacttt	gttgtcacc	840
ctgtcttaaa	tcctgccatc	tatactttaa	ggaacaaaga	tatgaagttt	gcaatgagaa	900
ggctgaatca	acataattta	aattctatgg	agacgacata	acacatttgg	ttgatgagag	960
cacaggataa	atgccatgga	cca				983

<210> 963

<211> 817

<212> DNA

<213> Unknown (H38g813 nucleotide)

<220>

<223> Synthetic construct

<400> 963

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ccctggctag	agacacccct	ctgtaatctt	tctgggtggc	tacatctttt	ccctatttgg	120
aaatatctcc	attatcctag	tttcccatct	ggatccccag	cttgacagtc	ccatgtactt	180
ttttgtctct	aattctatct	ttctggacct	ctgctatacc	accagcactg	tcccacagat	240
gctgggtcaac	ctccggggac	cagaaaagac	catttagctat	gggggttggt	ttgcccact	300
ctatatattt	ttggccctgg	gttctactga	atgcatactt	ctagccatca	tggcctttga	360
ccgttacgct	gccatagca	agcccttca	ctaccagtc	atcatgaacc	atagacgctg	420
tatccacatg	gctgctggca	cttggatcag	tggctttgct	aactcccttg	tccagtccac	480
tctcacagtg	gtggccccaa	gatgtggaca	gaggggtgtg	gaccatttct	tctgtgaagt	540
tccagccctt	ttgaaactag	cctgtattga	tattcgtgtg	aatgaaatgg	agctcaatgt	600
actaggecgt	ttgcttctcc	tgatgccact	caccctcatc	ctgggcactt	atgtgttcat	660
tgctcaggca	gtaatgagaa	tctgctctgc	tgaaagtcgc	tgggaaggctt	tcaatacctg	720
tgcctcacat	ttgctggtgg	tctccctctt	ctacttcaca	gccatcagta	tgtatgtcca	780
gcctccctct	agctattctc	atgaccgggg	gaagatc			817

<210> 964

<211> 945

<212> DNA

<213> Unknown (H38g814 nucleotide)

<220>

<223> Synthetic construct

<400> 964

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ttctcttggt	agtggacaat	tcagatcttc	ctcttctcac	tctttactac	aacatattgca	120
ctgactataa	cagggaaatgg	agccatttgt	tttgctctgt	gggtgtgaccg	gcgacttcac	180
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acagttccca	agatgttggt	caacttccct	tcagagaaaa	aaaacatctc	ctttgctgga	300
tgttttctcc	agtttttattt	cttcttctct	ttgggtacat	cagaatgctt	gcttttgact	360

gtgatggcct	ttgatcagta	ccttgcctatc	tgccgtccct	tgctctatcc	taatatcatg	420
actgggcatac	tctatgcca	actgggcata	ctgtgctggg	tttgtggatt	tctgtgggtc	480
ctgatcccca	ttgttctcat	ctctcagatg	cccttctgtg	gcccacacat	tattgaccat	540
gttgtgtgtg	accaggggcc	acgatttgca	ttggattgtg	tttctgcccc	aagaatccaa	600
ctgttttctg	acactcctaag	ctcattagtt	atcttttggtg	acttcctctt	tattattgga	660
tcctatactc	ttgtcctgaa	agctatgttg	ggatgcctt	caagcactgg	gagacataag	720
gccttctcta	cctgtgggtc	tcatttggct	gtggatcac	tgtgctatag	ctctcttatg	780
gtcatgtatg	tgagcccagg	actcggacat	tctacaggga	tgagaaaaat	tgaaactttg	840
ttctatgcta	tggtgacccc	actcttcaat	ccccttatct	atagcctcca	gaataaggag	900
ataaaggcag	ccctgaggaa	agttctgggg	agttccaaca	taatc		945

<210> 965

<211> 915

<212> DNA

<213> Unknown (H38g815 nucleotide)

<220>

<223> Synthetic construct

<400> 965

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tttatgttgt	tttttgtatt	ctatggagga	atcgtgtttg	gaaaccttct	tattgtcata	120
acagtgggat	ctgactccca	ccttcactct	cccattgact	tcctgctagc	caacctctca	180
ctcattgata	tgtctctgtc	ttcagtcaca	gcccccaaga	tgattactga	ctttttcagc	240
cagcgcaaa	tcattctctt	caagggctgc	cttggttcaga	tatttctcct	tcacttcttt	300
gggtgggagt	agatgggtgat	cctcatagcc	atgggctatg	acagatatat	agcaatatgc	360
aaaccactaa	actacactac	aattatgtgt	ggcaacgcac	gtgtcggcat	tatggctgtc	420
gcatggggaa	ttggctttct	ccattcgggt	agccagttgg	cctttgccgt	gcacttaccc	480
ttctgtggtc	ccaatgaggt	cgatagtttt	tattgtgacc	ttcctagggt	aatcaaaact	540
gcctgtacag	atacctacag	gctagatatt	atggctcattg	ctaacagtgg	tgtgctcact	600
gtgtgtttct	ttgttcttct	aatcatctca	tacactatca	tcctaatagc	catccagcat	660
cgccctttag	ataagtcgtc	caaagctctg	tccactttga	ctgtctacac	tacagttagt	720
cttttgttct	ttggaccatg	tgtctttatt	tatgcctggc	cattccccat	caagtcatta	780
gataaattcc	ttgctgtatt	ttattctgtg	atcacccctc	tcttgaaccc	aattatatac	840
acactgagga	acaaagacat	gaagacggca	ataagacagc	tgagaaaaat	ggatgcacat	900
tctagtgtaa	agttt					915

<210> 966

<211> 953

<212> DNA

<213> Unknown (H38g816 nucleotide)

<220>

<223> Synthetic construct

<400> 966

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cccaactttc	agagttggca	gcacttgctg	tccttgcccc	tcagcctcat	ttcctcctgg	120
ccatggggac	caacacccac	cccccccatc	accatccacc	tgagggcctc	tctgcacctg	180
ccctgtact	acctgcccag	cctcctctcc	ctgctggaca	tcgtgctctg	cctcaccgtc	240
atccccagg	tcctggccat	cttctggttt	gatcttaggt	cgatcggtt	ccctgcctgc	300
ttccttcaga	tgttcatcat	gaacagtttc	ctccccatgg	agtcctgcac	attcatgggtc	360
aaggactatg	atcattatgt	ggccatctgc	caccactgc	agtacctgtc	catcatcact	420
catcaatttg	tggccaaagc	tagtgtcttc	atttgtgtgc	agaatgcttt	gctgctttca	480
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tacaccttca	ttctaagagc	tgtgcttaga	ttcaagggtg	aggggggtggc	agtgaaggcc	720
ctgagcacat	gtggctccca	ctttatectc	atcctcttct	tcagcacctg	ctggttgttg	780
tgttgacaaa	tgtggccaga	aagaaggtec	ccatggacat	cctgatcctg	tttaatgtcc	840
ttcatccctt	tagtctcct	gcattaaacc	ctatcatatg	tggatttcaa	actaaagagt	900

taaagaagga attttagaag ttgctgcaga ggggcctttg aaaacacgga agg

953

<210> 967

<211> 954

<212> DNA

<213> Unknown (H38g817 nucleotide)

<220>

<223> Synthetic construct

<400> 967

aaacacaatc	acacggcagt	gaccaagggtg	actgaattta	ttctcatggg	gattacagac	60
aaccctgggc	tgcaggctcc	actgttttga	ctcttctca	tcatatatct	ggtcacagt	120
ataggcaatc	tgggcatggg	tatctttgac	ctactttgga	ctccaagcta	cacaccccca	180
tgtacttttt	ccttaaacad	ttggcaatca	ctgatctttg	gttactccac	tgtcattggg	240
cccaaagat	gtttagtga	acctcatatg	tgcacaaaga	acacaatttc	ttttacaatt	300
ggtatgcaa	tcacagagca	cgttttgaga	ggaacatcat	ctctcacccg	ggcattctat	360
cagcaacgaa	caatgagccc	tacaaacca	tcactaaaca	acttctgaac	ccgatcatca	420
tgccagagaa	aatacgggag	gagcaataaa	ccgttcccga	gctcgataaa	acgtgtgcgc	480
cactatttct	caaaaggaag	tgagtcaaaa	cagtctccac	caaccacagac	acaaccaaca	540
attgtcacgg	tgaagggacc	gctaaaatgt	gaatactccg	ttctgaaaaa	aagaaaataa	600
caataataaa	ggcgatgacc	gcaggaaacc	aacatgctca	tctccctctc	aattgttctc	660
atatectaca	tgtttattct	agtggccaat	ctcagaatga	actcaaggaa	agggagggtac	720
aaagccttct	ccacctgtag	ctctcatctg	acagtgggtga	tcatgttcta	tgggacattg	780
ttattttatt	acttgcaacc	caagtccagt	catactttgg	ctattgataa	aatggcctca	840
gtgttttata	ccctgttgat	tcctatgctg	aatccgttga	tctacagcct	aaggaacaaa	900
gaagtaaaag	atgctctaaa	gagaacttta	accaatcgat	tcaaaattcc	catt	954

<210> 968

<211> 660

<212> DNA

<213> Unknown (H38g818 nucleotide)

<220>

<223> Synthetic construct

<400> 968

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gacatgcagt	ctcatagcag	agtcattccct	tatgcgggct	gcctgacacg	gatgtctttc	120
ttggctcctt	ttgcatgtat	agaagacatg	ctcctgactg	tgatggccta	tgactgcttt	180
gtagccatct	gtcgccctct	gcactacca	gtcatcatga	atcctcacct	ctgtgtcttc	240
ttcgtttttg	tgtccttttt	ccttagcctg	ttggattccc	agctgcacag	ttagattgtg	300
ttacaattca	ctttcttcag	taatgtggaa	attgctaatt	ttgtctatga	gccatctcaa	360
cttctcaacc	ttgactgttc	tgacaccgtc	atcaatagca	tatttatata	tttcgatagt	420
actgttttgt	tttcttccca	tttcagggat	cctttgtctt	agtataaaat	tgtcccctcc	480
attctaagga	tgatcatcgtc	agatgggaag	tataaagcct	tcgccacctg	tggtctctac	540
ctagcagttg	tttgctgatt	tgatggaaca	ggcattggca	tgtacctgac	ttcagctgtg	600
tcaccacccc	ccaggaatgg	tgtggcgggc	tcagtgatgt	acgtgtgggt	cacccccatg	660

<210> 969

<211> 933

<212> DNA

<213> Unknown (H38g819 nucleotide)

<220>

<223> Synthetic construct

<400> 969

atggaaaaaa	gcaataatag	cactttgttt	attctcttgg	ggttttccca	aaataagaac	60
attgaagtcc	tctgctttgt	attatttttg	ttttgctaca	ttgctatttg	gatgggaaac	120
ttactcataa	tgattttctat	cacgtgcacc	cagctcatcc	accaaccat	gtatttcttc	180

ctcaattacc	tctcactctc	cgacctttgc	tacacatcca	cagtgacccc	caaattaatg	240
gttgacttac	tggcagaaag	aaagaccatt	tcctataata	actgtatgat	acaactcttt	300
accacccatt	tttttggagg	catagagatc	ttcattctca	cagggatggc	ctatgaccgc	360
tatgtggcca	tttgcaagcc	cctgcactac	accattatta	tgagcaggca	aaagtgtaac	420
acaatcatca	tagtttggtg	tactggggga	tttatacatt	ctgccagtca	gtttcttctc	480
accatctttg	taccattttg	tggcccaa	gagatagatc	actacttctg	tgatgtgtat	540
cctttgctga	aattggcctg	ttctaata	cacatgatag	gtctcttagt	cattgtcta	600
tcaggcttaa	ttgctttggt	gacatttgtt	gtcttggtgt	tgtcttatgt	ttttatattg	660
tatacatca	gagcatactc	tgcagagaga	cgcagcaaag	ctcttgccac	ttgtagttct	720
catgtaattg	ttgtggctct	gttttttgct	cctgcattgt	tcatttacat	tagaccggtc	780
acaacattct	cagaagataa	agtgtttgcc	cttttttata	ccatcattgc	tcccattgtc	840
aacctctca	tatacacgct	gagaaacaca	gagatgaaga	acgccatgag	gaaagtgtgg	900
tgttgctaaa	tactcctgaa	aagaaatcaa	ctt			933

<210> 970

<211> 666

<212> DNA

<213> Unknown (H38g820 nucleotide)

<220>

<223> Synthetic construct

<400> 970

cggaacttct	ctttcttaga	aatctcattt	acaaccgtat	gcacccccag	atttctgggg	60
gcaattatca	ccaggaataa	gactattttc	tataacaact	gtgcagccca	actctttttc	120
tttatcttca	tgggggtgac	tgaattttac	attttaactg	ccatgtccta	tgaccgctat	180
gttgccatct	gcaagccctc	tcattacaca	tccatcatga	acaggaaact	ctgcactcta	240
cttggtgctg	gtgcctggct	aagtgggttt	cgcaccattt	tcccaccctc	tatgtctctc	300
ctccagctgg	actactgtgc	ttccaacgtc	attgatcact	ttgcatgtga	ctattttccc	360
ctcttacaac	tatcttggtc	agatacatgg	ctcctagaag	taattgggtt	ttactttgct	420
ttggttactt	tgctgttcac	tttggcatta	gtgattttat	cttacatgta	cattatcagg	480
accattttga	gaatcccgtc	tgccagtc	agaaaaaagg	ctttctccac	ttgttcttct	540
cacatgattg	tcattttccat	ttcttatgga	agctgtatat	tcatgtatgc	taatccatct	600
gcaaaagaaa	aggcatcatt	gacaaaagga	atagctattc	tcaatacatc	tgttgccccc	660
atgctg						666

<210> 971

<211> 799

<212> DNA

<213> Unknown (H38g821 nucleotide)

<220>

<223> Synthetic construct

<400> 971

ataattttgt	gttttttcat	cataggtaac	tctcaggata	attcccaa	gactttgatg	60
gataacattt	cagaagtga	agaattcg	ctcgtgggt	taacagatg	cctagagctt	120
caggtccctt	tatttatcat	ctttactgtc	atttatctca	ccactctggt	tgggaacttt	180
gggatgatca	tgttgattct	gttggaactc	cggctccaca	ttcccatgta	ctttttcctt	240
ggcaaaactc	ctctgggtga	cagtgtttgt	cctgctagtc	actggctcct	acatctgtgg	300
actctttcaa	tccctcatcc	atgttgcttt	tactttccat	ctctccttct	gtcattctaa	360
tgtgggtta	cacttttttt	gtgatattcc	accactctta	gctctttctt	gctctgat	420
ttacgcacat	gagattgtgc	tcttcatatt	ggcagcattt	aatatctttt	tcactctctt	480
gattatcttg	aactcttatg	tttttatttt	tatttgctatc	ctgaggatgc	attcagctga	540
gggacaaaag	aaggtctttt	ccacctgtgc	ctatcacctc	actactgttt	ccatcttcta	600
tgggacaate	acctttatgt	acttacagcc	aagttctggt	cattccatgg	acacagacaa	660
aatctcatct	gtgttctaca	ccatggtc	ccccatgctt	aacctcttag	tctatagcct	720
gaggaacaaa	gaagtccaga	gtgcattcaa	ggtggttatt	ggaaaagcaa	agtcttcatt	780
gggcttagcc	tactatttta					799

<210> 972

<211> 946
 <212> DNA
 <213> Unknown (H38g822 nucleotide)

<220>
 <223> Synthetic construct

<400> 972

tggtaacctg	tcttcaacca	gtctgcccc	ctgagtttgt	gttccgtgtg	ttcaccacag	60
tccctgaatt	tcagggttctt	ctcttccttc	tcttcctcct	cttctacttg	atgatectct	120
gtggcaacac	agccatcatc	tgggttgtgt	gcacatacag	cgttctccga	accccaatgt	180
atttcttctt	gtccaacctg	tcctttgtag	agatctgcta	caccaccgtt	gtgggtgccct	240
tgatgcttcc	caacattttt	ggggcccaga	agcccatgcc	attggctgga	tgtggggccc	300
aaatgttctt	ctttctcaca	cttgggtggtg	ctgactgttt	cctcttggcg	atcgtggcct	360
atgaccgcta	tgtggccatc	tgccaccctt	tgcactaccc	ctcatcatga	cctgcaatct	420
gtgctgagag	atgctgggag	gcgctgtggg	cctggccctc	ttcctctccc	tgcagctcac	480
cgccttaata	ttcaccttgc	ccttctgcgg	ctaccgccag	gaaattaacc	acttctctctg	540
cgatgtacct	ccgctcctgc	gcctggcctg	cgtgcctatc	cgtgttcacc	aggctgtcct	600
ctatgtcgtg	agcatcctcg	tgtgaccgt	ccccttcttg	ctcatctgcg	tctcctacgt	660
gttcatcacc	tgtgccatcc	tgagcatccg	ttctgtctgag	ggcgcgccacc	aggccttctc	720
cacctgctcc	tcccacctca	ccgtggctct	gctgcagtat	ggctgctgtg	ccttggcata	780
cttgcacccc	cagtccagct	cctctgcaga	tgaggatcgc	cagtttgccc	ttgtttacac	840
ctttatcaca	ccattactca	accctttgat	ttacaccctt	aggaacaagg	atgtcaaagg	900
tgcccttgaa	aaaagtgtc	agtaccaaag	ggacacctga	gtcctt		946

<210> 973
 <211> 936
 <212> DNA
 <213> Unknown (H38g823 nucleotide)

<220>
 <223> Synthetic construct

<400> 973

atgtagaaca	gtagagaggc	gtcacagttc	atcttcctag	gactaagcaa	tgtcccagaa	60
ctgcagggtcc	ccttcttttat	catgtttgtt	ctcatctatc	tcataaatgt	agttggaaac	120
ttggggatga	tcattttgat	tctctgggtac	tctcagctcc	acaatccaat	gtacttcttc	180
ttcagtaata	tgtctctggt	agactttttt	tactcttcag	ttgtcactcc	aaaggctcatg	240
actgggctcc	ttagagaaga	caaaatcatt	tcctatactg	tgtgggctac	tcagacattc	300
ttttctgatt	cctttgccag	tgtggtaaat	ttattattgg	ccttaatggc	ctctggccac	360
tatgcagcag	tgtgcaaacc	cctgcattac	accaccacca	tgatgacaag	tgtgtgtaca	420
tgtctggcca	taggttgata	cgttggtggt	ttcctgaatg	cctccattca	cactggggaa	480
acattcagtc	tctttctgta	tgtccagtga	agtcacatc	ttttctctgtg	aggttccagc	540
agtcatggct	ctgtcttgct	ctgatagaca	tgtgaatgta	gtgggttcttg	tttatgtaac	600
cagctcaata	tctcttttgc	ccttctagtt	atcttgatat	cctacttatt	gatgtttatc	660
accatcctaa	agatgcactc	aactgcagga	taccagaagg	ctttggccat	ttgtgcctct	720
cacctcactg	cagttgccat	cttctatggg	actattatct	tcatgcatat	acagcccagc	780
tccagtcatt	ccattgacac	agacaaaatt	gcagctgtgt	tttatactat	tgtcttcccc	840
atggtgaacc	atgtggtcta	aagattgaag	aacaagggtga	agagtacatt	caagaaaatt	900
gttgagaagg	taaaattgtc	cctaggattg	tgagtt			936

<210> 974
 <211> 954
 <212> DNA
 <213> Unknown (H38g824 nucleotide)

<220>
 <223> Synthetic construct

<221> misc_feature
 <222> (1)...(954)

<223> n = A,T,C or G

<400> 974

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aaggccctgc	agggccccct	gttctgggtg	gtgcttctgg	tctacctggt	caccttgctg	120
ggtaactccc	tgatcatect	cctcacacag	gtcagccctg	ccctgcactc	ccccatgtac	180
ttcttctgc	gccaactctc	agtgggtggag	ctcttctaca	ccactgacat	cgtgcccagg	240
acctggcca	atctgggctc	cccgcatccc	caggccatct	ctttccaggg	ctgtgcagcc	300
cagatgtacg	cttctattgt	cctgggcac	tcggagtgt	gcctgtcac	ggccatggcc	360
tatgaccgat	atgttgccat	ctgccagccc	ctacgctatt	ccacctctt	gagcccacgg	420
gcctgcatgg	ccatgggtggg	tacctctgg	ctcacaggca	tcatacggg	ccaccacca	480
tgcctcectc	atcttctctc	tacctttctg	cagccaccgg	atcatccgc	actttctctg	540
tgacatectg	ccagtactga	ggctggcaag	tgctgggaag	cacaggagcg	agatctccgt	600
gatgacagcc	accatagtct	tcattatgat	ccccctctct	ctgattgtca	cctcttacat	660
ccgcatectg	ggtgccaatc	tagcaatggg	cctcaccacg	agccgccgca	agtcttctcc	720
acctgtctct	cccataggct	cgtggtctct	ctcttctttg	ggacagccag	catcacnnac	780
aaccggccgc	aggcaggctc	ctctgaaacc	acagaccgcg	tcatacgtct	cttcnacaca	840
gtcatcacac	ccatgtctca	ccccatcata	aacaccacag	ggaacaagga	cgtgaggagg	900
gccctgcggt	acttggtgaa	gaggcggcgc	ccctcgccgg	gaaggggctc	gggt	954

<210> 975

<211> 933

<212> DNA

<213> Unknown (H38g825 nucleotide)

<220>

<223> Synthetic construct

<400> 975

atggagacaa	agaattatag	cagcagcacc	tcaggcttca	tctctctggg	cctctcttcc	60
aaccctaagc	tgcagaaacc	tctctttgcc	atcttctca	tcatagtacct	actcactgcg	120
gtggggaatg	tgctcatcat	cctggccatc	tactctgacc	ccaggctcca	caccctatg	180
tacttttttc	tcagcaactt	gtctttcatg	gatattctgt	tcacaacagt	catagtgcct	240
aagatgctgg	tgaattttct	atcagagaca	aagattatct	cttatgtggg	ctgcctgatc	300
cagatgtact	tcttcatggc	atttgggaac	actgacagct	acctgctggc	ctctatggcc	360
atcgaccggc	tggtggccat	ctgcaacccc	ttacactatg	atgtggttat	gaaaccatgg	420
cattggcctac	tcatagtatt	gggttcttgc	agcatctccc	acctacattc	cctgttccgc	480
gtgctactta	tgtctcgtt	gtctttctgt	gcctctcaca	tcattaagca	ctttttctgt	540
gacacccagc	ctgtgctaaa	gctctctgc	tctgacacat	cctccagcca	gatgggtgtg	600
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tttaggcctc	tgtccatgta	ctcagtgatg	aagggccggg	tagccacagt	tatgtacaca	840
gtagtgcac	ccatgctgaa	ccctttcatc	tacagcctga	ggaacaaaga	tatgaaaagg	900
ggtttgaaga	aattaagaca	cagaatttac	tca			933

<210> 976

<211> 390

<212> DNA

<213> Unknown (H38g826 nucleotide)

<220>

<223> Synthetic construct

<400> 976

atgaaaaata	aaaccgtggt	aactgagttt	atccttctgg	gtctaacaga	tgtccctgaa	60
ctccagggtg	cagttttcac	ctttcttttc	cttgcgattt	tactcagcat	ccttggaat	120
ctgactatcc	tcatactcac	cttgctggac	tcccaccttc	agactcccat	gtatttcttt	180
ctccggaact	tctccttctt	ggaaatttcc	ttcacaaaca	tcttcattcc	aagggtcctg	240
attagcatca	caacagggaa	caagagtatc	agctttgctg	gctgcttcac	tcagtatttc	300
tttgccatgt	tccttggggc	tacagagttt	taccttctgc	tgccatttct	atgaccgcta	360

tgtgccatct gcaaactgat gactatgcac

390

<210> 977

<211> 933

<212> DNA

<213> Unknown (H38g827 nucleotide)

<220>

<223> Synthetic construct

<400> 977

atggagataa	agaactacag	cagcagcacc	tcaggcttca	tcctcctggg	cctctcttcc	60
aaccctcagc	tgcagaaacc	tctctttgcc	atcttctcca	tcattgtacct	gctcgtgcg	120
gtggggaatg	tgctcatcat	cccggccatc	tactctgacc	ccaggctcca	caccctatg	180
tacttttttc	tcagcaactt	gtctttcatg	gatatctgct	tcacaacagt	catagtgcct	240
aagatgctgg	tgaattttct	atcagagaca	aaggttatct	cctatgtggg	ctgcctggcc	300
catagtgtact	tctttatggc	atttggggaa	actgacagct	acctgctggc	ctctatggcc	360
atcgaccggc	tggtggccat	ctgcaacccc	ttacactatg	atgtgggttat	gaaaccacgg	420
cattgcctgc	tcattgctatt	gggttcttgc	agcatctccc	acctacattc	cctgttccgc	480
gtgctactta	tgtctcgctt	gtctttctgt	gcctctcaca	tcattaagca	ctttttctgt	540
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gtagtgacac	ccatgctgaa	ccctttcatc	tacagcctga	ggaacaaaga	tatgaagagg	900
ggtttgaaga	aattacagga	cagaattttac	cggttgaaga			933

<210> 978

<211> 939

<212> DNA

<213> Unknown (H38g828 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(939)

<223> n = A,T,C or G

<400> 978

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ggaacctgaa	tcattcatcag	ccatgacctt	gctggacacc	cgcattgcaga	catctatgta	180
cttattttctc	cagaatctgt	cctgcttaga	aatttgttcc	agacagtcat	cgtgcccacg	240
atgctgctca	acattgccat	ggggaccaag	accgttagct	ttgctgggtg	cattaccacg	300
gactttttcc	acattcttctg	ggggccacag	agttcttctc	cctgacagcc	atggcctatg	360
accagtatat	tgccatctgc	aagccctctc	actaccccat	gctcataagt	agtagagtct	420
gcacacagct	catctctcacc	tgctggctac	taggtttctc	cttcatcatc	atgcctgtca	480
tcctgaccag	tcagcttcca	ttctgtgata	cccacatcaa	gcatttcttc	tgtgactaca	540
cgcctctaata	ggaggtgggtc	tgcagtgggc	caaagtggtc	ggagatgggtg	gattttaccc	600
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tccagacaat	tgtcagaatc	cccgtgttcc	aggagaggaa	gaaggctttc	tctacctgtt	720
cctctcatgt	cattatgggtt	accatgtgtt	atgacagctg	cttctttatg	tatgtcaagc	780
cctctccagg	aaagtgggtt	gatgtcaaca	angggagtgt	ctctaataca	tacaattatt	840
gccccactgt	taaatccctt	catctgtact	ctgaggaacc	aacaagttaa	gcaggtaatg	900
aaagacctag	tcagaaaaat	gactttgtcc	gaaaataaa			939

<210> 979

<211> 951

<212> DNA

<213> Unknown (H38g829 nucleotide)

<220>

<223> Synthetic construct

<400> 979

atgaactcag	agaacctcac	ccggggccgcg	gttgcccctg	ctgaattcgt	actcctgggc	60
atcacaaatc	gctgggacct	gcgtgtggcc	ctcttcctga	cctgcctgcc	tgtctacctg	120
gtgagcctgc	tgggaaacat	gggcatggcg	ctgctgatcc	gcattggatgc	ccggctccac	180
acacctatgt	acttcttcc	ggccaacctc	tccctgctgg	atgcctgcta	ttcctccgcc	240
atcgccccca	agatgctagt	ggacctgctg	ctgccccgag	ccaccatccc	ttacaacagcc	300
tgtgccctcc	agatgtttgt	ctttgcaggt	ctggctgata	ctgagtgttg	cttgctggca	360
gccatggcct	atgaccgcta	cgtggccatc	agaaacccac	ttctctatac	aacagctatg	420
tcgcagcgtc	tatgcctggc	cttgctggga	gcattcaggcc	tgggtggggc	agtgagtggc	480
tttgttcaca	caacctcac	cttccgcctg	agcttctgcc	gctcccggaa	gatcaatagc	540
ttcttctcgc	atataccctc	actgctggcc	atctcgtgca	gtgacaccag	tctcaatgaa	600
ctccttctct	tcgccatctg	tggcttcac	cagacagcca	cgggtgttagc	tatcacgggtg	660
tcttatggct	tcacgctgg	ggctgtgate	cacatgcgct	cggctcgaggg	cagtcggcga	720
gcagcctcca	ccgggtggtc	ccacctcaca	gccgtggcca	tgatgtacgg	gacactcatt	780
ttcatgtacc	tgcgccccag	ctccagctat	gccctggaca	ctgacaagat	ggcctctgtg	840
ttctataccc	tggtcacccc	gtctctcaac	ccactcatct	acagcctccg	caataaggag	900
gtcaaggagg	ccctcaggca	gacctggagc	cgattccact	gtccagggca	g	951

<210> 980

<211> 948

<212> DNA

<213> Unknown (H38g830 nucleotide)

<220>

<223> Synthetic construct

<400> 980

atgggtgatcc	tgtcctggga	aaaccaaacg	atgagagtgg	aattcgtgct	tcaaggattc	60
tcttccatca	gacagttaaa	tattttcctc	tttatgataa	ttttagtttt	ctacatctta	120
actgtttctg	gaaacatect	cattgtcctt	ctagttttag	tcagacatca	tctccacacc	180
cctatgtact	tcctcctggg	gaacttgtcc	tgtctggaga	tctggtatac	ctctaaccatc	240
atccccaaaa	tgttgcctgat	tatcataget	gaatagaaga	ctatctctgt	ggctggctgg	300
ctggcacaat	tctaattctt	cggatccctg	gctgccacgg	agtgcctctt	gctcactgtg	360
atgtcctatg	atcgtacct	agccatctgc	cagcctcttt	gctaccgtgt	cctcatgact	420
ggcccccttt	gcattcaggct	agctgctggc	tcttggttct	gctgcttctt	ccttacagca	480
atcaccatgg	tcttgctatg	tagactaacc	ttctgtggac	cctatgaaac	tgatcacttc	540
ttttgtgact	tcacccctct	ggttcatctc	tcctgcatgg	atacctcagt	gactgagacc	600
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tactcctgcg	tcctttctgc	tatcctaaga	atcccatctt	gcacaggcca	gaaaaaggcc	720
ttctccacct	gctcttccca	cctcactgtg	gtcatagtgt	tttatgggac	actgattgcc	780
acataccttg	tgcctcagc	caactcatcc	caactcttgt	gcaaagggtc	ctctctgctc	840
tacatcatcc	tgacacccat	gtttaacccc	atcatttata	gcctgagaaa	tagagacatc	900
catgaagctc	tgaagaagtg	cttgaggaag	aagtcagggtg	tttgcctt		948

<210> 981

<211> 925

<212> DNA

<213> Unknown (H38g831 nucleotide)

<220>

<223> Synthetic construct

<400> 981

gagtaaatgg	gaacaagtaa	taatgttaca	gaatttgtcc	tcccaggcct	ctctcaggat	60
cctgatgtgc	aaaaagcatt	atttghtaatg	tttttactca	catacaatgt	gactatgggtg	120
ggcaaccttc	tcattgtggg	gaccattatt	gccatgcct	ccttgggactc	cccagtgtcc	180

ttcttctctcg	catgcctgtc	atattattgat	gctgtatatt	ccacttcctt	ttccccctaag	240
ttgatgatag	acttactctg	tgataaaaaa	gactgtttct	ttcctggctt	gcatgggcca	300
gctatttata	aactacccat	ttgggtggtat	tgaggctctt	cttttggtgg	gtatggcctg	360
tgatcactat	gtggacatct	gtaagctact	gcactatttg	accatcatga	actggcaggt	420
ttgcatcctc	ctgtttatgg	tggtctgtgac	tgagggtttt	tgcattctat	gtttcaaatt	480
gttgttgtgt	acagtctccc	tttctgtggc	cccaatgtca	ttgaccattt	tgtgacatgt	540
accattattt	ggaaatgggtg	tgacttgaca	cttactttat	aggcctcact	gtgattgcca	600
atgggtggagc	agtctgtatg	gtcatcttca	tccttctact	aatctcctat	ggagtcaccc	660
taaactccct	taaaacttat	agtcaggaag	gcgggcataa	agccctgtct	acctgcagct	720
ccaacattac	tggtgtgtcc	ccttttttga	tcctgtattt	ttcatctatg	ttagacctga	780
ttcaaaacttt	cctattgata	aattcatgac	tgtgttttat	acaattatca	cacctatgtt	840
gaatccatta	atatacacac	tgagaaattt	agagggtgaga	attgctgtga	aaaatctctg	900
gtgtaaaaac	taaactatag	taaga				925

<210> 982

<211> 958

<212> DNA

<213> Unknown (H38g832 nucleotide)

<220>

<223> Synthetic construct

<400> 982

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tgaggatgac	atccttttct	tttttggttc	ttctctgtgt	tctacatggg	aattatcctg	120
gaaaatctct	tcatttgtgt	cacagtaatt	attgactctc	atttaaattc	cccagggtact	180
gcctactggc	caacattttat	cttcttgatc	tggtgtctct	cctacagttc	tgactttttc	240
actaactgca	gcatcatttc	ttttccaaga	tgcatgatac	agatattttt	catttgtgtc	300
atgctgtaaaa	attgagatgg	tgctgctcat	aaccatggca	tagagcaggt	acactgcca	360
tctgtaagcc	tccccattac	ctgaccacaa	tgaaccccaa	aatgtgtgtt	tactttgttg	420
gaggcatcct	ggatagtcag	gataatccat	gctgtatctc	agtttgtttt	tgccataaac	480
ttgccttttt	gtggccctaa	tagagtaggt	agttttcact	gtgattttcc	ttatgtcatg	540
aaacttgctt	gtgtagacac	ttacaaacta	gagggtgtag	tcactgctaa	cagtgggctt	600
atatccatag	ctacctgttt	cttattaata	atatcctata	ttttcatttc	ggtaaccgtc	660
tagaatcctt	cttcaggaga	cttatctaaa	gcatttgtgt	catgttagat	cacatcacag	720
tagggatttt	gttttttatg	ccatgtatat	ttctctatgt	gtagcctttg	cctaaaacaa	780
cacatgatta	atatttgttc	attgttcctt	ttgctatcac	ccctgtctag	gatctacaca	840
ttaagaaaca	aagacatgaa	cgtctccatg	gaaagactgg	gaaaatggat	tgagggttct	900
agcaggatgt	cataataaat	ggtgcataac	cagagtgcac	gatgattcag	tctcacca	958

<210> 983

<211> 927

<212> DNA

<213> Unknown (H38g833 nucleotide)

<220>

<223> Synthetic construct

<400> 983

atggaaggaa	taaataaaaac	tgcaaagatg	cagtttttct	ttcgtccatt	ctcacctgac	60
cctgagggtcc	agatgctgat	ttttgtgggc	ttcctgatga	tgtatctgac	cagcctcggt	120
ggaaatgcta	caattgcagt	cattgttcag	atcaatcatt	ccctccacac	ccccatgtac	180
tttttctctg	ctaactcttc	agttctagaa	atcttctata	catcttccat	caccccatgt	240
gccttgggcaa	acctcctttc	aatgggcaaa	actcctgttt	ccatcacggg	atgtggcacc	300
cagatgtttt	tctttgtctt	cttgggtggg	gctgattgtg	tcctgctggg	agtcattggc	360
tatgaccggg	ttatagcgat	ctgtcaccct	ctgcgataca	ggctcatcat	gagctgggtc	420
ttgtgtgtgg	agctgctggg	aggtcctttg	gtgctggggg	tcctgttggt	actgccactc	480
accatttttaa	tcttccatct	cccattctgc	cacaatgatg	agatctacca	cttctactgt	540
gacatgcctg	cagtcatgcg	cctggcttgt	gcagacacac	gcgttcacaa	gactgctctg	600
tatatcatca	gcttcatcgt	ccttagcatc	ccccctctcat	tgatctccat	ctcctatgtc	660
ttcatcgtgg	tagccatttt	acggatccgg	tcagcagaag	ggcgccagca	agcctactct	720

acctgctctt	ctcacatctt	agtggctctc	ctgcagtatg	gctgcaccag	ctttatatac	780
ttgtccccc	gttccagcta	ctctcctgag	atggggcggg	tggtatctgt	ggcctacaca	840
tttatcactc	ccattttaaa	ccccttgatc	tatagtttga	ggaacaagga	actgaaagat	900
gccctaagga	aagcattgag	aaaattc				927

<210> 984

<211> 987

<212> DNA

<213> Unknown (H38g834 nucleotide)

<220>

<223> Synthetic construct

<400> 984

gattcagtg	accaagtaaa	tgactctctg	gtaacagaat	ttgtattact	tggaacttgca	60
caatccttg	aaatgcagtt	tttccttttt	ctcttcttct	ctttattcta	tgtgggaatt	120
atcctggga	acctcttcat	tgtgttcaca	gtgatctttg	atcctcactt	acactccccc	180
atgtatatc	tgctggccaa	cctatcgctc	attgacttga	gcctttcatc	taccacagtt	240
cctaggttg	tctacgatct	ttttactgat	tgtaaagtta	tttccttcca	taattgtatg	300
atacaaaagt	tctttatcca	tgttacggga	ggagttgaaa	tggtgctgct	gatagtcatg	360
gcatatgata	ggtacactgc	gatctgcaaa	cctctccact	atccaactat	tatgaatccc	420
aaaatgtgca	tgtttttggg	agcagcagct	tgggtcattg	gggtgattca	tgctatgtct	480
cagtttgttt	ttgtcataaa	tttacccttc	tgtggcccta	ataatgtggg	gagcttttat	540
tgtgattttc	ctcgggttat	taaacttgca	tgcatggaca	cttatgggct	agaatttgtg	600
gtcactgcca	acagtggatt	catatcgatg	ggcaccttct	ttttcttaat	tgtatcatac	660
atttttatc	tggtcactgt	ccaacgacat	tcctcaaagt	atttatccaa	agcattcttc	720
acttcgtagg	ctcacatcac	cgtagtggtt	ttgttttttg	ctccatgcat	gtttctctac	780
gtgtggcctt	tcctactata	gtcattggat	aaattttttg	ccatcatgaa	ctttgttgtc	840
accctgtctt	taaactcctg	catctatact	ttaaggaaca	aagatatgaa	gtttgcaatg	900
agaaggctga	atcaacatat	tttaaattct	atggagatga	cataacacat	ttggttgatg	960
agagcacagg	ataaatgcc	tggaacca				987

<210> 985

<211> 770

<212> DNA

<213> Unknown (H38g835 nucleotide)

<220>

<223> Synthetic construct

<400> 985

tccatgtact	tcttctctgac	aaactttgca	ggctctggaga	tcttctactt	tttcaccatt	60
gccccctctga	ctctggccaa	tgctctaccc	atggggagaa	acctcatttc	cctgcccggc	120
tgtggaggcc	agatgttctt	cttcatcttc	ctgggaaggg	ctgactgcat	cctgctggcc	180
gtcatggcct	ttgactgggt	tgtggccatc	tgttgctctc	tctgttacgg	cctcatcatg	240
agctggagggt	tgtgtgtcca	gctgaccctg	gggtctctgc	tgttgggggt	cttcttagcc	300
atgcagctga	cctgtcttat	cttccaactc	cctttatgca	gcagcaaaga	aatcagcacg	360
ttctactgtg	atgtctctcc	tgctcatgaga	ctggcctgtg	cagataacctg	ggtccatgag	420
gccactatgt	ctatggtcag	caccaccttt	ctcaccgtcc	ccttctctgt	catcactctt	480
tcctatgtct	ccatcatggc	cgccatcttg	aagatttget	ctgcagaggg	gaggcacaag	540
gccttctcca	cctttctctc	cacctgactg	tggttctcct	ccaggactga	tgtacacgcc	600
tcgccttctt	gtgtccagc	tctagctact	atcctgagag	gggccaggca	gtgtctgttg	660
tttacacctt	cattaccctt	gtgtgaacc	ctttgatcta	cagcatgagg	aacacagaac	720
ttaaggatgc	tttgaagaga	gcaatgacga	gggtcccgtc	gctctaaaca		770

<210> 986

<211> 915

<212> DNA

<213> Unknown (H38g836 nucleotide)

<220>

<223> Synthetic construct

<400> 986

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tttatgttgt	tttttgtatt	ctatggagga	atcgtgtttg	gaaaccttct	tattgtcata	120
acagtgggtat	ctgactccca	ccttcactct	cccatgtact	tcctgctagc	caacctctca	180
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ggtgggagtg	agatgggtgat	cctcatagcc	atgggctttg	acagatatat	agcaatatgc	360
aaacccctac	actacactac	aattatgtgt	ggcaacgcat	gtgtcggcat	tatggctgtc	420
gcatggggaa	ttggctttct	ccattcgggtg	agccagttgg	cctttgccgt	gcacttaccc	480
ttctgtggtc	ccaatgaggt	cgatagtttt	tattgtgacc	ttcctagggg	aatcaaaactt	540
gcctgtacag	atacctacag	gctagatatt	atggtcattg	ctaacagtgg	tgtgctcact	600
gtgtgttctt	ttgttcttct	aatcatctca	tacactatca	tcctaattgac	catccagcat	660
tgcccttttag	ataagtcgtc	caaagctctg	tccactttga	ctgctcacat	tacagttagt	720
cttttgttct	ttggaccatg	tgtctttatt	tatgcctggc	cattccccat	caagtcatta	780
gataaattcc	ttgctgtatt	ttattctgtg	atcacccctc	tcttgaaccc	aattatatac	840
acactgagga	acaaagacat	gaagacggca	ataagacggc	tgagaaaatg	ggatgcacat	900
tctagtgtaa	agttt					915

<210> 987

<211> 958

<212> DNA

<213> Unknown (H38g837 nucleotide)

<220>

<223> Synthetic construct

<400> 987

atggatagag	taaataattc	tgcggtatct	aaatttgtat	tgattggact	ttcaagctct	60
tgggagatgc	atctttttct	tttttgggtc	ttctctgtgt	tctacatggg	aattatcctg	120
gaaaatctct	tcatttgtgt	cacagtaatt	attgactctc	atttaaattc	cccagggtact	180
gcctactggc	caacatttat	cttcttgatc	tgggtcttct	cctacagtcc	tgactttttc	240
actaactgca	gcattcattc	ttttccaaga	tgcatgatac	agataatttt	catttgtgtc	300
atgcgtaaaa	attgagatgg	tgtgtctcat	aaccatggca	tagagcaggt	acactgccaa	360
tctgtaagcc	tccccattac	ctgaccacaa	tgaaccccaa	aatgtgtgtt	tcctttgttg	420
gaggcatcct	ggatagtcag	gataatccat	gctgtatctc	agtttgtttt	tgccataaac	480
ttgccttttt	gtggccctaa	tagagttagt	agttttcact	gtgattttcc	ttatgtcatg	540
aaacttgctt	gtgtagatac	ttacaaacta	gaggttgtag	tcactgctaa	cagtgggctt	600
atatccatag	ctacctgttt	cttattaata	atatccata	ttttcatttc	ggtaaccgtc	660
tagaatcctt	cttcaggaga	cttatctaaa	gcatttgtgt	catgttagat	cacatcacag	720
tagggatttt	gttttttatg	ccatgtatat	ttctctatgt	gtagcctttg	cctaaaacaa	780
cacatgatta	atatttggtc	attgttcctt	ttgtctacac	ccctgtctag	gatctacaca	840
ttaagaaaca	aagacatgaa	cgtctccatg	gaaagactgg	gaaaatggat	tgcagggtct	900
agcaggatgt	cataataaat	ggtgcataat	cagagtgcac	gatgattcag	tctcacca	958

<210> 988

<211> 982

<212> DNA

<213> Unknown (H38g838 nucleotide)

<220>

<223> Synthetic construct

<400> 988

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gaacaaaata	atggcactga	agtgcactgaa	ttcattctcc	tgggatttgc	tgggtcaacac	120
aagtcttggc	atattcctctc	catagcattt	ctagcaatct	atgtgggttac	cccagtaggt	180
aatattggaa	tgatcctact	tatcaaaatt	gatgtctctc	ttcatatccc	catgtaaatt	240
ttcctccaac	acttggcatt	tgttgatctc	tgttacacct	ctgctatcac	tcccaagatg	300
ttgaaaaact	ttgtagaaac	aaaaaaatct	atctcatgta	taggatgtat	ggtgcaatta	360

ctagtttatg	gtactttgca	acaagtgact	gctacatcct	ggctgctatg	gcagtagacc	420
gttatgtggc	cttctgtaac	ccactccatt	atccaggggt	tatgtcccag	agactctgca	480
ttaagctatt	agtttagttca	tatgtcatgg	gtttcctaaa	tgcctctata	aacataagtt	540
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ctccaattat	tgccttacca	tgtcctaata	ttgacctcaa	catcatgtta	ttaacagtat	660
ttgtgggatt	aaatttgatg	tgcactgtga	tgggtggcat	catttcctgc	atatatgtcc	720
tggttgccat	cctgaggata	tcttctgctg	caggggaagaa	aaaagtctct	ctacatgtgc	780
ctcccacctg	acagcagtc	ccattttcta	tggggttctc	tcttacatgt	atctatgcc	840
tcgtattaat	gagtcctaaa	aacaagaaaa	agtggcctct	gtgttttatg	gcattattat	900
tcccatgtta	aaccccttga	tttacagcca	gagaaaccaa	gatgtgattg	aagccataaa	960
actaacagaa	aaaaagtatt	tc				982

<210> 989

<211> 1006

<212> DNA

<213> Unknown (H38g839 nucleotide)

<220>

<223> Synthetic construct

<400> 989

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ttccacttcc	acttcttttc	aacagacctg	gtgggtggctt	cctttataat	tgtggccttg	120
atgttgacc	aagaagcctt	gttgacact	tcacctttgg	gcccacagtc	tggcaagatc	180
ccttctctca	tattccaatg	tatttatatt	tatttttttg	gcattgacta	tgttggaat	240
tggctactcc	accaacattt	ctctctcaac	actggctacc	gtcctttaca	tggggaagat	300
gcttatctcc	ctccctggct	atggaactca	gatgctcttt	gtcatccttt	tgagaggatc	360
tgagtgtgtc	ttgcttgctg	tcatggctta	tgataggtat	ataaccatct	gtcatccatt	420
caattacaat	ctcatcatga	gtgggtagct	ctgtgggcag	atgacttttg	gctctttgag	480
gctgggattc	ctgttgtagc	tgtttttgac	tatgttgatc	tgacaccctc	cattctgtgg	540
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ttctctcttg	tctgctctcc	ctatggctgc	cttgacagcca	ccatcttgag	gatgcattca	720
gctaagagaa	agcactaggc	cttctctacc	agttctctcc	acctcattgt	ggttctctctg	780
aagtattggt	gttgcatcct	catctgcctt	tgccccagct	ctagttactc	cccagaggag	840
ggctgggagg	tatctcttgt	tcacatgttt	ttctcccggg	gtggaatccc	ttgatctata	900
gcgtatggaa	ccaagacgta	actgatgcag	tagagagact	tgtggcaaga	atgtccttgt	960
tctaacagcc	agaaatattc	cttcttaaaa	aatatttccc	taacta		1006

<210> 990

<211> 987

<212> DNA

<213> Unknown (H38g840 nucleotide)

<220>

<223> Synthetic construct

<400> 990

gattcagtg	accaagtaaa	tgactctctg	gtaacagaat	ttgtattact	tggacttgca	60
caatccttgg	aaatgcagtt	tttctttttt	ctcttcttct	ctttattcta	tgtgggaatt	120
atcctgggaa	acctcttcat	tgtgttcaca	gtgatctttg	atcctcactt	acactcccc	180
atgtatatcc	tgtctggcaa	cctatcgctc	attgacttga	gcctttcacc	taccacagtt	240
cctaggttga	tctacgatct	ttttactgat	tgtaaagtta	tttcttcca	taattgtatg	300
atacaaaagt	tctttatcca	tgttacagga	ggagttgaaa	tgggtgctgct	gatagtcatg	360
gcatatgata	ggtacactgc	gatctgcaaa	cctctccact	atccaactat	tatgaacccc	420
aaaatgtgca	tgttttttgg	agcagcagct	tgggtcattg	gggtgattca	tgtatgtct	480
cagtttgttt	ttgtcataaa	tttacccttc	tgtggcccta	ataatgtggg	gagcttttat	540
tgtgattttt	ctcgggttat	taaacttgca	tgcattggaca	cttatgggct	agaatttgtg	600
gtcactggca	acagtggatt	catatcgatg	ggcaccctct	ttttcttaat	tgtatcatac	660
atttttatcc	tggctactgt	ccaacgacat	tcctcaaatg	atttatccaa	agcattcttc	720
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gtgtggcctt	tcctactaa	gtcattggat	aaatTTTTTg	ccatcatgaa	ctttgttgtc	840
acccctgtct	taaatectgc	catctatact	ttaaggaaca	aagatatgaa	gtttgcaatg	900
agaaggctga	atcaacatat	tttaaattct	atggagatga	cataacacat	ttggttgatg	960
agagcacagg	ataaatgcc	tggacca				987

<210> 991

<211> 736

<212> DNA

<213> Unknown (H38g841 nucleotide)

<220>

<223> Synthetic construct

<400> 991

atgcaatcag	aacaccttgc	agaatTTTTca	gaattcctca	ttttgagcct	ctcaggagat	60
ccagaactgc	agccccctct	tgggctgttt	ctgtccatga	acctgggtcac	agtgccttgg	120
aacctgtctca	ttatcctggc	catcagttct	gactcccacc	tccacaagcc	tatgtacttc	180
ttactctcca	aattgtccat	ggctgccatt	tgTTTTgtct	tcaccatgat	ccaaaagatg	240
atggtaaacc	tcagggcaca	gagcaaagac	atctttactc	agccaagtgg	tagtccaatt	300
ccattctaaa	tgtgtagtct	tatcagattt	cttctaattc	agcagaaatc	tgttgtttta	360
atcttcgaat	actcactggg	tctaattctc	ctatttgaat	ctgaagatgt	aaactaatta	420
ttcttttgta	tgagcctttc	aaaataattg	aagacagtta	tgctcttttc	ttgataatca	480
ccatactttc	ttcacactaa	ttgatacaca	attgttaata	agtcatggat	tttctactca	540
aacaaccttt	attctatcat	cttatgtctc	tggttatgca	acagttgact	ctcaatgctt	600
tatttatttt	ttaaacatga	tgattactat	taacctcttt	gtaagattta	aaaaatatct	660
tatgcacagt	agtatctcaa	taaattacaa	ctattatttt	aaaaaataaa	ataaagggtg	720
tatctatgag	atatat					736

<210> 992

<211> 915

<212> DNA

<213> Unknown (H38g842 nucleotide)

<220>

<223> Synthetic construct

<400> 992

atgggtgactg	aattcatttt	tctgggtctc	tctgattctc	aggaactcca	gaccttccta	60
tttatgttgt	ttttgtatt	ctatggagga	atcgtgtttg	gaaaccttct	tattgtcata	120
acagtgggtat	ctgactccca	ccttcactct	cccatgtact	tcctgctagc	caacctctca	180
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aaacccctac	actacactac	aattatgtgt	ggcaacgcat	gtgtcggcat	tatggctgtc	420
gcatggggaa	ttggctttct	ccattcgggt	agccagttgg	cctttgccgt	gcacttaccc	480
ttctgtgggc	ccaatgaggt	cgatagtttt	tattgtgacc	ttcctagggt	aatcaaactt	540
gcctgtacag	atacctacag	gctagatatt	atgggtcattg	ctaacagtgg	tgtgctcact	600
gtgtgtttct	ttgttcttct	aatcatctca	tacactatca	tcctaataac	catccagcat	660
cgcccttttag	ataagtcgtc	caaagctctg	tcacttttga	ctgtctacat	tacagtagtt	720
cttttgttct	ttggaccatg	tgtcttttatt	tatgcctggc	cattccccat	caagtcatta	780
gataaattcc	ttgctgtatt	ttattctgtg	atcacccctc	tcttgaaccc	aattatatac	840
acactgagga	acaaagacat	gaagacggca	ataagacggc	tgagaaaatg	ggatgcacat	900
tctagtgtaa	agttt					915

<210> 993

<211> 927

<212> DNA

<213> Unknown (H38g843 nucleotide)

<220>

<223> Synthetic construct

<400> 993
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 gcagacctcc agctccccct ctttctcctc ttctctggga tctacttggt caccatcggt 120
 gggaaacctgg gcatgatcac tctaatttgt ctgaactctc agctgcacac ccccatgtac 180
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 ctctacttct tcttgtttt tgtcattgct gagtggtaca tgctgacagt gatggcctac 360
 gaccgctatg ttgccatctg ccaccctttg ctttacaaca tcattatgtc tcatcacacc 420
 tgctgtctgc tgggtggctgt ggtctacgcc atcggactca ttggctccac aatagaaact 480
 ggctcatgt taaaactgcc ctattgtgag cacctcatca gtcactactt ctgtgacatc 540
 ctccctctca tgaagctgtc ctgctctagc acctatgatg ttgagatgac agtcttcttt 600
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 ctctccagca tctcggcat cagcaccaca gaggggagat ccaaagcctt cagcacctgc 720
 agctcccacc ttgcagccgt gggaaatgtt tatggatcaa ctgcattcat gtacttaaaa 780
 cctccacaaa tcagttcctt gaccaggag aatgtggcct ctgtgttcta caccacggta 840
 atccccatgt tgaatccctt aatctacagc ctgaggaaca aggaagtaaa ggctgccgtg 900
 cagaaaacgc tgaggggtaa actgttt 927

<210> 994

<211> 930

<212> DNA

<213> Unknown (H38g844 nucleotide)

<220>

<223> Synthetic construct

<400> 994
 atggcagcca aaaactcttc tgtgacagag tttatcctcg aaggettaac ccaccagccg 60
 ggactgcgga tccccctctt ctctctgttt ctgggtttct acacggtcac cgtgggtggg 120
 aacctgggct tgataaccct gattgggctg aactctcacc tgcacactcc catgtacttc 180
 ttctttttta acctctcttt aatagatttc tgtttctcca ctaccatcac tcccaaatg 240
 ctgatgagtt ttgtctcaag gaagaacatc atttcttca cagggtgtat gactcagctc 300
 ttcttcttct gcttctttgt cgtctctgag tcttctatcc tgtcagcgat ggctgatgac 360
 cgctacgtgg ccatctgtaa cccactgttg tacacagtca ccatgtcttg ccagggtgtg 420
 ttgtctcttt tgttgggtgc ctatgggatg ggggttctgt gggccatggc ccacacagga 480
 agcataatga acctgacctt ctgtgctgac aacctgtca atcatttcat gtgtgacatc 540
 ctctctctcc ttgagctctc ctgcaacagc tcttacatga atgagctggg ggtctttatt 600
 gtgggtggctg ttgacgttg aatgccatt gtcactgtct ttatttctta tgccctcatc 660
 ctctccagca ttctacacaa cagttctaca gaaggcagg ccaaagcctt tagtacttgc 720
 agttcccaca taattgtagt ttctcttttc tttggttctg gtgctttcat gtatctcaaa 780
 cccctttcca tcttgcctct cgagcaaggg aaagtgtcct ccctgttcta taccataata 840
 gtccccgtgt taaaccatt aatctatagc ttgaggaaca aggatgtcaa agttgccctg 900
 aggagaactt tgggcagaaa aatcttttct 930

<210> 995

<211> 473

<212> DNA

<213> Unknown (H38g845 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(473)

<223> n = A,T,C or G

<400> 995
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 gtccagcatc tggggaatgt cttttctctg gtgcacctgc tggcatacct ggctccatc 120
 atggcaaaca tgctcataat caccatcacc tgggctgacc atcacctcca gacacctatg 180

tattttcttcc	tcagcagttt	ttccttctgt	gaatgctgtt	ttatcaccac	agttattcct	240
aaacttctgg	tcatectttc	tttcaggcag	ggcaaataat	ccccctttct	actaccttgt	300
ctcatgcagt	ccccctttca	tttttatntt	cttgggtcaa	cagtttttct	tcccttaatg	360
gctgtgatgt	ccccctggat	tgatacctgg	ccatttgcaa	gcctctgcat	tactccacca	420
tcatgagcct	gaggactage	ttccacaagg	tcactgcctg	gctttgtcct	ggg	473

<210> 996

<211> 998

<212> DNA

<213> Unknown (H38g846 nucleotide)

<220>

<223> Synthetic construct

<400> 996

acagaccac	agaatctaac	aacagatgtc	tcaatattec	tcgtcctaga	actctcagag	60
gatccagaac	tacagccggt	cctcgctggg	ctgttcctgt	ccatgtgect	ggatcatgggtg	120
ctggggaacc	tgctcatcat	cctggccgct	agccctgact	cccacctcca	cacccccatg	180
tacttcttcc	tctccaacct	gtccttgcc	gacatgggtt	cacctccacc	atgggtcccca	240
agatgattgt	ggacatccaa	tctcacagca	gtcatctcct	atgcgggctg	cctgactcag	300
atgtctcttt	ttgccatttt	tggaggcatg	gaagaaagac	atgctcctga	gtgtgatggc	360
cctatgaccg	gtttgtagcc	atctgtcacc	ctctatatta	ttcagccatc	atgaacccat	420
gtttctgtgg	ctttctagtt	ctgttgtctt	gttgtctcag	tcttttagac	tcccagctgc	480
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tgtatttccc	tgctgccata	tttggttttc	ttcccacctc	ggggatcctt	ttctcttact	660
ataaaaattgt	ttcctccatt	ctgagggttt	catcatcagg	tgggaactat	aaagccctct	720
ctgcctgtgg	gtctcacctg	tcagttgttt	gcttatttta	tggaaacaggc	gttggagggt	780
acctcagttc	agatgtgtca	tcttccccca	gaaagggtgc	agtggcctca	gtgatgtaca	840
cgggtggcac	ccccatgctg	aaccccttca	tctacagcct	gagaaacagg	gatattaaaa	900
gtgtcctgcg	ggcctgcac	ggcagaacag	tctaattctca	atatcttatt	atctgttcca	960
ttccttttgt	agtgtgggtt	taaaaaggca	gcaagggtc			998

<210> 997

<211> 666

<212> DNA

<213> Unknown (H38g847 nucleotide)

<220>

<223> Synthetic construct

<400> 997

agtcaactgt	cccttatgga	cctcatgctc	atctgcacca	ctctacccaa	gatgatcttc	60
agctacttgt	ctgggaagaa	atctatctct	ctggcagggt	gtggaactca	gatattcttc	120
tatgtgtccc	tgcttgagc	tgaatgtttc	ttgttggtctg	tcattggctta	tgaccgctat	180
gtggctatat	gtcacctctc	tcagtacacc	atcctcatga	atccggaact	ctgtgtcttc	240
atgactgttg	cttctctggac	cttgggggtct	cttgatggga	tcatagtgtct	tgcagctgtc	300
ctgtcatttt	cttactgcag	ctctctggaa	attcatcatt	ttttctgtga	tgttgctgcc	360
cttttacctc	tatcctgcac	agaaacatct	gcatttgaaa	gactacttgt	catttggtgt	420
gtggtaaatgc	taatctttcc	agtttcagtt	atcatacttt	cctattccca	tgtccttcga	480
gccgtcatcc	acatgggctc	tggggaaagt	cgtcgcaagg	ccttcactac	ctgtcctcct	540
caccgcgtctg	tggtcggact	ctactacggg	gctgctatgt	tcatgtacat	gagaccagct	600
tctaaacata	cgccagacca	ggacaagatg	gtgtcggcct	tctacactaa	tctcaccctc	660
atgctg						666

<210> 998

<211> 342

<212> DNA

<213> Unknown (H38g848 nucleotide)

<220>

<223> Synthetic construct

<400> 998

cttgccctgca	tagttggata	gaagtttgca	tttattattt	ctccaaacca	tcacttcatg	60
ataatgggtca	cattcatttt	agttaacatt	taaaaacatt	cttcaggaaa	cttatccagt	120
gctcttatca	ttttgttcat	tttcatccct	gttgtttctc	tatttttcac	tccatgcgta	180
gttctctatg	tttggcctac	tttgccacca	tcacttgata	aaaatatgtt	cattgttgac	240
tttgttgca	accctgtctt	gaagcctgcc	acctacatat	tacagaacaa	agacataaag	300
gtagcacttt	gaaatttgca	tgaaaagaga	acttattcca	gc		342

<210> 999

<211> 915

<212> DNA

<213> Unknown (H38g849 nucleotide)

<220>

<223> Synthetic construct

<400> 999

atggtgactg	aattcatttt	tctgggtctc	tctgattctc	agggactcca	gaccttcccta	60
tttatgttgt	tttttgtatt	ctatggagga	atcgtgtttg	gaaaccttct	tattgtcata	120
acagtgggat	ctgactccca	ccttcactct	cccatgtact	tcctgctagc	caacctctca	180
ctcattgac	tgtctctgtc	ttcagtcaca	gcccccaaga	tgattactga	ctttttcagc	240
cagcgcaaag	tcattctctt	caagggtctg	cttggtcaga	tatttctcct	tcacttcttt	300
ggtgggagtg	agatgggtgat	cctcatagcc	atgggctttg	acagatatat	agcaatatgc	360
aaacccctac	actacactac	aattatgtgt	ggcaacgcac	gtgtcggcat	tatggctgtc	420
gcatggggaa	ttggttttct	ccattcgggtg	agccagttgg	cctttgccgt	gcacttaccc	480
ttctgtggte	ccaatgaggt	cgatagtttt	tattgtgacc	ttcctagggg	aatcaaactt	540
gcctgtacag	atacctacag	gctagatatt	atggtcattg	ctaacagtgg	tgtgtctact	600
gtgtgttctt	ttgttcttct	aatcatctca	tacactatca	tcctaattgac	catccagcat	660
cgcccttttag	ataagtcgtc	caaagctctg	tccactttga	ctgctcacat	tacagtatgt	720
cttttgttct	ttggaccatg	tgtctttatt	tatgcctggc	cattccccat	caagtcatta	780
gataaattcc	ttgctgtatt	ttattctgtg	atcacccctc	tcttgaacct	aattatatac	840
acactgagga	acaaagacat	gaagacggca	ataagacagc	tgagaaaatg	ggatgcacat	900
tctagtgtaa	agttt					915

<210> 1000

<211> 669

<212> DNA

<213> Unknown (H38g850 nucleotide)

<220>

<223> Synthetic construct

<400> 1000

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gacatccaat	ctcacagcag	tcattctcct	atgcaggctg	cctgactcag	atgtctctct	120
ttgccatttt	tggaggcatg	gaagagacac	atgctcctga	atgtgatggc	ctatgtccgg	180
ttttagacca	tctgtcaccc	tctatatcat	tcagccatca	tgaacctgtg	tttctgtggc	240
ttcttacttt	tgttgtcttt	tttttttctc	agtcttttag	acgcccagct	gcacaacttg	300
attgccttac	aaatgacctg	cttcaaggat	gtggaaattc	ctaatttctc	ctgtgacctt	360
tctccactcc	cccatcttgc	atgttgtgac	accttcacca	ataacataat	catgtatttc	420
cctgtcgcca	tatttggttt	tcttcccatc	tcggggaccc	ttttctctta	ctataaaatt	480
gtttcctcca	ttctgagggt	ttcatcatca	gggtgggaagt	ataaggcctt	ctccacctgt	540
gggtctcacc	tgtcgggtgt	ttgctgattt	tatggaaacag	gcgttgaggg	gtacctcggt	600
tcagatgtgt	catcttcccc	gagaaagagt	gcagtggcct	cagtgatgta	cacggtgggtc	660
accccatg						669

<210> 1001

<211> 986

<212> DNA

<213> Unknown (H38g851 nucleotide)

<220>

<223> Synthetic construct

<400> 1001

gattcagtgg	accaagtaaa	tgactctctg	gtaacagaat	ttgtattact	tggaacttgca	60
caatccttgg	aatgcagtt	tttccttttt	ctcttcttct	ctttattcta	tgtgggaatt	120
atcctgggaa	acctcttcat	tgtgttcaca	gtgatctttg	atcctcactt	acactccccc	180
atgtatattc	tgtggccaa	cctatcgctc	attgacttga	gcctttcatc	taccacagtt	240
cctaggttga	tctacgatct	ttttactgat	tgtaaagtta	tttccttcca	taattgtatg	300
atacaaaagt	tctttatcca	tgttacggga	ggagttgaaa	tgggtgctgct	gatagtcag	360
gaatatgata	ggtacactgc	gatctgcaag	cctctccact	atccaactat	tatgaatccc	420
aaaatgtgca	tgtttttggg	agcagcagct	tgggtcattg	gggtgattca	tgctatgtct	480
cagtttgttt	ttgtcataaa	ttaaccttct	gtggccctaa	taatgtgggg	agcttttatt	540
gtgattttcc	tcgggttatt	aaacttgcac	gcatggacac	ttacgggcta	gaatttgtgg	600
tcactgccaa	cagtggattc	atategatgg	gcaccttctt	tttcttaatt	gtatcataca	660
tttttattct	ggtcactgtc	caacgacatt	cctcaaatga	tttatccaaa	gcattcttca	720
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cccctgtctt	aaatcctgcc	atctatactt	taaggaacaa	agatatgaag	tttgcaatga	900
gaaggctgaa	tcaacatatt	ttaaattcta	tggagacgac	ataacacatt	tggttgatga	960
gagcacagga	taaatgccat	ggacca				986

<210> 1002

<211> 659

<212> DNA

<213> Unknown (H38g852 nucleotide)

<220>

<223> Synthetic construct

<400> 1002

agtgtgctgt	ctattttctga	gacctattat	accgtggcca	tcaaccccca	aatgctgtcc	60
gggtctcctca	gtcctcaaca	aaccatctcc	atcccaggct	gtgccgctca	gctctttttc	120
tatctcactt	ttgggtgcaa	taaatgcttc	ctgctcacag	ccatggggta	tgaccactat	180
gtggccatct	gcaacctctt	acagtattca	gtcatcatgg	gcaaaaaggc	ttgtatacaa	240
ctggtcagtg	gatcctggaa	cattggcctg	agcacagcta	tcattcaggt	gtcttctgta	300
ttcagccttc	ccttctgtga	tgctaattct	atctcccact	tcttttgtga	tatccggccc	360
ataatgaagc	ttgcctgtgc	agacactact	atcaaggagt	ttattacttt	gctcatcagt	420
ctctgtgtcc	ttgttctgcc	catgggtattg	atcttcatct	cctatgtcct	aattgtcacc	480
accatcctca	agattgcac	agctgagggc	ggagaaaggc	ctttgctact	tgtgcctcac	540
acctcacagt	ggtcattgtc	cactatggcc	gtacttcttt	catctaccta	aaacccaaat	600
ccccaaaattc	cctgcaggac	agacttatct	ctgtgacata	cactgttatt	actcctctg	659

<210> 1003

<211> 939

<212> DNA

<213> Unknown (H38g853 nucleotide)

<220>

<223> Synthetic construct

<400> 1003

atgtctacgt	ctaatacacac	ccagttccat	ccttcttcat	tcctactgct	gggtatccca	60
gggctagaag	atgtgcacat	ttggattgga	gtcccttttt	tctttgtgta	tcttgttgca	120
ctcctgggaa	acactgctct	cttgtttgtg	atccagactg	agcagagtct	ccatgagcct	180
atgtactact	tcctggccat	gttggattcc	attgacctgg	gcttgtctac	agccaccatc	240
ccccaaatgt	tgggcatctt	ctggttcaat	accaaagaaa	tatcttttgg	aggctgcctt	300
tctcacatgt	tcttcatcca	ttcttccact	gctatggaga	gcattgtgtt	gggtggccatg	360
gcctttgacc	gctacattgc	catttgcaaa	cctcttcggg	acaccatgat	cctcaccagc	420

aaaatcatca	gcctcattgc	aggcattgct	gtcctgagga	gcctgtacat	ggttgttcca	480
ctggtgtttc	tccttctgag	gctgcccttc	tgtgggcac	gtatcatccc	tcatacttat	540
tgtgagcaca	tgggcattgc	ccgtctggcc	tgtgccagca	tcaaagtcaa	cattaggttt	600
ggccttggca	acatatctct	cttggttactg	gatgttatcc	ttattattct	ctcctatgtc	660
aggatectgt	atgctgtctt	ctgcctgccc	tcctgggaag	ctcgactcaa	agctctcaac	720
acctgtgggt	ctcatattgg	tgttatctta	gcctttttta	caccagcatt	tttttcattc	780
ttgacacatc	gttttggcca	taatatccca	cagtatatac	atattatatt	agccaacctg	840
tatgtggttg	ccccaccage	cctcaatcct	gtaatctatg	gagtcaggac	aaagcagatt	900
cgagagagag	tgctgaggat	ttttctcaag	accaatcac			939

<210> 1004

<211> 877

<212> DNA

<213> Unknown (H38g854 nucleotide)

<220>

<223> Synthetic construct

<400> 1004

tacatgataa	ccatcttatg	ggaaatatct	aagccagtaa	ataatatattt	tctaacactt	60
tctgtaagat	atcaaagtct	aatcactact	gtgtcataat	tgtaaataaa	attataatat	120
aaattttactg	agttttttctg	agtacctaata	gagttaaaaa	atatgggagc	atatgtagta	180
ctgtgcttgt	atcaatatgg	ataaggtatc	tggaagtctt	ttctgaacat	ctttcgggtgc	240
tgtctgagatt	attccactga	tggggatggg	ccatggctgc	tatgtgacca	tctgcaactgc	300
atgaaaaatca	tgactcaata	taggtgtggc	catcttgcctg	gaatggcatg	caactggaaga	360
tttatccagg	cacagtttag	atcctctccc	cagtctgact	tcctttctat	aattccaatg	420
tcacaatatg	aatagcccat	tcatatgtga	cttaaacact	ttgttgaagc	tcctctgcat	480
aggtagtatg	atacacttgg	tctctttgtt	gctgccaatg	atgggttcaa	ctgcctgtta	540
aacatcatct	tcttgatggg	ttcttaagtg	gccatcctat	atactttgaa	atcccacagc	600
ttggaggaaa	gatacaaagc	tctctctacc	tgtgtctctc	acaccaccgt	ggccatctaa	660
tcttttgtgt	tctgtatact	tgtttatctg	tgcccagtg	cccttcccca	gtcagtaaaag	720
cagtggctgt	gctttacacc	atgataacgc	ctacattaaa	ccctttagtc	taacctcag	780
aaatgcagag	gtgaaaagtg	ttgagaaact	tctgggtcaa	aagatgactt	gaagagagaa	840
ataatccaaa	cataagatga	ttttactctt	tcaatgg			877

<210> 1005

<211> 927

<212> DNA

<213> Unknown (H38g855 nucleotide)

<220>

<223> Synthetic construct

<400> 1005

atggagaaga	aaaagaatgt	gactgaattc	attttaatag	gtcttacaca	gaaccccata	60
atggagaaag	tcacgtttgt	agtatttttg	gttcttttaca	tgataaacact	ttcaggcaac	120
ctgctcattg	tggttaccat	taccaccagc	caggctctga	gtcccccat	gtacttcttc	180
ctgacccacc	tttctttgat	agacacagtt	tattcttctt	cttcagctcc	taagttgatt	240
gtggattcct	ttcaagagaa	gaaaatcatc	tcctttaatg	gggtgatggc	tcaagcctat	300
gcagaacaca	tttttggtgc	tactgagatc	atcctgctga	cagtgatggc	ctgtgactgc	360
tatgtggcca	tctgcaaacc	tctgaactac	acaaccatta	tgagccacag	cctgtgcatt	420
ctcctggtag	cagtggcctg	gggtgggagga	tttcttcatg	caactattca	gattctcttt	480
acagtattgc	tgcccttctg	tggccccaat	gtcataggcc	acttcatgtg	tgacttgtac	540
ccattgttaa	aacttggttg	catagacact	catacccttg	gtctctttgt	tgctgtgaac	600
agtgggttta	tctgcttatt	aaacttcctt	atcttggttg	tatcctatgt	gatcatcttg	660
agatctttaa	agaacaatag	cttggagggg	agggtgaaag	ccctctccac	ctgtatttct	720
cacatcatag	tagttgtctt	attctttgtg	ccctgtatat	ttgtgtatct	gcgctcagtg	780
accactctgc	ccattgataa	agctgttgct	gtattttata	ctatgggtgt	cccaatgtta	840
aatcccgtgg	tctacacact	cagaaatgct	gaggtaaaaa	gtgcaataag	gaagctttgg	900
agaaaaaaag	tgacttcaga	taatgat				927

<210> 1006
 <211> 738
 <212> DNA
 <213> Unknown (H38g856 nucleotide)

<220>
 <223> Synthetic construct

<400> 1006
 tgtattcaac aacattgata tccactttgt ctctgcatgt tctcctttta ttttaatttg 60
 taccattttt ttcccaaata aaagtacttg cactcactta gagatgctga aataaattga 120
 ttggtataaa gtaaggatgc tgattaacca aatttacact aaagccaatt ggccttttca 180
 tggattataa cactatgcac aaccactcca tactcaaaca tgcattttct tctccaatgt 240
 tatatgatgc agcacctagc tctttacagg acattttttt cttggtgggt cacagatttt 300
 ccttctgttg gtgatggcct aggcactat agggccatct gcaagtcctt gcagtatttg 360
 gttgtcatga agcaatggct gtgtgttggt ctgctggtgg tgccttgggc tggaggattt 420
 ttgcacatag taattcaact tggacttatt tatgggctcc catcttatga cccaatgtc 480
 attggtcatt ttatttggta catggacccc ttaatgaagc ttgtctgtga ctacacactc 540
 aacagatttg cctattttgc aggtcatgat taaatactag gttttatgta tttcacttat 600
 gctcagactg gactgtttcc ttttgggtgat tgcacctcat tattcttttg tcattttttc 660
 cctagaggac ttggttctat aaatcttgct atacatagtt attatccctg tggcatctct 720
 agagatacgg agcctacc 738

<210> 1007
 <211> 786
 <212> DNA
 <213> Unknown (H38g857 nucleotide)

<220>
 <223> Synthetic construct

<400> 1007
 ctaattgtag tcaccgtaac tgtcagtgag accctgggct caccaatgta cttctttctt 60
 gctggccttat catttataga tatcatttat tcttcaccca tttccacagc attgatttca 120
 gacttgttct ttgggaataa ttccatatcc tcccatctt gcttggccca gctctttaca 180
 gagcaccttt ttggtgggtc agaggctctt cttctgttgg tgatggccta tgaccttgca 240
 ttacttggtt atcatgagac aatgggtgtg tgttttgctg ctggtagcgt cctgggttgg 300
 aggatttctg cactcagtat ttcaacttag tgttatttat gggctcccat tctgtgacct 360
 caatgtcatt gatcattttt tctgtgatat gcaccttta ttgaaactgg tctgtactga 420
 taccatgtt attggcctct tagtggtggc caatggagga ctagggtgca ctattgtgtt 480
 tctgtcttta ctcatctct atggtgtcat ctgcactctc taaagaacct tagtcagaaa 540
 gggagggtgaa aagccctctc aacctgcagt tccacataa ctgtgggttg tttcttcttt 600
 gttccctgta tttttatgta tgctagacct gctaggacct tccccattga caaatcagtg 660
 agtgtgtttt atacagtcac aactccaatg ctgaaccctt taatctacac tctgagaaat 720
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<210> 1008
 <211> 930
 <212> DNA
 <213> Unknown (H38g858 nucleotide)

<220>
 <223> Synthetic construct

<400> 1008
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 cttgcctgcc tgtcatttat agatgctgca tattccacta caatttctcc caaattgatt 240
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atagaccagc	ctggatggcg	gagctgaggt	cgtgcttctt	gtggtgaagg	cctgtgatca	360
ccatgtggac	atctggaagc	cactgcgcta	tctcgactat	catgaatcga	cagggctgaa	420
tgcggctgct	cgtggctgtc	gtcgcactgcg	aggtgttctg	cattcgctgt	ctcatattgt	480
gagtgtgtat	acagtctcgc	ctactgtggc	cccaatgtca	ttgactactt	tgtctgtgac	540
atgtaccag	ttattggaac	tggtatgcac	tgacacctac	tttattggcc	ttactgtttt	600
tgtcaatggt	ggaacaatct	gtatagtcgt	cttcaccctt	ctactaatct	cctatggagt	660
cacctaatac	tcccttaaaa	cttacagtca	agaagggagg	cataaagtcc	tgtttacctg	720
cagctccac	attatcgtct	ttgccctctt	ttttgttccc	tgtattttca	tgtatgttag	780
acctgtttca	aacatccttt	tgataaatc	ctgacagtgt	tttatacagt	tatcaccccc	840
atgttgaatc	ctttaatata	cacattgaga	aattcagaga	tgagaaatc	tgtagaaaca	900
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<210> 1009

<211> 915

<212> DNA

<213> Unknown (H38g859 nucleotide)

<220>

<223> Synthetic construct

<400> 1009

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aatagcacc	tcatcgtgtt	gatctgtaat	gactcccacc	tccacacacc	catgtatttt	180
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ctagtgatct	gcattctctga	agacaaaagc	atctcctttg	ctggctgcct	gtgtcagttc	300
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atcaccagtg	tcttgaggat	ctcctctctc	aagggctacc	tcaaagcctt	ctccacatgc	720
tcttcccacc	tgacctctgt	cactttatac	tatggctcca	ttctctacat	ctacgtctc	780
cccagatcta	gctattcttt	tgatatggac	aaaatagttt	ctacatttta	cactgtggta	840
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aaaaaacttc	tccca					915

<210> 1010

<211> 948

<212> DNA

<213> Unknown (H38g860 nucleotide)

<220>

<223> Synthetic construct

<400> 1010

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ggcaactttc	ttattgtcac	agttaccagt	gtggatctcg	cacttcaaac	acccatgtac	180
ttctttcttc	aaaatctgtc	acttcttgaa	gtatgtttca	ccttggttat	ggtgccaaaa	240
atgctttag	atctagtgtc	cccaaggaaa	attatctctt	ttgtgggctg	tggtagccag	300
atgtacttct	tcttcttctt	tggcagttct	gaatgtttcc	ttctctccat	gatggcttat	360
gatcgctttg	tggccatctg	taaccctctc	cattattcag	tcataatgaa	caggtcccta	420
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gcctccacac	tcctgtttat	catgtttccc	ttttgtctca	ttttggtttc	ctacaccgcg	660
attatcataa	caattctgag	gatgtcctct	gccactggcc	gccagaaggc	atcttctact	720
tgttctctac	acctcattgt	ggtgtccctc	ttctacggaa	cagccagtct	gacctacctg	780
cggcccaaat	caaaccagtc	ccctgagagc	aagaagctag	tgtcattgtc	ctacactgtc	840

atcacaccta tgctaaaccc catcatctac ggcctgagga acaatgaagt gaaaggggct 900
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<210> 1011

<211> 927

<212> DNA

<213> Unknown (H38g861 nucleotide)

<220>

<223> Synthetic construct

<400> 1011

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gtgtcatttg	tggtcacccat	cactgccagc	ccatcactga	gatcccccat	gtactttttc	180
ctggcctatc	tctcctttat	tgatgcctgc	tattcctctg	tcaatacccc	taagctgac	240
acagattcac	tctatgaaaa	caagactatc	ttattcaatg	gatgtatgac	tcaagtcttt	300
ggagaacatt	ttttcagagg	tgttgagggtc	atcctactta	ctgtaatggc	ctatgaccac	360
tatgtggcca	tctgcaagcc	cttgcaactat	accaccatca	tgaagcagca	tgtttgtagc	420
ctgctagtgg	gagtgtcatg	ggtaggaggc	tttcttcatt	caaccataca	gatcctcttc	480
atctgtcaat	tacctttctg	tggtccta	gtcatagatc	actttatgtg	tgatctctac	540
actttgatca	atcttgccctg	cactaatacc	cacactctag	gactcttcat	tgctgccaac	600
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tactccttaa	agaccacacag	cttagaggca	aggcatgaag	ccctctctac	ctgtgtctcc	720
cacatcacag	ttgtcatctt	atcctttata	ccctgcata	ttgtgtacat	gagacctcca	780
gctactttac	ccattgataa	agcagttgct	gtattctaca	ctatgataac	ttctatgtta	840
aaccctttaa	tctacacctt	gaggaatgct	caaataaaaa	atgccattag	gaaattgtgt	900
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<210> 1012

<211> 488

<212> DNA

<213> Unknown (H38g862 nucleotide)

<220>

<223> Synthetic construct

<400> 1012

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ccatagccca	agataactaag	tattatagga	ttgaaatgaa	atataaatga	aactttgtaa	120
atgttaaatt	ataacacaaa	tcataatggtc	agtgtcgatg	tcctaattgt	tcctaactcc	180
tcacacact	ctcctacttc	ttcattgtgg	ctgccatcct	gatatccgct	ctgcagaggg	240
gaggcacaag	gcttttccca	cctgtctcct	ccacctgggt	taattctcct	ccagcacaat	300
gaacaagcct	cacctatttg	tgccccagct	ccatcttctc	ttatgagagg	ggcaaggtag	360
tgtctacggg	ttacacatgc	atcactcctg	tgccaaaccc	cttgatctgc	agcatgagga	420
agaaggaact	caagcatgct	cttaaaaaaa	aagaagaaat	tgcaagggtc	ttgctgctca	480
gaacacat						488

<210> 1013

<211> 953

<212> DNA

<213> Unknown (H38g863 nucleotide)

<220>

<223> Synthetic construct

<400> 1013

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acttatgcac	tataggagga	aatatcatca	tcactctcct	gatctggatc	acccctgccc	180
tgcacactcc	aatgtatttc	ttcctggtga	acctctcatt	tctggagatg	tgctatacca	240

ccagtgtggt	gcctcatgct	gggtgcacctg	ctgggtggaga	ccaaaaccat	aagtgtgggt	300
ggctgtgcaa	cccagatgta	catatttgcc	atcttgggac	tgacagaatg	ctgcttgcta	360
gcagctatgg	cttacgatcg	ctttgtagct	atttggtacc	cactgcatta	cactctcttc	420
atgggcccctc	gtgtttgttt	gaaattggct	gcagcatctt	ggttcactgg	agtgggtggtg	480
gagtcagccc	agatcaccct	gatcttcact	ttgcctttct	gtggaacagg	aaagattcaa	540
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tgttcactta	tctgcaacct	aagactgcac	acactccaga	aacagacaaa	gcaactgcac	840
tcatgtacac	aatggtcaca	cctgctttga	atcctgttat	ctataccttg	aggaacaagg	900
aagtaaagga	agcctttcaa	aggataaccc	aaaggaactc	tcttagacaa	acg	953

<210> 1014

<211> 873

<212> DNA

<213> Unknown (H38g864 nucleotide)

<220>

<223> Synthetic construct

<400> 1014

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ttcacctcgg	ccacagttcc	caagatgatt	gtggacatgc	agtcgcatag	cagagtcac	180
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tgcaactaccg	agtcacatcg	aatcctcacc	tctgtgtctt	cttagttttg	gtgtcctttt	360
tccttagcct	gttggtatcc	cagctgcaca	gctggattgt	gttacacaa	tcaccttctt	420
caagaatgtg	gaaatctata	atttttttct	tgtagcccat	ctcaacttct	caaccttgcc	480
tgttctgaca	gcacatcaaa	taacatatta	tgtattttag	atatccctat	atttggtttt	540
cttcccattt	cagggatcct	tttgtcttac	tataaaattg	tctcctccat	tccaagaatt	600
ccatcgtcag	atgggaagta	taaagccttc	tccacctgtg	gctctcacct	ggcagttggt	660
tgcttatattt	atgaaacagg	cattggcggtg	tacctgactt	cagctgtgtc	atcatctccc	720
aggaatggag	tggtggcatc	agtgatgtac	gctgtggtea	tcccatgct	gaaccctttc	780
atctacagcc	tgagaaacag	ggacattcat	agtgccctgt	ggaggctgcg	cagcagaaca	840
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<210> 1015

<211> 981

<212> DNA

<213> Unknown (H38g865 nucleotide)

<220>

<223> Synthetic construct

<400> 1015

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tgcccttcag	ccctgactcc	cacctccaca	cccacatgta	cttcttcttc	tccaacctgt	180
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ttggaggcat	ggaagacaga	catgtccttg	agtgtgatgg	cctatgaccg	gtttgtagcc	360
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catatttggt	ttccttccca	tctcggggac	ccttttctct	ttaaaactgt	tctctccatt	660
ctgagggttt	catcatcagg	cgggaagtat	aaaaccttct	ccacctgtgg	gtctcacctg	720
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aaccccttca	tctacagcct	gagaaacagg	gatatgaaaa	gtgtcctgcg	gcggccgcac	900
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aaaaaaggca	gcaaggtcaa	a				981

<210> 1016

<211> 762

<212> DNA

<213> Unknown (H38g866 nucleotide)

<220>

<223> Synthetic construct

<400> 1016

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gttcttttgg	ggaacattag	tgtgatgaca	atcattgtaa	ctgattccca	gctgaacaca	180
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ctccaagtca	gtgtaacatt	ctcagtgctc	ttctgtgctt	ccagagtcac	tgctcacttc	540
tactgtgatt	cttatcaaat	tgaaaagatt	tcctgttcta	atctctttgt	caataagatg	600
gtatctctga	gtttgagtgt	catcattatt	ttgcctacaa	ttgttggtat	tatagtatct	660
tacctgtata	ttgtatcctc	agtcttgaag	atccccctca	gtgaaggagg	aaagaaagac	720
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<210> 1017

<211> 1008

<212> DNA

<213> Unknown (H38g867 nucleotide)

<220>

<223> Synthetic construct

<400> 1017

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gatccaaaac	tgcagctggc	cctcgagtgg	gcgtgaaccg	tgtacatgta	cctagtcatt	120
gggtgctggag	aatctgctca	ttatcctggc	cgctcagctct	gacttccacc	tcacaccccc	180
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gactcagatg	tctctctttg	ctgtttttgg	aggcatggaa	gaaagacatg	ctcctgagtg	360
tgagggccta	tgaccgggtt	gtagccatct	gtcaccctct	atattattca	gccatcatga	420
acccatgttt	ctgtggcttc	ctagttttgt	gttttttttt	ttctcagctc	tttagactcc	480
cagctgcaca	atltgattgc	cttacaaatg	acctgcatca	aggatgtgga	aattcctaata	540
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atagtcatgt	atltccttgc	tgccatattt	ggttttcttc	ctatctcacg	gatcattttc	660
tcttactata	aaattgtttc	ctccatgctg	agtgtttcat	catcagggtg	gaagtataaa	720
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atcaaaaagg	tcctgtgggt	gttgcattgg	agaacagttt	aatctcatta	ttttattatc	960
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<210> 1018

<211> 949

<212> DNA

<213> Unknown (H38g868 nucleotide)

<220>

<223> Synthetic construct

<400> 1018

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agcatcctgg ctgtcagctc tgactgcccc ctccacaccc ccatgtactt ctctctctec      180
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gcagcagagc attcgaatct catgatctgt tccatccttt ttcttgtgt      949

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<210> 1019

<211> 939

<212> DNA

<213> Unknown (H38g869 nucleotide)

<220>

<223> Synthetic construct

<400> 1019

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atccttctag ggaatgttgg gatgatgacc attattatga ctgacctcg gctgaacaca      180
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acagctctgt gtactcagtt ggtggctggt tcctattttt gtggctgcat tagctcagtt      480
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<210> 1020

<211> 828

<212> DNA

<213> Unknown (H38g870 nucleotide)

<220>

<223> Synthetic construct

<400> 1020

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ctctgtcatt tctcccaaaa tgacaataag ctttgtgaca gaaaagaaca tcatcacata      240
tgtgacatca aacactcagc cttttcctct ggcttctttg tcattagtga ttactccata      300
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acatggacca	attcctgttt	tgtgatcaca	gttgcattgag	ccttaacttg	tgtaacatag	480
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agaaccagca	gtgtaccatg	ctgtgttatc	attttcatat	tttgttttca	ttcttttcaa	600
catttttcat	taaccacagt	gtccaaatct	tcagccagat	tccataaatc	tgttttatttc	660
tttttttgga	ttagggacat	tcagtgtacct	cagatctcca	gaagctatgg	gttagtgtaa	720
attacagtgt	ccttcaccaa	gatggggcca	gtgatgaacg	gtctgttcaa	caccttgagg	780
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<210> 1021

<211> 1001

<212> DNA

<213> Unknown (H38g871 nucleotide)

<220>

<223> Synthetic construct

<400> 1021

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gatgattgtg	gacatccagt	ctcacagcag	agtcacatctc	tatgcaggct	gcctgactca	300
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cggtggtcac	ccccatgctg	aaccccttca	tctacagcct	gagaaacagg	gatatgaaaa	900
gtgtcctgcg	gcggccgcac	agcagcgcag	tctaattctca	atatcttctt	atctgttcca	960
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<210> 1022

<211> 1025

<212> DNA

<213> Unknown (H38g872 nucleotide)

<220>

<223> Synthetic construct

<400> 1022

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ctggggaacc	tgtcatcat	cctggccgctc	agccctgact	cccacctccc	caccccatgt	180
tacttcttcc	tctccaacct	gtccttgccct	gacatcggtt	tcacctccac	cacgggtcccc	240
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caaattgtctc	tctttgccat	ttttggaggc	atggaaaaaa	gacatgtctc	tgagggtgatg	360
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gtctttttaga	ctcccagctg	cacaacttga	ttgccttaca	aatgacctac	ttcaaggatg	540
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tcaaa

1025

<210> 1023

<211> 1044

<212> DNA

<213> Unknown (H38g873 nucleotide)

<220>

<223> Synthetic construct

<400> 1023

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accattggag	gcaccctcag	caccctggcg	gccatcctta	tggaaaccaa	actccacagc	180
cccattgact	tcttctctgg	gaacttgtcc	ctgccagatg	tggggtgtgt	cagtgtcact	240
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tggggaatcc	agcaagccct	ggtgggcatg	tcatgtgtct	tttcttccac	caatgcactg	480
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aacactgtca	tcagcccat	gctgaaccca	ctcatctact	ggacatctct	gctggacgtc	900
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tcacctctta	atagccatgg	ccta				1044

<210> 1024

<211> 688

<212> DNA

<213> Unknown (H38g874 nucleotide)

<220>

<223> Synthetic construct

<400> 1024

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aaaaccgtag	tgggggcccct	catcttgatc	actctagttt	tccttaattc	tcagcttcac	180
ctccccatgt	actacgtcat	cagaaattta	tcatttatgg	atcactgcaa	ttgctctatt	240
agtaccctta	aaatactggg	gaagtttgtg	ttagagaaga	ccatcatctc	ctatgaggac	300
ggcatgtcac	agctttgtag	tgtttcgtgt	ttatattgtc	atggccaagc	gtaacatgag	360
gaccagcaac	tgtgtgcatc	acatttcac	aagtcagctc	cctgctggta	gttgtagtat	420
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attttctttt	ttacttgatg	caatatgtga	gtcactagat	taacagttgt	ttcctactcc	600
ttttctctcc	agcatcctcc	acatcagctt	tacaaagggc	aagctctggg	tttttcccgt	660
aggtctgacg	cattcatgct	gttgccct				688

<210> 1025

<211> 993

<212> DNA

<213> Unknown (H38g875 nucleotide)

<220>

<223> Synthetic construct

<400> 1025

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atgggtgctga	ggaacctgct	caacatcctg	gctgtcagct	ctgactcccc	cctccacacc	180
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ctgacacaga	tttcttcttt	gtcctttttt	gcatgtatag	aaggcatgct	cctgactgtg	360
atgacctatg	actgctttgt	agccatctgt	tgccctctgc	actaccagct	catcgtgaat	420
cctcacctct	gtgtcttctt	cgttttgggt	tcctttttcc	ttagcctggt	ggattcccag	480
ctgcacagtt	ggattgtggt	acaattcacc	atcatcaaga	atgtggaaat	ctctaattct	540
gtctgtgacc	cctctcaact	tctcaaactt	gcttgttctg	acagcgatc	caatagcata	600
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caaagtgcc	tgtggaggct	gctcagcaga	acagtcgaat	ctcatgatct	gttccatcct	960
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<210> 1026

<211> 965

<212> DNA

<213> Unknown (H38g876 nucleotide)

<220>

<223> Synthetic construct

<400> 1026

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cggtgctgag	gaacctgtgc	agcctcctgg	ctgtccgctc	tgactcccc	ctccacaccc	180
ccatatactt	cttctctctc	aacctgtgct	gggctgacat	cggtttcacc	tcggccacag	240
ttcccaagat	gattgtggac	atgcagtcgc	atagcagagt	catctctcat	gcaggctgcc	300
tgacgcagat	gtctttcttg	gtcctttttg	catgtataga	aggcatgctc	ctgactgtga	360
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aaagtgccct	gtggggggctg	cacagcagaa	cagtcgaatc	tcattgatctg	ttccatcctt	960
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<210> 1027

<211> 945

<212> DNA

<213> Unknown (H38g877 nucleotide)

<220>

<223> Synthetic construct

<400> 1027

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acgggtcaggg	gcaacctcag	catcctggca	gctgtcttgg	tggagcccaa	actccacacc	180
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gttccatcaa	tgttgagtcg	tctctgtccc	cgcaagcgtg	cagttccctg	tggggcctgc	300
cttaccacgc	tcttcttctt	ccatctgttc	gttggagtgg	actgcttctt	gctgaccgcc	360
atggcctatg	accaattcct	ggccatctgc	cggccctcca	cctacagcac	ccgcatgagt	420

cagacagtcc	agaggatggt	ggtggctgcg	tcctgggctt	gtgctttcac	caacgcactg	480
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aactatatgc	gactgggttc	aaccaagctt	tcagacaagg	ataaagctgt	tgggaattttc	840
aacactgtca	tcaatcccat	gctgaacca	atcatctaca	gcttcagaaa	ccctgatgtg	900
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<210> 1028

<211> 969

<212> DNA

<213> Unknown (H38g878 nucleotide)

<220>

<223> Synthetic construct

<400> 1028

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tttctctttg	tttatcttat	cacctggga	ggtaacttgg	ggatgatcac	tctcatatgg	180
attgatccca	gactccacac	tcctatgtac	ttttttctta	ggcacttgct	ctttgtagat	240
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gctgatggga	agcaaaaagc	tttcttcacc	tgtttttctc	accttgccgc	tgtctccatc	780
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agcttgagga	ataaggaggt	gaaagatgca	ttcagaagaa	aaattgagag	gaaaaaattt	960
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<210> 1029

<211> 687

<212> DNA

<213> Unknown (H38g879 nucleotide)

<220>

<223> Synthetic construct

<400> 1029

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tttttctgtc	acgttcctgg	tcattttacct	tattatggta	atgggcaatt	tgagcatgat	180
tttgatcatt	agaagtgact	gaaaacttca	cattccaatg	tacttcttcc	tcagtcacct	240
ctccttttga	gttctctgtt	atactctcaa	tgtcactcct	cagatattgg	ttaatttctt	300
atccaagaga	aaaaccattt	tcttcattgg	ttgtgtaagt	gttttataat	tctacttttt	360
cattgtcctg	ataatcagag	attatcatat	gcttacagtg	atggctaattg	actgctacat	420
ggccatttgc	aagcccttgt	tatatggtag	taaaatgtcc	agatttgtct	gcctctctct	480
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tcttctgtcc	ttctgaggat	ccaatgagat	caaccacttt	gactgtgcgg	acccccctct	600
gttagtcctc	ccttgccgag	gtacctgtgt	caaataaatc	atcatgttga	tggagccaca	660
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<210> 1030

<211> 859

<212> DNA

<213> Unknown (H38g880 nucleotide)

<220>

<223> Synthetic construct

<400> 1030

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atcaatagca	tattcatata	ttttgataat	actatgtttg	gttttcttcc	catttcaggg	540
atccttttgt	cttactataa	aattgtcccc	tccattctaa	ggatttcac	atcagatggg	600
aagtacaaag	ccttctcagc	ctgtggctgt	cacctggcag	ttggttgctt	attttatgga	660
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ggcgtcagt	atgtacgctg	tggtcacccc	catgtgaac	cctttcatct	acagcctgag	780
aaacagggac	attcaaagt	ccctgtggag	ggtgtgcaac	aaaacagtcg	aatctcatga	840
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<210> 1031

<211> 975

<212> DNA

<213> Unknown (H38g881 nucleotide)

<220>

<223> Synthetic construct

<400> 1031

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actggaaact	tgggaatgat	tgtcctcacc	cgaattgatt	cccgccttca	cacacccatg	180
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cagcagtggg	tctttggggt	ctttgtggca	gcagactggt	tctctttgga	gtccatggcc	360
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gcagtgattc	ctatgttgaa	cccacttatc	tacagcttga	gaaacaagga	agtcaaagat	900
gccatccaca	ggactgtcac	tcagaggaag	ttttgcaagg	cctaaattct	tatccagaag	960
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<210> 1032

<211> 941

<212> DNA

<213> Unknown (H38g882 nucleotide)

<220>

<223> Synthetic construct

<400> 1032

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cctatgctat	gtgccatttt	cttcgtgttt	tttctagcag	tttatatagt	tactataccg	120

ggaaatatta	gcataatcct	cttaatccaa	agcagcccac	agcttcacac	gctaattgtac	180
ctttttctca	gccatttggc	ttctgtggac	attgggtatt	ccatatcagt	tacgccaatc	240
attctcatca	atttcttaag	agagaaaacg	actatttcctg	tcacaggctg	tatagcacag	300
cttggctctg	atgtcatgtt	tgaaccaca	gagtgtcttc	tgctggtcac	tatgtggcta	360
tctgctctcc	cctgctttac	tccatccaaa	tgcctccagt	cgtctgtctc	ctcctactgg	420
gagcctccta	cctgggtgga	tgcctgaacg	cttcgtcttt	tacaggctgt	ttgatgaacc	480
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agctttcttg	tggccatgtt	tacattgctg	aaatatcccc	tgccatctcc	tctgcatctg	600
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tgaagggtgtg	ctctactgag	ggaaggaaga	aggctttctc	cacctgcgct	tcccacctca	720
ctgcagtcac	tttgttctat	gggaccattt	tgtttgttta	tgtgatgccc	aagtcaagct	780
attcagcgga	tcaggtaacg	gtggcatttg	tgatctacac	gggtgggtgatt	cccatgctga	840
acccctcat	ctacagtctc	aggaataagg	agggtgaaaga	ggccatgaga	aaattgatgg	900
caagaacaca	ttggttttcc	tgaattaaat	cagtataatc	c		941

<210> 1033

<211> 606

<212> DNA

<213> Unknown (H38g883 nucleotide)

<220>

<223> Synthetic construct

<400> 1033

atctttgcca	tcttgaccac	cattgactgc	tgtgtatttg	tctgggaatt	cctggagtgc	60
acagtctttg	tgaataagag	ggcatgtgac	cagctggcgt	gtgggtgcctt	ttgcattggc	120
ctgatcatga	cagtgggtcta	aataaccaca	gtgtcacaga	ggtacaaaag	gagcacatat	180
gctatattga	ctgcttcttg	tttgacaccc	ttcttgtcat	gaaactctcc	tgcattgaca	240
atactatcta	tgaataaaac	agtattttat	tcaccacaca	tgtgtgcagg	tgtccatggg	300
tttggtttgc	atttctcata	ttgacatccc	tgttacctcc	atcgtgctta	gaatttctta	360
atctgaggtc	tttgccacct	gtgtccccc	acccccacct	catcatgggc	attgtctata	420
tgtctgtgct	tgtactgctt	acctcaagca	caagccaatg	aattcaatag	aaaacaggtc	480
ttctataaga	gacctacatt	atcatcattc	attctgcctc	tggacactgt	tgtttacact	540
ctgaggtaca	tggaggccaa	ggataccatg	tacagagctg	tggacagaaa	tatttcttaa	600
cagatt						606

<210> 1034

<211> 945

<212> DNA

<213> Unknown (H38g884 nucleotide)

<220>

<223> Synthetic construct

<400> 1034

atggagccag	aagctgggac	caataggacc	gctgttgctg	agttcattct	actgggccta	60
gtgcaaacag	aagagatgca	gccagttgtc	tttgtgctcc	tcctctttgc	ctatctgggc	120
acaactgggg	gcaacctcag	catcctggca	gccgtcttgg	tggagcccaa	actccacgcc	180
cccattgact	tcttcttggg	gaacctgtca	gtgctggatg	tcggatgtat	cactgtcact	240
gttcttgcaa	tgttgggtcg	tctcttgtcc	cacaagtcca	caatttctta	tgacgcctgc	300
ctctcccagc	tcttcttctt	ccacctctcg	gctgggatgg	actgcttctt	gctgaccgcc	360
atggcctatg	accgactcct	ggccatctgc	cagcccccca	cctacagcac	ccgcatgagt	420
cagacagtcc	agaggatgtt	ggtggctgcg	tccttggctt	gtgccttcac	caacgcactg	480
acccacactg	tggccatgtc	cacgtcctac	ttctgtggcc	ccaatgaggt	caatcacttc	540
tactgtgacc	tcccacagct	cttccagctc	tcctgtctca	gcacccaact	caatgagctg	600
ctgctctttg	ctgtgggttt	catcatggca	ggcacacctt	tggttctcat	catcactgcc	660
tacagccacg	tggcagctgc	agttctacga	atccgttcag	tggagggccg	aaagaaggcc	720
ttctccacgt	gtggctccca	cctcaccgtg	gtttgccttt	tctttggaag	aggtatcttc	780
aactacatga	gactgggttc	agaggaggtc	tcagacaagg	ataaaggggg	tggagttttc	840
aacactgtta	tcaaccctat	gctgaacctt	cttatctaca	gcctcagaaa	ccctgatgtt	900
cagggtgctc	tgtggcaaat	atttttgggg	aggagatcac	tgacc		945

<210> 1035
 <211> 927
 <212> DNA
 <213> Unknown (H38g885 nucleotide)

<220>
 <223> Synthetic construct

<400> 1035
 atgaagagaa agaacttcac agaagtgtca gaattcattt tcttgggatt ttctagcttt 60
 ggaaagcatc agataaccct ctttgtgggt ttcctaactg tctacatttt aactctgggt 120
 gctaacatca tcattgtgac tatcatctgc attgaccatc atctccacac tcccatgtat 180
 ttcttcctaa gcatgctggc tagttcagag acggtgtaca cactgggtcat tgtgccacga 240
 atgcttttga gcctcatttt tcataaccaa cctatctcct tggcaggctg tgctacacaa 300
 atgttctttt ttgttatctt ggccactaat aattgcttcc tgcttactgc aatgggggtat 360
 gaccgctatg tggccatctg cagacccttg agatacactg tcatcatgag caaggggacta 420
 tgtgcccgagc tgggtgtgtg gtcctttggc attgggtctga ctatggcagt tctccatgtg 480
 acagccatgt tcaatttgcc gttctgtggc acagtggtag accacttctt ttgtgacatt 540
 taccagtcga tgaactttc ttgcattgat accactatca atgagataat aaattatggt 600
 gtaagtcat ttgtgatttt tgtgcccata ggctgatata ttatctccta tgtccttgtc 660
 atctcttcca tcttcaaat tgcctcagct gagggccgga agaagacctt tgccacctgt 720
 gtctcccacc tcaactgtgt tattgtccac tgtggctgtg cctccattgc ctacctcaag 780
 ccgaagtcag aaagttcaat agaaaaagac cttgttctct cagtgcagta caccatcatc 840
 actcccttgc tgaaccctgt tgtttacagt ctgagaaaca aggaggtaaa ggatgcccta 900
 tgcagagttg tgggcagaaa tatttct 927

<210> 1036
 <211> 958
 <212> DNA
 <213> Unknown (H38g886 nucleotide)

<220>
 <223> Synthetic construct

<400> 1036
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 ctcttgaggga tctcagagag tcttgagcag cagcagatgc tgttttggat gttcctgggtc 120
 aggtacctgg tcacgggtgct gggaaatgtg ctcacatcc ctcacatcc tggccatcag ctctgattcc 180
 cgctgcaca ccccatgta cttcttctct gccaacctct ccttcaactga cctcttcttt 240
 gtcaccaaca caatcccaa gatgctgggt aacctccagt cccagaacaa agccatctcc 300
 tacacagggt gtctgacaca gctctaactc ctggtctcct tgggtggcct ggacaacctc 360
 aacctggcgg tgatggcgta tgatcgctat gtggccatct gccgtcccct ccactatgtc 420
 acagccatga tccctgggct ctgtatcttg ctctctcct tgtgttgggt gttctctgcc 480
 ctctatggcc tcatccatat cctctcatg accaggtgac cttctgtggg tctcaaaaga 540
 tccactacct cttctgtgag atgtacttcc tgctaaggct ggcattgtcc aacatccacg 600
 tcaaccacac agtactgggt gccacgggct gcttcatctt cctcatcccc ttaggtttca 660
 tgatcacatc ctacgcccgc attgtcagag ccatcctcca aataccctca gccactggga 720
 agtacaaagc cttctccacc tgtgcttccc atttggtgtg ggtctccctc ttctatggga 780
 ctctgggtat ggtgtacctg cagccctcc aaacctactc catgaaggac tcagtagcca 840
 cagtgatgta tgcgggtggg acgccatgat taacctttc atctacagcc tgaggaacaa 900
 ggacatgcat ggggctctgg gaagacttcg ccaaggaaaa gccttccaga agttgaca 958

<210> 1037
 <211> 828
 <212> DNA
 <213> Unknown (H38g887 nucleotide)

<220>
 <223> Synthetic construct

<400> 1037

atgcgaagaa	agaacctcac	agaggtaaca	gagtttggtt	tcctgggatt	ctccagattc	60
cacaaacatc	acatcactct	ctttgtgggt	tttctcatcc	tgtacacatt	aactgtggct	120
ggcaatgcc	tcacatgac	catcatctgc	attgaccgtc	acctccacac	tcccatgtac	180
ttcttcctga	gcacgtctgg	tagctcaaag	acagtgtaca	caactgttcat	cattccacag	240
atgctctcca	gcttcgtaac	ccagacccag	ccaatctccc	tagccgggtg	taccacccaa	300
acgtttctct	ttgttacctt	ggccatcaac	aattgcttct	tgctcacagt	gatgggctat	360
gaccactata	tggccatctg	caatcccttg	agatacaggg	tcattacgag	caagaagggtg	420
tgtgtccagc	tgggtgtgtg	agccttttagc	attggcctgg	ccatggcagc	tgtccaggta	480
acatccatat	ttaccttacc	tttttgtcac	acgggtgggtg	gtcatttctt	ctgtgacatc	540
ctccctgtca	tgaacctctc	ctgtattaat	accactatca	atgagataat	caatttttgtt	600
gtcagggttat	ttgtcatcct	gggtcccatg	ggctctggct	tcactctccta	tgtcctcatc	660
atctccactg	tcctcaagat	tgcctcagct	gagggttgga	agaagacctt	tgccacctgt	720
gccttccacc	tcactgtgtg	cattgtccat	tatggctgtg	cttccattgc	ctacctcatg	780
cccaagtcag	aaaactctat	agaacaagac	ctccttctct	cagtgtacc		828

<210> 1038

<211> 936

<212> DNA

<213> Unknown (H38g888 nucleotide)

<220>

<223> Synthetic construct

<400> 1038

atggatggag	ataaccagag	tgagaactca	cagttccttc	tcctggggat	ctcagagagt	60
cctgagcagc	agcagatcct	gttttggtatg	ttcctgtcca	tgtacctggt	cacgggtgctg	120
ggaaatgtgc	tcacatcctt	ggccatcagc	tctgattccc	acctgcacac	ccccatgtac	180
ttcttctctg	ccaacctctc	cttcaactgac	ctcttctttg	tcaccaacac	aatccccaaag	240
atgctgggtga	acttccagtc	ccagaacaaa	gccatctcct	atgcaggggtg	tctgacacag	300
ctctacttcc	tgggtctcctt	ggtagccctg	gacaacctca	tcctggccgt	gatggcgat	360
gatcgctatg	tggccatctg	ctgccccctc	cactatgtca	cagccatgag	ccctgggctc	420
tgtgtcttgc	tcctctcctt	gtgttggggg	ctgtctgttc	tctatggcct	cctcctcacc	480
ttcctcctga	ccaggggtgac	cttctgtggg	cctcgagaga	tcactacct	cttctgtgac	540
atgtacatcc	tgtgtgtggct	ggcatgttcc	aacacccaca	tcattcacac	agcattgatt	600
gccactggct	gcttcatctt	cctcaccctc	ttagggttca	tgaccacatc	ctatgtacgt	660
attgtcagaa	ccatcccttca	aatgccctcg	gcctctaaga	aatacaaaac	tttctctacc	720
tgtgcctcgc	atttgggtgt	gggtctccctc	ttttatggga	cgcttgctat	gggtgtacctg	780
cagccccctc	atacctactc	catgaaggac	tcagtagcca	cagtgtatga	tgtgtgtctg	840
acacctatga	tgaacctttt	catctacagc	ctgaggaaca	aagacatgca	tggggctccg	900
ggaagagtcc	tatggagacc	ctttcagagg	cctaaa			936

<210> 1039

<211> 898

<212> DNA

<213> Unknown (H38g889 nucleotide)

<220>

<223> Synthetic construct

<400> 1039

atggctgatg	gaaatataaa	aggatcacag	aattcatttt	tgtaggctta	aggtatcatc	60
ttcagctgca	agtcttctct	ttcttaccat	ttctaccttt	tttacctcat	tactatgaca	120
gaaaacttgg	gcacatgagt	tcgcatctgg	ctcgattcct	gctttcacac	acctatgtac	180
tttgtctcca	gctacctgtc	ctttgtggac	atctgcttct	catccgttgt	gggccacaag	240
ttgtctactg	acttatttgc	tgttaaggaaa	gccatctctt	tcctgggctg	tccttgcag	300
cagtgggtct	ttgggttctt	cgtagtcatt	gagtatcttc	tcttggcttc	catggcctat	360
gacaattatg	tggccatctg	taaccattg	ttgtactcag	tggccatgta	atagagactg	420
tgcacccagc	tgggtgtgtg	acgttatgca	gctgatttct	tcaacaccat	aactcacaca	480
acggctgctt	ttcattttcc	cttttttcc	tccaacatta	tcaatcattt	cttctgtgac	540
atgtctctcc	ttctttctct	ctgtgtgtgt	gacgcccggg	tcaataaatt	gttagttttc	600

attgtggctg	gagctgtact	agttgtcagt	agcctgacca	ttataatctc	ctatTTTTac	660
atccttactg	acattctgag	gatctgctct	gctaattggg	aagaacaaaa	ctTTTTccac	720
ctgctcttca	cacttaacag	ctgtttccat	cttttatggg	tctctcttct	ttagctacgt	780
ttcgaccagg	tgcaactttt	tacccggaac	tcaataaaat	agtgttggtg	ttctgtacat	840
ccccatgttg	aaacctctca	tctacagctt	gataaataaa	gaagtatcct	agccacta	898

<210> 1040

<211> 934

<212> DNA

<213> Unknown (H38g890 nucleotide)

<220>

<223> Synthetic construct

<400> 1040

atggaaaaaa	taaacaacgt	aactgaattc	atTTTTctggg	gtctttctca	gagcccagag	60
attgagaaag	tttgTTTTgt	ggtgtTTTTct	ttcttctaca	taatcattct	tctgggaaat	120
ctctcatca	tgctgacagt	ttgcctgagc	aacctgttta	agtcacccat	gtatttcttt	180
ctcagcttct	tgtctTTTTgt	ggacatttgt	tactcttcag	tcacagctcc	caagatgatt	240
gttgacctgt	tagcaaagga	caaaaccatc	tcctatgtgg	ggtgcatgtt	gcaactgctt	300
ggagtacatt	tctttgggtg	cactgagatc	ttcatcctta	ctgtaatggc	ctatgatcgt	360
tatgtggcta	tctgtaaacc	cctacattat	atgaccatca	tgaaccggga	gacatgcaat	420
aaaatgttat	taggggacgtg	ggtaggtggg	ttcttacact	ccattatcca	agtggctctg	480
gtagtccaac	tacccttttg	tggacccaat	gagatagatc	actacttttg	tgatgttcac	540
cctgtgttga	aacttgccctg	cacagaaaca	tacattgttg	gtgttggtgt	gacagccaac	600
agtgggtacca	ttgctctggg	gagttttgtt	atcttgctaa	tctcctacag	catcatccta	660
gtttccctga	gaaagcagtc	agcagaaggc	aggcgcaaa	ccctctccac	ctgtggctcc	720
cacattgcca	tggtcgttat	ctttttcgag	cccctgtact	tttatgtaca	tgcgccctga	780
tacgaccttt	tcagaggata	agatgggtgg	tgtattttac	accattatca	ctcccatggt	840
aaatcctctg	atTTatacac	tgagaaatgc	agaagtaaag	aatgcaatga	agaaactgtg	900
gggcagaaat	gttttcttgg	aggctaaagg	gaaa			934

<210> 1041

<211> 951

<212> DNA

<213> Unknown (H38g891 nucleotide)

<220>

<223> Synthetic construct

<400> 1041

atggactata	gaaatcaaac	tttggttact	gaattttttt	ccgtgggatt	aacaaatctc	60
tttcagcaca	agattgctct	ctttctggta	tttctcttgg	tttatcttgt	cactgttccg	120
ggaaacttgg	gaatgatcac	tcttatttgg	atggattctc	gactccagac	ccccaaagta	180
ttttctctct	gccacttgte	ctttgtggat	gtctgtcctt	cttctgccat	cggteccaa	240
atggtgactg	atatcttcgt	ggagaaaaaa	gtaatctctt	tggttggtgt	gcccagttat	300
ggttttttgg	ccatttttga	gtaactgaat	gtttctctct	ggctgccatg	gcatatgacc	360
ggtataggct	atctataagc	ctttgttgta	tacactcatt	atgtcccaac	aggtctgtgt	420
gcagctgggtg	gtgggcctta	tgctgtgggc	cttataagca	ccatgaccca	tatgactttc	480
acctttcgcc	tactctactg	tggtccaaac	atcatcaatc	acttcttctg	tgaccttctc	540
cctgtcctct	ccctggcata	tgcagatacc	catattaata	aatgttttact	ttttatcttg	600
gtgggtgccc	tgggagtact	cagtgggtgtg	atcatcttgg	tctcctacat	ttacattgtc	660
attgccatcc	tgagaattcg	ctctgtgac	gcgagacgca	aagacttctc	cacttgctct	720
tcacacctga	tggtgtctct	catcctgtat	gggacactct	tctttatctg	tgtatgtcca	780
agctctagtt	tctctatcaa	catcaataaa	gtggtttccc	tgttctacac	agcagtgatc	840
cccatgttga	atcccccttat	ctacagcctg	agaacaag	aggtaaaaga	ttcattcagc	900
aagaagtttg	aaagaaagaa	gtttcttata	ggtaggtgaa	ctagaatacc	a	951

<210> 1042

<211> 930

<212> DNA

<213> Unknown (H38g892 nucleotide)

<220>

<223> Synthetic construct

<400> 1042

atggtgaatt	ttacacatgt	ctcagaattt	gttctacttg	ggttccaagg	gggtcccggg	60
atgcaggcta	tgctatttct	gatttttctg	atcctgtatg	gcatagctgt	gggtgggaaac	120
cttggcatga	ttgtaattat	ctgggtagat	gcacacctcc	acacccaat	gtatgccttc	180
ctgcaaagcc	tttcattgtt	ggacatctgc	tattcctcca	caattgcacc	cagggtctctg	240
gcgaactcca	tgcaagagga	ccacacaatt	tcctttggcg	gatgtgctgc	tcagtctctt	300
ttcttgtctc	tctttgggat	cacagaggct	ttcctcctgg	ctgccatggc	ctatgaccgc	360
ttcatcgcca	tctgcaaccc	tcttctgtac	tctgtgagca	tgtctcacca	ggctctgtgtg	420
ctgttaatat	caggatccta	cttgtggggt	gtagtcaatg	ccattgctca	aacaaccatg	480
accttcagggt	tgcttttctg	tgggtccaat	gagatcaacg	actttttctg	tgatgttccc	540
ccactcttgt	ccctctcatg	ttcagatacc	tttataaacc	aactgggtct	tcttgggtta	600
tgtggctcca	ttattgtcag	tacctttttg	attgtcctgg	tctcatacat	ttacatcatc	660
tcaacaattc	tgaggatccc	gaccatgcag	ggacgctaga	aagcctcttc	cacgtgcgct	720
tcccacctaa	caggagtgtg	cttgtttttt	ggtagtggtt	tcttcatgta	tgcacaaccc	780
agtgccatct	tcttcatgga	gcaaagtaaa	atagtgtcca	tattctacac	tatgggtcatc	840
cccattgctga	atccccctgat	atacagcctg	aggaacaaag	aggccaagca	ggctctgaga	900
cggagcatgc	agaagctgtc	tttgtgatca				930

<210> 1043

<211> 927

<212> DNA

<213> Unknown (H38g893 nucleotide)

<220>

<223> Synthetic construct

<400> 1043

atgagggaaa	ataaccagtc	ctctacactg	gaattcatcc	tcctgggagt	tactgggtcag	60
caggaacagg	aagatttctt	ctacatcctc	ttcctgttca	tttaccocat	cacattgatt	120
ggaaacctgc	tcattgtcct	agccatttgc	tctgatgttc	gccttcacaa	ccccatgtat	180
tttctccttg	ccaacctctc	cttgggtgac	atcttctctt	catcggtaac	catccctaag	240
atgctggcca	accatctctt	gggcagcaaa	tccatctctt	ttgggggatg	cctaacgcag	300
atgtatttca	tgatagcctt	gggtaacaca	gacagctata	ttttggctgc	aatggcatat	360
gatcgagctg	tggccatcag	ccaccactt	cactacacaa	caattatgag	tccacgggtct	420
tgtatctggc	ttattgtctg	gtcttgggtg	attggaaatg	ccaatgccct	ccccacact	480
ctgctcacag	ctagtctgtc	cttctgtggc	aaccaggaag	tggccaactt	ctactgtgac	540
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ctaggggttg	gcattttctc	tgtgccatta	ctatgcatca	ttgtctccta	tattcgagtc	660
ttctccacag	tcttccaggt	tccttcacc	aaggcgctgc	tcaaggcctt	ctccacctgt	720
ggttccacc	tcacggttgt	ctctttgtat	tatggtacag	tcatgggcac	gtatttccgc	780
cctttgacca	attatagcct	aaaagacgca	gtgatcactg	taatgtacac	ggcagtgacc	840
ccaatgttaa	atcctttcat	ctacagtctg	agaaatcggg	acatgaaggc	tgccctgcgg	900
aaactcttca	acaagagaat	ctcctcg				927

<210> 1044

<211> 927

<212> DNA

<213> Unknown (H38g894 nucleotide)

<220>

<223> Synthetic construct

<400> 1044

atgaagaaag	aaaatcaatc	ctttaacctg	gattttattc	tcctgggagt	tactagtcag	60
caagaacaga	ataatgtctt	ctttgtgatt	tttttgtgca	tttaccocat	cacactgact	120
ggaaatctgc	tcatcatctt	ggccatctgt	gctgacattc	gccttcacaa	ccccatgtat	180

tttctccttg	ccaacctctc	cttggttgac	atcatcttct	catccgtaac	catccctaag	240
gtgctggcca	accatctctt	gggcagcaag	ttcatctcct	ttgggggatg	cctaatagcag	300
atgtatttca	tgatagcctt	ggccaaggca	gacagctata	ccttggctgc	aatggcatac	360
gatcgagctg	tggccatcag	ctgcccactt	cattacacaa	caattatgag	tccacgggtct	420
tgtatcctgc	ttattgctgg	gtcttgggtg	attggaaaca	ccagtgtctt	ccccacact	480
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ctaggggtcg	gcgttttctc	tttgccatta	ctatgcatca	ttgtctccta	tggttcagggtc	660
ttttccacag	tcttccaagt	tccatctacc	aagagtctat	tcaaagcctt	ctgcacctgt	720
ggctcccacc	tcacagttgt	ttttttatat	tatggtacaa	cgatgggcat	gtatttccgc	780
cctctgacca	gttacagccc	caaagatgca	gtgataactg	tgatgtatgt	ggcagtgacc	840
ccagcattaa	atcctttcat	ctatagtctg	agaaattggg	atatgaaggc	agccctacag	900
aaactcttca	gcaagagaat	ctcctca				927

<210> 1045

<211> 990

<212> DNA

<213> Unknown (H38g895 nucleotide)

<220>

<223> Synthetic construct

<400> 1045

gctcttcttt	tccattccta	caaacatccc	accagagga	gaatgactgt	caaaagtcac	60
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cacttcctca	ttttccttga	tatccatatg	gtcacatgg	tggggaactt	gggcatgac	180
actctaattt	gtcttaactc	tcagcttcac	accccatgt	actacttctt	cagcaatctg	240
tcactcttgg	atctctgcta	ttcctccatt	actaaccta	agatgctggg	gaactttgtg	300
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tgctgccctt	tgctttgcaa	cgctcatctc	tctcatgtca	cctgctccct	gatgggtggc	480
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tcctgatcta	gtgccttatg	atgttgagat	ggcagttctc	ttttttgcta	gattgcaacc	660
tgagaatcat	gatcttaaca	gttcttgttt	tcttacacct	tcattctctt	cagcatectg	720
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tccttgcccc	aagagaatgt	ggcctctgtg	ttctacacta	cagtaatcta	cgtgccgaat	900
cccctaattg	acagcctgaa	aaacaaggat	gtaaaagctg	ccatgcagaa	aacactaagg	960
agtaagtttt	gttgccagatg	taattatctt				990

<210> 1046

<211> 948

<212> DNA

<213> Unknown (H38g896 nucleotide)

<220>

<223> Synthetic construct

<400> 1046

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gctgggaacc	tgctcattgt	cctggccatt	ggcactgaca	cacacctcca	caccctatg	180
tacttcttcc	ttgccagctt	gtcgtgtgca	gatatctttt	ccacctccac	cactgtgccc	240
aaggccctgg	tgaatatcca	gacccagagc	aggtccattt	cctacgcagg	gtgtttggca	300
cagctctact	tcttcttgac	ttttggggac	atggacatct	ttctcccggc	tacaatggcc	360
tatgaccgct	atgtggccat	ttgccacctg	ctccactata	tgatgatcat	gagcctccac	420
cgctgtgcct	tcctgggtgac	agcctgctgg	accctcacaa	gtcttctcgc	catgactcgc	480
accttctcta	tattccggct	ttccttgtgc	tcttagatcc	ttcctggctt	cttctgtgat	540
ttgggaccgc	tgatgaaggt	gtcttgctct	gacgccagg	tcaatgagct	tgtgctcctc	600
ttcctagggg	gagcagtcac	tttaatccct	tttatgtctc	tcctgggtctc	ttatatccgc	660

attgtttcag	ccatcctcag	ggccccctct	gcccaggga	ggcgcaaggc	cttctctacc	720
tgcgactctc	acctcgttgt	tgttgctttg	ttctttggga	cagtgatcag	ggcttatctg	780
tgcccccat	cctcttcttc	caactcagta	aaggaggata	cagcggtgc	tgtcatgtac	840
acagtgggtga	ctccccgtct	gaacccccctt	atttacagca	tgcggaacaa	ggacatgaag	900
gcggcggttg	ttagacttct	caagggcagg	gtctccttct	cacagggc		948

<210> 1047

<211> 1007

<212> DNA

<213> Unknown (H38g897 nucleotide)

<220>

<223> Synthetic construct

<400> 1047

gatacagacc	cacagagtct	aacagatgtc	tctatatctc	tcctcctcaa	actctcagag	60
gatccagaac	tgcagcaggt	cgtcgctggg	ctgttcctgt	ccatgtgcct	ggtcacggtg	120
ctggggaacc	tactcatcat	cctggccgtc	agccctgact	cccacctcca	cacccccatg	180
tacttggtcc	tctccaacct	gtcccttgcc	tgacatcggt	ttcacctcca	ccacggtccc	240
caagatgatt	gtggacatcc	agtctcacag	cagagtcac	tcctatgcag	gctgcctgac	300
tcagatgtct	ctctttgcca	tttttgagg	tatggaagag	agacatgctc	ctgagtgtga	360
tggcctatga	cgggtttgta	gccatctgtc	accctctata	ttgttcagcc	atctttaacc	420
cgtgtttctg	tggcttctca	gatttggtgt	cttttttttt	ttttttctca	gtctttcaga	480
ctcccagctg	cacaacttga	ttgccttaca	aatgacctgc	ttcaaggatg	tggaaattcc	540
taattttctc	tgggaacctt	ctcaactctc	ccatcttgca	tgttgtagca	ccttcaccag	600
gaacatcagt	atttccctgc	tgccatattt	ggttttcttc	ccatcttggg	gacctttttc	660
tcttactgta	aaattgtttc	ctccattctg	aggggttcat	catcaggtgg	gaagtataaa	720
ccttctccac	ctgtgggtct	cacctgtcag	ttgtttgctg	attttatgga	acaggcattg	780
gagggtagct	cgggttcagat	gtgtcatctt	ccccgagaaa	gggtgcagtg	gcctcagtg	840
tgtacatggt	ggtcaccccc	atgctgaacc	ccttcactca	cagcctgaga	aacagggata	900
tgaaaagtgt	cctgcggcgg	cgcgatggca	gcacagtcta	atctcaacat	cttcttatct	960
gttccattcc	ttttgtagg	tggtttaaaa	aaggcgccaa	ggtcaaaa		1007

<210> 1048

<211> 926

<212> DNA

<213> Unknown (H38g898 nucleotide)

<220>

<223> Synthetic construct

<400> 1048

atgagacaga	ataataatat	tacagaattt	gtcctcctgg	gcttctctca	ggatctggat	60
gtgcaaaaag	cattatttgt	catattttta	ctcacatact	tggtgacagt	gggtggggaac	120
ctgctcattg	tggtgactat	tattaccagc	ccttccttgg	gctccccaat	gtacttcttc	180
cttgccctgc	tgctatttat	agatgctgca	tattccacta	caatttctcc	caaattgatt	240
gtagacttac	tctgtgataa	aaagactatt	tctttcccag	cttgcatggg	ccagttattt	300
atataccact	tgtttggtgg	ttctgaggtc	ttccttcttg	tggtgatggc	ctgtgatcac	360
tatgtggcca	tctgtaagcc	actgcactat	ttgaccatca	tgaatcgaca	ggtttgaatc	420
cttctgttgg	tggtggctgt	gactggagg	tttctgcatt	ctgtgtttca	aattgttgtt	480
gtatacagtc	tcgctttctg	tggccccaat	gtcattgact	actttgtctg	tgacatgtac	540
ccattattgg	aactggatg	cactgacacc	tactttattg	gccttactgt	ttttgtcaat	600
gggtggaacaa	tctgtatagt	cgtcttcacc	cttctactaa	tctcctatgg	agtcactcta	660
aactccctta	aaacttacag	tcaagaagg	aggcataaag	tcctgtttac	ctgcagctcc	720
cacattatcg	tctttgccct	cttttttggt	ccctgtatgt	tcatgtatgt	tagacctgtt	780
tcaaacatcc	ttttgataaa	ttcctgacag	tgttttatac	agttatcaca	cccatgttga	840
atcctttaat	atacacattg	agaaattcag	agatgagaaa	ttctgtagaa	acactcttgt	900
gtaaaagtta	actgtattag	agtaag				926

<210> 1049

<211> 939

<212> DNA

<213> Unknown (H38g899 nucleotide)

<220>

<223> Synthetic construct

<400> 1049

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ctcaggctaa	ggacactcct	ttttgtgttc	ttttttctaa	tctacatcct	gactcagctg	120
ggaaacctgc	ttattttaat	cactgtctgg	gcagacccaa	ggctccatgc	ccgccccatg	180
tacatctttc	ttggtgttct	ctcagtcatt	gatatgagca	tctcctccat	cattgtccct	240
cgctcatga	tgaacttcac	tttaggtgtc	aaacccatcc	catttggtgg	ctgtgttgct	300
caactctatt	tctatcactt	cctgggcagc	acccagtgtc	tcctctacac	cctaattggcc	360
tatgacaggt	acctggcaat	atgtcagccc	ctgcgtacc	ctgtgctcat	gactgctaag	420
ctgagcgcct	tgtttgtggc	tggagcctgg	atggcaggat	ccatccatgg	ggctctccag	480
gccatcctaa	ccttccgcct	gccctactgt	gggcccgaatc	aggtggatta	cttcttctgt	540
gacatccctg	cagtgttgag	actggcctgt	gctgacacaa	cagtcaacga	gctggtgacg	600
tttgtagaca	ttgggggtgg	ggttgccagt	tgcttctccc	tgatcctcct	ctcctacata	660
cagatcattc	aggccatcct	gagaatccac	acagctgatg	ggcggcgcgc	ggctttttca	720
acttgtggag	cccatgtaac	cgtggtcacc	gtgtactatg	tgccctgtgc	cttcatctac	780
ctgaggcctg	aaaccaacag	ccccctggat	ggggcagctg	ccctagtccc	cacggccatc	840
actcctttcc	tcaacccctt	tatctacact	ctgcggaacc	aagaggtgaa	gctggccctg	900
aaaagaatgc	tcagaagccc	aagaactccg	agtgaggtt			939

<210> 1050

<211> 954

<212> DNA

<213> Unknown (H38g900 nucleotide)

<220>

<223> Synthetic construct

<400> 1050

atgggaaaga	ccaaaaacac	atcgctggac	actgtggtga	gagatttcat	tcttctgggt	60
ttgtctcacc	ccccgaatat	aagaagcctc	ctcttcctgg	tcttcttctg	catttacatc	120
ctcactcagc	tggggaacct	gctcattctg	ctcaccgtgt	gggctgaccc	gaagctccgt	180
gctcgcccca	tgtacattct	tctgggagtg	ctctcattcc	tggacatgtg	gctctectca	240
gtcatcgttc	cttgaattat	tttaaaactt	actcctgcca	acaaggctat	cccgtttggt	300
ggctgtgtgg	ctcaactgta	tttctttcac	ttcctgggca	gcacccagt	cttctctac	360
accttgatgg	cctatgacag	gtacctggca	atatgtcagc	ccctgcgcta	cccagtgtct	420
atgaatggga	ggttatgcac	agtccttggt	gctggagctt	gggtcgccgg	ctccatgcat	480
gggtctatcc	aggccacctt	gaccttcgc	ctgccctact	gtgggcccac	tcaggtagat	540
tactttatct	gtgacatccc	cgcagtattg	agactggcct	gtgctgacac	aactgtcaat	600
gagcttgtga	cctttgtgga	catcggggta	gtggccgcca	gttgcttcat	gttaattctg	660
ctctcgtagt	ccaacatagt	aaatgccatc	ctgaagatac	gcaccactga	tgggaggcgc	720
cgggccttct	ccacctgtgg	ctcccaccta	atcggtgtca	cagtctacta	tgccccctgt	780
attttcatct	accttagggc	tggctccaaa	ggccccctgg	atggggcagc	ggctgtgttt	840
tacactgttg	tactccatt	actgaacccc	ctcatctata	cactgaggaa	ccaggaagtg	900
aagtctgccc	tgaagaggat	aacagcaggt	caagggactg	aatgaaaata	agta	954

<210> 1051

<211> 930

<212> DNA

<213> Unknown (H38g901 nucleotide)

<220>

<223> Synthetic construct

<400> 1051

atgggaaaga	ccaaaaacac	atcgctggat	gccgtggtga	cagatttcat	tcttctgggt	60
ttgtctcacc	ccccaaatct	aagaagcctc	ctcttcctgg	tcttcttcat	catttacatc	120

ctcactcagc	tggggaacct	gtcattctg	ctcaccatgt	gggctgaccc	gaagctctgt	180
gtcgcgccca	tgtacattct	tctgggagtg	ctctcattcc	tggacatgtg	gtctctctca	240
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ggctgtgtgg	ctcaactgta	tttctttcac	ttcctgggca	gcacccagtg	cttctcttac	360
accttgatgg	cctatgacag	gtacctagca	atatgtcagc	ccctgcacta	cccagtgtct	420
atgaatggga	ggttatgcac	agtccttgtg	gctggagctt	gggtcgcccg	ctccatgcat	480
gggtctatcc	aggccacctt	gaccttccgc	ctgcccact	gtgggcccaa	tcaggtggat	540
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attttcatct	accttagggc	tggctccaaa	gacccctgg	atggggcagc	ggctgtgttt	840
tacactgttg	tcactccatt	actgaacccc	ctcatctata	cactgaggaa	ccaggaagtg	900
aagtctgccc	tgaagaggat	aacagcaggt				930

<210> 1052

<211> 900

<212> DNA

<213> Unknown (H38g902 nucleotide)

<220>

<223> Synthetic construct

<400> 1052

atgtttatat	tgacaggctt	cacagatgat	tttgagctgc	aagtcttcct	atttttacta	60
ttttttgcaa	tctatctctt	taccttgata	ggcaatttag	ggctggttgt	gttggtcatt	120
gaggattcct	ggctccacaa	ccccatgtat	tattttctta	gtgttttatc	attcttggat	180
gcttgctatt	ctacagttgt	caactccaaa	atgttggtea	atttcctggc	aaaaaataaa	240
tccatttcat	ttatcggatg	tgcaacacag	atgcttcttt	ttgttacttt	tggaaactaca	300
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gctggcattt	tacatgctac	tatacatata	gtggctacat	ttagcctgtc	cttctgtgga	480
tccaatgaaa	ttaggcattg	cttttgtgat	atgcctcttc	tccttgctat	ttcttgttct	540
gacactcaca	caaaccagct	tctactcttc	tactttgttg	gttctattga	gatagtcact	600
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gctaaggga	ggcaaaaggc	cttctctaca	tgtggctctc	acctaactgg	agtgacaatt	720
tatcatggaa	caattctcgt	cagttatatg	agaccaagtt	ccagctatgc	ttcagaccat	780
gacatcatag	tgtcaatatt	ttacacaatt	gtgattccca	agttgaatcc	catcatctat	840
agtttgagga	acaaagaagt	aaaaaaggca	gtgaagaaaa	tgttgaaatt	ggtttacaaa	900

<210> 1053

<211> 974

<212> DNA

<213> Unknown (H38g903 nucleotide)

<220>

<223> Synthetic construct

<400> 1053

cacacagagc	cacggaatct	cacagggtgc	tgagaattcc	tcctcctggg	actctcagag	60
gatccagaac	tgcagccagt	cctcgctttg	ctgtccctgt	ccctgtccat	gtatctggtc	120
acgggtgctga	ggaacttget	gagcatcctg	gctgtccgct	ctgagtcctc	gctccacaca	180
accatgtact	tcttctcttc	catcctgtgc	tgggctgaca	tcggtttcac	ctcagccaca	240
gttcccaaga	tgattgtgga	catgcagtg	tatagcaaag	tcattctctca	tgcgggctgc	300
ctgacacaga	tgtctttctt	ggtccttttt	gcattgtatg	aaggcatgct	cctgactgtg	360
atggcctatg	actgctttgt	aggcatctgt	cgcctctctc	actaccaggt	catcgtgaat	420
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ctgcacagtt	ggattgtgtt	acaattcacc	atcatcaaga	atgtggaaat	ctctaatttt	540
gtctgtgacc	cctctcaact	tctcaaaact	gcctgttctg	acagcgtcat	caatagcatc	600
ttcatatatt	ttggtagtac	tatgtttggg	tttcttccca	tttcagggat	ccttttgtct	660
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atacaaagtg	ccctgcgagg	gctgcccac	aaaacagtcg	aatctcatga	tctgttccat	960
cctttttctg	gtgt					974

<210> 1054

<211> 1006

<212> DNA

<213> Unknown (H38g904 nucleotide)

<220>

<223> Synthetic construct

<400> 1054

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gatccagaac	tgcaaccggt	cgtcgctggg	ctgttcctgt	ccatgtgcct	cgtcagtgtg	120
ctgggggaacc	tgetcatcat	cctggacgtc	agccctgact	cccacctccc	cacccccatg	180
tactttcttcc	tctccaacct	gtccttgcc	gacatcgggt	tcacctccac	cacgggtccc	240
aagatgattg	tggacatcca	gtctcacagc	aaagtcattc	atgcaggctg	cctgactgtg	300
atgtctctct	ttgccatttt	tggaggcatg	gaaaaaagac	atgctcctga	gtgtgatggc	360
ctatgaccgg	tttgtaccce	tctgtcaccc	tctatatcgc	tcagccatct	tgaacccgtg	420
tttctgtggc	ttcctaaatt	tgttgtcttt	tttttttttc	cctcagtctt	ttagactccc	480
agctgcacaa	cttgattgcc	ttacaaatga	cctgcttcaa	ggatgtggaa	attcctaatt	540
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tcagcatgta	tttccctgct	gccgtatttg	gttttctttc	catctcgggg	accttttct	660
cttactgtaa	aatggtttcc	tccattctga	gggtttcatt	atcagggtgg	aagtataaac	720
cttctccacc	tgagggtccc	acctgtcagt	tgtttgctga	ttttatggaa	caggcgttgg	780
agagtacctc	ggttcagatg	gtcatcttc	cccagaaag	ggtgcagtgg	cctcagtgat	840
gtacacgggtg	gtcaccceca	tgctgaaccc	cttcatctac	agcctgagaa	acggggatat	900
taaaagtgtc	ctgcggcggc	cgcaaggcag	cacagtctca	tctcaatacc	ttcttatctg	960
ttccattcct	tttgtagggt	gggttaacaa	agacagcaag	gtcaaa		1006

<210> 1055

<211> 929

<212> DNA

<213> Unknown (H38g905 nucleotide)

<220>

<223> Synthetic construct

<400> 1055

atggaaaata	ggaaaaattg	acttaattca	tcctcttggg	gctcacacag	aaccctgagg	60
gccaaaaagt	tttatttgtc	acattcttac	tcattctacat	tgtgacgata	atgggcaacc	120
tccttatcat	ggtgaccatc	atggccagcc	agtccttggg	ttcccccatg	tacttttttc	180
tggcttcttt	atcattttata	cataccgtct	attatactgc	cattgctccc	aaaatgattg	240
ttgacctgct	ctctgagaaa	aagaccattt	cttttcaggg	ttgtatggct	caacttttta	300
tggatcattt	atttgctggg	gctgaagtca	ttcttctggg	ggtaaatggc	tatgatcaat	360
atgtggccat	ctgtaagcct	cttcattatt	tgatcatcat	gaatcgtcga	gtctgtgttc	420
tcattgctgt	ggtggcctgg	attggaggct	ttcttcactc	attggttcaa	tttctcttta	480
tttatcagct	ccctttctgt	ggacccaatg	tcattgacaa	cttcctgtgt	gatttgtatc	540
ccttattgaa	acttgcttgc	accaataact	atgtcactgg	gctttctatg	atagctaagt	600
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ccacctttcc	cattgataaa	tccatgactg	tgggttttaac	ttgtataact	cccatgctga	840
aaccactaat	ctatgccctg	aggaatgcag	aaatgaaaag	tgccatgagg	aaacttttga	900
gtgaaaaagt	aagcttagct	ggaaaaggg				929

<210> 1056

<211> 925

<212> DNA

<213> Unknown (H38g906 nucleotide)

<220>

<223> Synthetic construct

<400> 1056

cacatgcctc	ccaacaatgt	gactgaattc	attctcttgg	ggctcacaca	gaatccacac	60
ttgcagaaaa	tactctttat	tgtattttta	tttatttttc	tatttaccat	gctggccaat	120
ctgttcattg	tcacacccat	ctcctgtagc	cccacacttt	catcacccat	gtacttcttt	180
ctcacttact	tatcctttat	agatgcctcc	tacacctctg	tcacaacccc	caaaatgac	240
accgacctgc	tctaccagag	gagaactatt	tccttggtg	gctgcctgac	tcagctcttt	300
gtggagcact	tgtctggagg	ctcagagatc	atcctcctta	ttgtcatggc	ctatgaccgc	360
tacgtggcca	tctgcaagcc	cctgcactac	acaaccatta	tgcaacaagg	gatctgccac	420
cttctggtgg	tgatagcctg	gattggaggc	atcctgcatg	ccactgtgca	gattcttttc	480
atgaccgact	tgcccttctg	tggtcccca	tgctattgac	cactttatgt	gtgatctctt	540
cccattgttg	aaacttgcc	gcagagacac	ctacagactt	gggatgctgg	tggcagccaa	600
cagtggagcc	atgtgcttgc	tcactttttc	cctgctcgtc	atctctaca	tagtcatcct	660
gagctccctg	aaatcctata	gctctgaagg	acagcacaaa	gccctctcca	cctgtggctc	720
ccactttact	gtcgttgtag	tcttttttgt	gccttgcata	ttcacctaca	tgcactcctgt	780
ggtcacctac	tctgtggaca	agttggtgac	tgtgttcttt	gcaatcctca	ctcccatggt	840
aaatcctata	atttacactg	tgagaaacac	agaggtaaaa	aatgccgtga	ggagtttggt	900
gaggaaaaga	gtaacagttt	atgca				925

<210> 1057

<211> 499

<212> DNA

<213> Unknown (H38g907 nucleotide)

<220>

<223> Synthetic construct

<400> 1057

atgtacacga	ctttactcat	ggcccagggt	gtgtctctgt	gcagacaatg	gatccacac	60
tctttctgtg	atatgtctgc	tctgctgaag	ctggccctct	ctgacactcg	agttaatgaa	120
tgagtgatat	ttatcatggg	agggctcatt	ctgtgcatcc	catccatact	catccttggg	180
tcctatgcaa	gaattgtctc	ctccatcctc	aaggctcctt	cttctaagtg	tatctgcaag	240
gccttctcta	cttgtggctc	ccaccctgtc	tgtgggtgtc	ctgttctatg	gaaccgttat	300
tggtctctac	ttatgctcat	cagctaatag	ttctactcta	aaggacactg	tcattggctat	360
gatgtacact	gtggtgaccc	ccatgctgaa	ccccttcctc	tacagcctga	ggaacagaga	420
catgaaggga	gccctgagca	gagtcattca	tcagaagaaa	actttcttct	ctctctgatg	480
ataacacttg	gagctatta					499

<210> 1058

<211> 996

<212> DNA

<213> Unknown (H38g908 nucleotide)

<220>

<223> Synthetic construct

<400> 1058

atgggacca	agaatcta	tcgtgttttg	gaattcttcc	tcctccactt	cttagatgac	60
ttggaactgc	agcctttcct	cttcaggctg	tccctgaacc	atgcacctag	tcacagtgt	120
tgcgaacttg	ctcacatcct	tctgactgtc	agctttgccc	tcacctccac	aaccccatga	180
acttcaacct	gtccttagct	gacattggtt	tcaccctgtc	cacaatttca	aagataactg	240
tagacctcca	aactcacagc	agaatcattt	tatacatgag	ctgcctgaaa	tagatgtctt	300
ttaaaattat	ttttggatgt	ttgcacaatc	tactcatgac	tgtgatggcc	tatgacccat	360
ttgtggcgac	ctgtcatctc	ttgtactaca	cagtgatcag	gaatccccac	ctctgtggcc	420
tcttgcctt	gggtctctc	tctctctctc	tttttttttt	ttgatcagtc	ttttggaaac	480
ccagctgtac	agtttgatgg	tgtcacaagt	tctctcatgc	aatgtagac	attcctcatt	540

tcttctgtga	cccttctcag	tttctccacc	tttctgttc	tgacactgcc	accaataaca	600
cattaatgca	ttttattggt	gccatctctg	tgggtccattc	tcagggatcc	tttactgtta	660
tactcaaatt	atgttctcca	tactcataaac	cctataaaat	gtgggaagta	taaagcaaac	720
cttctccacc	catcgctctc	acctgtcagt	tgtttgctta	ttttatggaa	caggccttgg	780
agtatacctt	agtttggtcg	gctcaccttc	cccaagaaca	ggtgtggtgg	cctcaatggt	840
atataccaca	gtcacctca	tgttgaaccc	tgcattcaca	gcctgaggaa	cagagacatc	900
aagaatacct	ggtggtggct	cctcagcata	actgcctggt	atcaatacct	gtgctatcct	960
ttatggagtg	tggttagaaa	aaacagcaaa	ctcaaa			996

<210> 1059

<211> 923

<212> DNA

<213> Unknown (H38g909 nucleotide)

<220>

<223> Synthetic construct

<400> 1059

atggggactt	caaataatga	gactgaattc	attctttttg	gcattacaaa	aaatccagaa	60
ctaaggaaaa	tattctctgc	tttgtttcta	gccatgtatg	tgaccacagt	gttgggaaat	120
ctattcattg	tggtgactct	ggctgcaagt	tggagtctga	gatcacctat	gtacttttcc	180
cttacttctt	tgtctctcat	gggtgccacc	tactcttcca	tcactgcccc	taagatgact	240
gtggactctt	tgagaacact	accatttccc	ttgaaggctg	catgaccag	ctctttgcag	300
agcatttctc	tgatggtgta	gcgatcatcc	ttctcactgt	gatggtctgt	gactgctatg	360
aggccatcag	taagccccctg	catgacacaa	ccatcatgag	tccacgggtg	tgctgctgtt	420
ggtggttagaa	gcttggtggg	ggggattaac	acatgccaca	atacagcttt	ttttttttca	480
tatatcaaat	acccttctgt	ggtcccaata	ttattgacca	ttttatatgt	gatttgtttc	540
cattgttaaa	acttgcttac	atggacaccc	acatgctggg	tctcttagtc	atcctcaaca	600
gtgggggtgat	gtgtatggcc	atcttccctta	tcctaattgc	atcctacatt	gtcacctctg	660
actctctgaa	gtcttgccgc	tcggtaggtc	gacgcaacac	actttccacc	tgtggctccc	720
accacacagt	ggatcatctg	ttcttcgtgg	agtgtatttt	cttgtagata	agacctgtgg	780
tcacttaccc	catagacaag	gatatggcta	tttcctttac	tattgttgca	cccatgttaa	840
atcctctgat	ctataccctg	aggggcatca	aggtaaaaaa	tgccataaga	aaaatgtgga	900
tgaaacaggg	gaccctaggt	ggt				923

<210> 1060

<211> 950

<212> DNA

<213> Unknown (H38g910 nucleotide)

<220>

<223> Synthetic construct

<400> 1060

atggctccga	ccaacctcac	atctgcccc	gctgttcttc	ctcctcggcc	tggtggacgg	60
aacagacgcc	caccgcgtgc	tgttctctgt	ctgccttggg	tctatctgct	caacgccctg	120
agcaacctga	gcatggtggc	gctggtgaga	tccgacgggg	ccctccgctc	ccccatgtat	180
tacttcttgg	gtcactgagc	ctcgtggacg	tctgctttac	caccgtcacg	gtccccaggc	240
tgctggccgg	cctgctccac	ccgggccagg	ccatatcctt	ccaggcgtgt	ctgccgagat	300
gtactttctt	gtgactctgg	catcacccag	agctacctca	tggcggccat	gtcctagcga	360
gcccgaacgc	gcgtgccggc	acctctgtac	ggcgcgctgg	tgacgccatc	ggcgtgcgcc	420
tgctggtgcg	tgcgtcgtgg	gccgtgacgc	acctgcactc	gctgctgcac	acgctgctcc	480
tctccgcgct	ctcctacccc	taccccaccc	ccgtgcgccc	cttcttttgc	gacatgacgg	540
tgatgctgag	cttggcgacc	tcggacacgt	ccgccgcgga	gacggccatc	ttctccgagg	600
gcctggccgt	ggtgttgccc	ccgctgtccc	tcgtgttccc	tttctctacg	gcgcactcctg	660
gtcgcggtgc	tcggcttgcc	cggccgcgcc	gcgccttctc	cacctgcggg	gcccacctag	720
tggcgggtgg	ggtggcgctt	ttctttggct	ctgtctcttc	cgtgtatttc	ccgccgtcgt	780
ctgcctactc	agcccgcctac	gaccgcctgg	ccagcgtggt	ctacgctgtc	atcacgccga	840
ccttgaaccc	tttcatcaac	agccttcgca	acaaagaggt	caagggcgcc	ctgaaaaggg	900
ggctcagcat	ggagggctgc	accccaagag	gcgtgagggc	aaatctggct		950

<210> 1061
 <211> 933
 <212> DNA
 <213> Unknown (H38g911 nucleotide)

<220>
 <223> Synthetic construct

<400> 1061
 atgaaagggg caaacctgag ccaaggggatg gagtttgagc tcttgggcct caccactgac 60
 cccagctcc agaggctgct cttcgtgggtg ttctgggca tgtacacagc cactcfgctg 120
 gggaacctgg tcatgttctt cctgatccat gtgagtggca cctgcacac acccatgtac 180
 tccctcctga agagcctctc cttcttggtt ttctgtact cctccacggg tgtgccccag 240
 accctgggtga acttcttggc caagaggaaa gtgatctctt attttggctg catgactcag 300
 atgtttctt atgcggttt tgccaccagt gagtgctatc tcactgctgc catggcctat 360
 gaccgctatg ccgctatttg taacccctg ctctactcaa ccatcatgtc tcctgaggtc 420
 tgtgcctcgc tgattgtggg ctctacagt gcaggattcc tcaattctct tatccacact 480
 ggctgtatct ttagtctgaa attctgcggg gctcatgtcg tcaactcactt cttctgtgat 540
 gggccacca tctgtcctt gtcttgtgta gacacctcac tgtgtgagat cctgtctctc 600
 atttttgctg gtttcaacct tttagctgc accctcacca tcttgatctc ctacttctta 660
 attctcaaca ccatcctgaa aatgagctcg gccaggggca ggtttaaggc attttccacc 720
 tgtgcatccc acctactgc catctgcctc ttctttggca caacactttt tatgtacctg 780
 cgccccaggc ccagctactc cttgacccag gaccgcacag ttgctgtcat ctacacagtg 840
 gtgatcccg tgctgaacc cctcatgtac tctttgagaa acaaggatgt gaagaaagct 900
 ttaataaagg tttggggtag gaaaacaatg gaa 933

<210> 1062
 <211> 948
 <212> DNA
 <213> Unknown (H38g912 nucleotide)

<220>
 <223> Synthetic construct

<400> 1062
 atgcaaaacc aaagctttgt aactgagttt gtctctctgg gactttcaca gaatccaaat 60
 gttcaggaaa tagtattttg tgtatttttg tttgtctaca ttgcaactgt tgggggcaac 120
 atgctaattg tagtaaccat tctcagcagc cctgctcttc tgggtgtctcc tatgtacttc 180
 ttcttgggct tctgtcctt cctggatgag tgcttctcat ctgtcatcac cccaaagatg 240
 attgtagact ccctctatgt gacaaaaacc atctcttttg aaggctgcat gatgcagctc 300
 tttgctgaac acttctttgc tggggtggag gtgattgtcc tcacagccat ggcctatgat 360
 cgttatgtgg ccatttgcaa gcccttgcat tactcttcta tcatgaacag gaggtctgtg 420
 ggcattctga tgggggtgag ctggacaggg ggcctcttgc attccatgat acaaattctt 480
 tttactttcc agcttccctt ttgtggcccc aatgtcatca atcactttat gtgtgacttg 540
 taccggttac tggagcttgc ctgcactgat actcacatct ttggcctcat ggtgggtcatc 600
 aacagtgggt ttatctgcat cataaacttc tccttgttgc ttgtctccta tgctgtcatc 660
 ttgctctctc tgagaacaca cagttctgaa gggcgctgga aagctctctc cacctgtgga 720
 tctcacattg ctggttgat tttgttctt gtcccatgca tatttgtata tacacgacct 780
 ccactgtctt tttcccttga caaatggcg gcaatatctt atatcatctt aaatcccttg 840
 ctcaatcctt tgatttacac tttcaggaat aaggaagtaa aacaggccat gaggagaata 900
 tggaacagac tgatgggtgt ttctgatgag aaagaaaata ttaaactt 948

<210> 1063
 <211> 930
 <212> DNA
 <213> Unknown (H38g913 nucleotide)

<220>
 <223> Synthetic construct

<400> 1063

atgcaactga	ataataatgt	gactgagttc	attctgcttg	gattgacaca	ggatcctttt	60
tggaagaaaa	tagtggttgt	tatttttttg	cgtctctact	tgggaacact	gttgggtaat	120
ttgctaataca	ttattagtgt	caaggccagc	caggcactta	agaaccaaat	gttcttcttc	180
cttttctact	tatecttata	tgataactgc	ctctctactt	ccatagcccc	tagaatgatt	240
gtggatgccc	ttttgaagaa	gacaactatc	tccttcagcg	agtgcagat	ccaagtcttt	300
tcattcccatg	tctttggctg	cctggagatc	ttcatcctca	tcctcacggc	tggtgaccgc	360
tatgtggaca	tctgtaagcc	cctgcactac	atgaccatca	taagccagt	ggtctgtggt	420
gttttgatgg	ctgtggcctg	ggtgggaccc	tgtgtgcatt	ctttagtcca	gatttttctt	480
gccttgagtt	tgccattctg	tggccccaat	gtgatcaatc	actgtttctg	tgacttgacg	540
cccttggtga	aacaagcctg	ttcagaaacc	tatgtgggta	acctactcct	ggtttccaat	600
agtggggcca	tttgtgcagt	gagttatgtc	atgctaataa	tctcctatgt	catcttcttg	660
cattctctga	gaaaccacag	tgctgaagtg	ataaagaaa	cactttccac	atgtgtctcc	720
cacatcattg	tggtcatctt	gttctttgga	ccttgcataa	ttatgtacac	atgccctgca	780
accgtattcc	ccatggataa	gatgatagct	gtattttata	cagttggaac	atcttttctc	840
aaccctgtga	tttacacgct	gaagaataca	gaagtgaaaa	gtgccatgag	gaagcttttg	900
agcaagaaat	tgatcacaga	tgacaaaaga				930

<210> 1064

<211> 964

<212> DNA

<213> Unknown (H38g914 nucleotide)

<220>

<223> Synthetic construct

<400> 1064

atggagacaa	caaatacactc	tgccgtgact	gaattctttc	tggtggggct	ttcccaatat	60
ccagagctcc	agctttttct	gttctgtctc	tgccctcatca	tgtacatgat	aatcctcctg	120
ggaaatagct	tcctcattat	catcaccatc	ttggattctc	gcctccatac	ccccatgtat	180
ttctttcttg	gaaacctctc	attcttgggc	atctgttaca	catcatcatc	cattcctcca	240
atgcttatta	tatttgtatc	tgagagaaaa	tccatctcct	tcattggctg	tgctctgcag	300
atgggttgtg	cccttggctt	gggtccatt	gagtgatcc	tcctggctgt	gatggcctat	360
gaccgctatg	tgcccatctg	caaccactg	aggtactcca	tcatcatgaa	cagagtgtctg	420
tatgtgcaaa	tggtgtcatg	gtcctggatc	ataggctgtc	tgacctccct	attgcaaca	480
gttctgacaa	tgatgttgcc	ttctgtggg	aataatatca	ttgatcatct	tacctgtgag	540
atcctggctc	ttcttaaagt	catatgtctc	gatctctcca	taaatgtgtt	tataatgaca	600
gtgtcaagta	ttgttttatt	ggtgattcct	cttaattttt	atctcctatg	tgttttattct	660
ctcttccatc	ttgagaatta	attctgtctg	gggaagaaag	aaagcctttt	ttacctgttc	720
agcgcaactg	actgtgggta	tcttattcta	tggttcagtt	cttttcacgc	acatgaagcc	780
caaatacaag	ttcacaacag	catctgatga	aatcattgga	ttgtcttatg	aagtgtatcac	840
cccaatgaac	cccatcatct	acagcctgag	gaataaggag	ataaaagaag	ctgtgaagaa	900
aatcctcagc	agacacgtgc	atctatggaa	aatatgaaag	gccttgaggc	atgtgacgtt	960
ctca						964

<210> 1065

<211> 620

<212> DNA

<213> Unknown (H38g915 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(620)

<223> n = A,T,C or G

<400> 1065

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ctttttcctg	aagaacctct	ctgttttgga	tctgtgtctac	atctcagtea	ctgtgcctaa	120
atccaatccg	aactccctga	ctgcagaag	ctccatctct	tatcttggct	gtgtggctca	180
agcctatttt	ttctctgcct	ttgcatctgc	tgagctggcc	ttccttactg	tcatgtctta	240

tgaccgctat	gttgccattt	gccaccccct	ccaatacaga	gccgtgatga	catcaggagg	300
gtgctatcag	atggcagtc	ccacctggct	aagctgcttt	tcctacgcag	ccgtccacac	360
tggaacatg	tttcgggagc	acgtttgcag	atccaatgtg	atccaccagt	tcttcctgta	420
catccctcag	gtgttgccc	tggtttctctg	ngagggttttc	ttttagagac	tttgacceng	480
ccctgagcct	caatgcttgg	ntctgggatg	ctttattccc	atgatgatct	ccnattttcc	540
anatcttctn	aanggggctc	nagaatccct	tnaggaccag	antcnagcta	aaagcctttn	600
ccnnctgct	tccccccacg					620

<210> 1066

<211> 611

<212> DNA

<213> Unknown (H38g916 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(611)

<223> n = A,T,C or G

<400> 1066	
gatgcatgct	cgagcggccg ccagtgatgat ggatatctgc agaattcgcc cttccaatgt 60
atattattct	ctctgacctc tcttcttgg acctctgctt taccacaagt tgtgtccccc 120
agatgctggg	caacctctgg ggcccaaaga agaccatcag cttcctggga tgctctgtcc 180
agctcttcat	cttctgtgcc ctggggacca ctgagtgcac cctcctgaca gtgatggcct 240
ttgaccgata	cgtggctgtc tgccagcccc tccactatgc caccatcatc ccccccgcc 300
tgtgctggca	gctggcatct gtggcctggg ttatgagtct ggttcaatcg atagtccaga 360
catcatccac	cctccacttg ccttctgtc cccaccagca gatagatgac tttttatgtg 420
aggtcccatc	tctgattcga ctctcctgng gagatacctc ctacaatgaa atccagttgn 480
ctgtgtccag	tgtcatcttt ggtggntgtg cctctcagcc tcatccttgc ctcttatgga 540
gccactgccc	aggcnggggc tgaggattaa ctttgccnna gccatggaag aaaggtcttt 600
nggacctngn	n
	611

<210> 1067

<211> 619

<212> DNA

<213> Unknown (H38g917 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(619)

<223> n = A,T,C or G

<400> 1067	
gatgcatgct	cgagcggccg ccagtgatgat ggatatctgc agaattcgcc ctttctttat 60
ttcgaagagt	atacactagt ggattgaaga gaaacaaata cataggaagg gcgaattcca 120
gcacactggc	ggccgttact agtggatccg agctcggtae caagcttgat gcatagcttg 180
agtattctaa	cgcgtcacct aaatagcttg gcgtaatcat ggatcatagct gtttctctgtg 240
tgaaattgtt	atccgctcac aattccacac aacatacgag ccggaagcat aaagtgtaaa 300
gcctgggggtg	cctaattgagt gagctaactc acattaattg cgttgcgctc actgtccgct 360
ttccagtcgg	gaaacctgtc gtgccagctg cattaatgaa tcggccaacg cgcgngnaga 420
ggccggnttg	cgtattgggc gctcttccgc ttctcgtcga ctgactcgtc gcgctcggga 480
cgtccggctg	cggcgagcgg taccagctta ctcaanggcc gtantacggt tattcncagg 540
aatnnggggt	taacgcncng naaagaacat tgtgngccan angncaagcn taatgcccag 600
gaaccgntan	aacgntccc
	619

<210> 1068

<211> 621

<212> DNA

<213> Unknown (H38g918 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(621)

<223> n = A,T,C or G

<400> 1068

gnnnnntntt	cantccattg	ggccctctag	atgcatgctc	gagcggccgc	eagtgtgatg	60
gatatctgca	gaattcgccc	ttattccgga	gggtatacat	gaagggattg	gtaactagac	120
gtaaactcga	agccaagaac	agaatttctc	ttagaaaaga	gaattgaaac	taaagagaaa	180
gaactagcaa	agaaggaaat	attgaatata	caagagagag	gagacagatg	atggaacaag	240
actctgaaag	aggtggaagg	gattgaatac	aatcaaaagt	atgggtgactg	ctagttccaa	300
gatgggtggcg	taggggcaag	ctggctttgc	ttacccccct	ggcagaaaac	caaaaacaaa	360
tagcaccaag	attatcacta	gcaatatccc	agaactcaca	tataaggatg	agacagttcc	420
cagggcccg	agaagatcag	aagcacaaagt	gggagaagtc	agctttggat	gctactttgt	480
tctaaggagg	acaagttggg	aggatgattg	cagatgtata	ttcaatgtta	taaaacagcc	540
cataaaacaa	agattggaaa	atgttgaatt	ttgcaaccag	gagcaaatac	tgggaaaggc	600
gaattccagc	cacttgcngc	c				621

<210> 1069

<211> 615

<212> DNA

<213> Unknown (H38g919 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(615)

<223> n = A,T,C or G

<400> 1069

gnnnnntnna	tcantgccct	ngggccctct	agatgcatgc	tcgagcggcc	gccagtgtga	60
tggatatctg	cagaattcgc	ccttggttgcg	caaggtgtaa	atgaaaggg	ttgcgcagga	120
gtaaatgaag	ggattacgca	ggagtaaatg	aagggattac	gcaggagtaa	atgaagggat	180
tacgcaggag	taaatgaagg	gattacgcag	gagtaaatga	agggattacg	caggagtaaa	240
tgaagggatt	acgcaggagt	aaatgaaggg	attacgcagg	agtaaatgaa	gggattacgc	300
aggagtaaat	gaagggatta	cgcaggagta	aatgaaggga	ttacgcagga	gtaaatgaag	360
ggattacgca	ggagcaaata	cataggaagg	gcgaattcca	gcacactggc	ggccggtact	420
agtggatccg	agctcggtac	caagcttgat	gcatagcttg	agtattctaa	cgcgtcacct	480
aaatagcttg	gcgtaatcat	ggtcatagct	gtttcctgtg	tgaaattgtt	atccgctcac	540
aattccacac	aacatacgag	cccgggaagca	taaagtgtaa	agnctgggg	gcctaattgag	600
tgacttactc	catta					615

<210> 1070

<211> 614

<212> DNA

<213> Unknown (H38g920 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(614)

<223> n = A,T,C or G

<400> 1070

ggnnttnant	cattgccccg	ctngatgcat	gctcgagcgg	ccgccagtgt	gatggatatc	60
------------	------------	------------	------------	------------	------------	----

tgcagaattc gcccttccga tgtattttct tctacgttaa ggtatttttaa attgttacta	120
atgcataagg gcaacacatt ctgtaatgct gacaagatga aagagccaaa agtaattaat	180
gatgctgtta cctcacaaat atgtatgtgt ggatgtatat atatctattc aatatatgta	240
actatacata tgtctgtttc taattgaaaa caccaggtaa ttatcatctg tagaaaccct	300
agtgtctcag ataagttggc tagttttttg tttcacataa aggaacaaac atttatagat	360
ttatatgtat attaaaaatg gtaaaaaattg gctgggtgca gtgggttcag cctataatac	420
cagcactttg ggaagccgag gtgggaggat tacttgaggt aaggagccca gcctgaccaa	480
caagggtgaaa ccccatccct actaaaaata caagaattag cccgggggatg gtgggtggcca	540
cctgtaatcc cagctacttg ggagactgaa gccaggaaaa tcacttgacc caggaagcng	600
aggttgcagg ngag	614

<210> 1071

<211> 857

<212> DNA

<213> Unknown (H38g921 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(857)

<223> n = A,T,C or G

<400> 1071

atggnnnnnn nntttnnnaa anttttnccc antttgggcc gneccccct tctttaaggn	60
aatgggcccga ttgggccctt cccggaaggc ccggggggcnc ccggccccaa aggtttgggt	120
tgggaaatgg ggggaattta aattcctttg ggccaaggna aaaattttcc ngccccctt	180
tttttccctt ttgggttttt anccggggga anggggggggt tgattaatta atcggaagn	240
tnggggggaa nttttttaa aaaaaccttg ggggaagggt ccaaccacac aagggtgggt	300
ttccanggga ccgttgggac caggcttttn gaatcaagaa tcccaaaggg cattcttttg	360
gattaaggaa nggtgccggg accggtgaaa gggaaaaaac tgggtggacc catacaaaa	420
tgagaaccac ggtgagatgc cgaggagcac gtggagaaag gctttgcttc cggccactgg	480
cagaggggat cctgaggatg gtgcttgatg atgtacacat agggagacaa ggggtgatgag	540
gcatgaactc aggataacca caacagcnat cacaaggcc acaaagctct actgcctgtg	600
tgttgggtgc aggccagggc aatccagggg tgcaatgtca caagaaagaa agtgggtgat	660
ggcacgggng ggccacagaa ggacaggcca ctgtgatgaag ggcttgtggg cactgcaatg	720
gccacgaaac caccagacc aggaaccan ggccaagctt gcgcctgaag agcaaggcta	780
ctcatgaatg gcttccgtag tngtaaagga tagcaagatg gcaaaggcaa gccggtcatn	840
aagccatggc ttgccng	857

<210> 1072

<211> 593

<212> DNA

<213> Unknown (H38g922 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(593)

<223> n = A,T,C or G

<400> 1072

aacgcagagt accgcccact acgtaatctg tacatgaaag ggtttaaaag agactgggaa	60
gagaggaatt ggcaagatca agcagaggca actccttcta gtccttctag taccgcaagg	120
ggcagataaa tggaatgggt aacacctaga ggaaagtata cttgccaaaa gcaaatncat	180
aggggggagt acattatcgg gttgaaaaaa gtattccatg cagataaaaa ccaaaagcaa	240
atacatcggg ggcgtacttc tgcgtcttt gagcgtagt atggtagcca gcttttgnct	300
ctttagtgag ggttaattgc gcgcttggcg taatcatggt catagctggt ttctgtgtga	360
aattgttatc ccgctcacia ttcacacaac atacgagccc gggagcataa agtgtaaagc	420
ctgggggtgcc taatgagtgg agcttactta cattaaattg cgttgcgctc actggccgct	480

tttccaagtc gggaaacctg tcgtgncagc ttcantaatg aatcggccaa cgccgcgggg 540
agaggcgggt tgcgtattgg gcgctcttcc gcttcttngt tnactgactt cgg 593

<210> 1073
<211> 624
<212> DNA
<213> Unknown (H38g923 nucleotide)

<220>
<223> Synthetic construct

<221> misc_feature
<222> (1)...(624)
<223> n = A,T,C or G

<400> 1073
gnnntttaac nccggngctn cnagcagtg aacaacgcag agtacgcccc cgatgtactt 60
tctttttcag tctcaagtct tectcttctc caaagatttt gtcttttcta ctacctgagc 120
taccaaatcc cttgtcatca atttcaataa ctgtattctc ttcattcattt caacttcaaa 180
cgtgtcatct cagaacaagc ttcattgttac ttccaatttt atccttcttg tttgtgtatt 240
ccaagaattc cagtcccatc taggcccgcga atgcattgtt cctgccaccc ttttcataatc 300
ctcaattccc ttgtatcatc actttccttt tatatagcac agattccatg attcataaca 360
ataattatgt ttttttttgc atgtgtctctt aatttccttt cttgtctcta ttatcttcta 420
tcatactttt ctggaaacac taattctggt gaaatatact ctttgtggac tttgcactta 480
tgctcagtcg gctgaagatg atggctagac aaatactcac aatcatgctg actggcccaa 540
tttatagtcg tgaccaccga ttacaaaccc cttcatttat tctccgcaac aggggcgtct 600
tctgcgcttg agcgtccggt gggg 624

<210> 1074
<211> 637
<212> DNA
<213> Unknown (H38g924 nucleotide)

<220>
<223> Synthetic construct

<221> misc_feature
<222> (1)...(637)
<223> n = A,T,C or G

<400> 1074
ttatnnccat tggagctcca aagcagtggt aacaaccgca gagtacgccc cccatgtatt 60
ttctttttct tggggnagct gnatgcttcc tncgtgctac catggnatat gaccggctat 120
gnggncatct gcagtccectt gnntceccag tcattatgaa ccaaaggaca cgggccaaac 180
tggttggtgn ttcttgggtc ccaagctttc ctgnagctac tngcaagac cacaatggct 240
cttnagnntt ccattctgng gcaccaacaa ggtgaaccac ttntttctgn gacagccggc 300
tgtgtgaaa gctggtctgn tgcaagacac agcactgttt gagatctacg ccatcgtcgg 360
aaccattctg gtggtcaatg aacccttctg tgctgatctt gngttcctat actcgnattg 420
gtgctgctat ccctcaagaa cccatcaagc taaangggaa gcaataaagn ccttttctcta 480
cgtgtctctt aacacctccc ttggtggcct ctcttttcta atataatcnt ctaagcctca 540
acctacttct tgggcctnaa ntcaaataaa ttcttctgga gaggcaagaa ggtggtattc 600
atztatncta cactggtngn gactccatgn tggaaact 637

<210> 1075
<211> 621
<212> DNA
<213> Unknown (H38g925 nucleotide)

<220>
<223> Synthetic construct

<221> misc_feature
 <222> (1)...(621)
 <223> n = A,T,C or G

<400> 1075

gtnatnccnt ttaatnccnt tggagctcca agcagtggtgta acaacgcaga gtacgcccgt	60
tcctcagaca gtatatgaat ggggttaaaaa tgggccagag cagatgcagg aagatcaaat	120
aggaggctac tgcagtagag tcaaactctag ggctgatggt ttcttgggat gcatagtaat	180
aggtagatag agaaagtctt taggaggttag aatggacagg acttcacaat gcattaaatg	240
tagggagaaa aaaaatgatt cctgggtttc tagcttgagc tagtagggat agtggtagaa	300
tttactgata tggaaaactg gaggaataag agtttggaag agaaagatgg caagttaaat	360
acctgtggga aatataatca cagacactaa ataggcagct gtgtgggtgg caaaggagag	420
ccatgggcta ggaacatata gtgggattcc ctggcatgtc attggttact gaagtcagag	480
tgtatgagac agcctaagga gagaatncac acaggagaag aaagaactaa acattcagtg	540
gtgggccaga ggatgagaaa cccaagagat tggactgttt aggagcaaca gtgttgngaa	600
aaggagaaaa nggttgaaat t	621

<210> 1076

<211> 631

<212> DNA

<213> Unknown (H38g926 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature
 <222> (1)...(631)
 <223> n = A,T,C or G

<400> 1076

ggntttannc nctggagctc caaagcagng gtaacaacgc agagtacgcc cattgcgtag	60
cgtgtacata aaggggttgg agctgaagga ggagataaag aagaagacag ccagaacctt	120
gtcctctgtc ggagatcgca gggatcttgg gccgtagata ggtataagca aaggggtgcat	180
agtagaaaagt cactacagtg aggtgggtgc tgcaggtcga ataggccttc ttctccctt	240
ctgcagagtg catgtggttag acagcaagga gaatccggcc ataggaacat gcaatacaaaa	300
tgaagggaaa cacaagaaaa atgggtggtgc tcaaaaacac cgtgcactca tagaccagg	360
tatccgtgca ggctagggtc aacatagctg gaacatcaca gaaaaaatga ttgatggctc	420
tggacttgca atatgggata cggagtgcat ataccgtgtg agcacaagag ttgatggagc	480
ctatcatcca agatcctgtt atcatcagtg cacacactct ttttctcata cggatgagat	540
agtggagagg aaagcaata gccacataac gatcataggc cattgatgtc aggagcagcg	600
cttctgcacc tgctaaagtc aggaagaaga t	631

<210> 1077

<211> 620

<212> DNA

<213> Unknown (H38g927 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature
 <222> (1)...(620)
 <223> n = A,T,C or G

<400> 1077

tgttantecn ntttntncc attggagctc ccaagcagtg gtaacaacgc agagtacgcc	60
ctccttggtt ctgagagtgt agatgaagg gttataggag ataaagatca gggcaatatg	120
taggacaagg acacagacac tgacaacaaa gttgattatc tcattgacag tgggtgtctgt	180
gcaggccagc ttcagcagg gtctcacatc acagaagaag tgggagatga caaagtcac	240
acaaaagggc aggccaaaca tagatgttac ttggacaata gccatgcccc ggccaatcct	300
cagtgaccca gatcccagtc agacacaagc cctcttacct atgaataaccg taaggggttg	360

cagaagacca	catagcaatc	atatcccatg	gctatgagaa	gaaagcagtt	gttgatgcc	420
aaagtcacat	agaagagctg	agtgacacag	ccttgcatga	caataagcta	gtgaggattc	480
aagaggcgag	aaagcatatg	gggagtaatg	gccaccatgt	agcagggtctc	agagatagac	540
agcaatgctt	aggaaaaagt	acatgggccc	tacttctgtc	gtccttgagcg	tactgatggt	600
accagctttt	tgttcccttt					620

<210> 1078

<211> 627

<212> DNA

<213> Unknown (H38g928 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(627)

<223> n = A,T,C or G

<400> 1078

tgtagctcca	aagcagtggg	aacaacgcag	agtagccct	cttggttacg	taaggggaata	60
gatgatgggg	ttcagcatgg	gggtgactac	agtgatcatg	acagtggcca	cacgggtccca	120
ctctgctcgc	gtcgggacgt	ggcctggaag	tagactgcaa	tgactgtcct	atagaaagag	180
gtcaccaca	nccagggtgg	agccacaggt	gggncacaag	tcccggagcc	tcccagaggc	240
ttgagggcag	ctggagcacg	ggnaagcttg	ntatggnccc	acaaggaggc	gaggatgagc	300
agnaagggag	tgaccaccac	ttgcngcgcc	ctnggtgaag	atgagcagct	tggatgtggt	360
ggntgtcaga	gcacgagagc	ctttaagaga	ggcttggtgg	gtcacagaag	aagtgggngc	420
actttgtggg	aaagcacaga	aaggacaagc	gagccatgag	caggatatac	aggagggagt	480
tgtccgtggg	acaccagcca	tgccattcca	accagggctg	cgcacatngc	cggggacatt	540
ctcgtgggat	aagggaaggg	gtgccggatn	ggcacgtatc	agtcataggc	cttggnccgc	600
agaagacagc	tttnaattta	ccccagg				627

<210> 1079

<211> 549

<212> DNA

<213> Unknown (H38g929 nucleotide)

<220>

<223> Synthetic construct

<400> 1079

gcagtggtaa	caacgcagag	taccgcccc	tatgtacttt	ttcttgggaa	acttgtctgt	60
gtttgacatg	ggtttctcct	cagtgacttg	tcccaaaatg	ctgctctacc	ttatggggct	120
gggccgactc	atctcctaca	aagactgtgt	ctgccagctt	ttcttcttcc	atttccctcg	180
gagcattgag	tgtctcttgt	ttacggtgat	ggcctatgac	cgcttccactg	ccatctgtta	240
tcctctgcga	tacacagtca	tcatgaaccc	aaggatctgt	gtggccctgg	ctgtggggcac	300
atggctgtta	gggtgcattc	attccagtat	cttgacctcc	ctcaccttca	ccttgccaca	360
ctgtgggtccc	aatgaagtgg	atcacttctt	ctgtgacatt	ccagcactgt	tgcccttggc	420
ctgtgctgac	acatccttag	cccagagggt	gagcttcacc	aacgttggcc	tcatatctct	480
ggctgctttc	tgctaaatct	tttatcctac	actagaatca	caaatatcta	tcttaagcat	540
tcgtacaac						549

<210> 1080

<211> 616

<212> DNA

<213> Unknown (H38g930 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(616)

<223> n = A,T,C or G

<400> 1080

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gnnnnnnnnt tcatnccatt gggccctcta gatgcatgct cgagcggccg ccagtgtgat      60
ggatatctgc agaattcgcc cttgttgctt agagtgtaaa taaaagggtt aacattggct      120
tagagggtgaa gagtaaatac ataggaaggg cgaattccag cactctggcg gccgttacta      180
gtggatccga gctcgggtacc aagcttgatg catagcttga gtattctaac gcgtcaccta      240
aatagcttgg cgtaatcatg gtcatactgt ttctctgtgt gaaattgtta tccgctcaca      300
attccacaca acatacgagc cggaagcata aagtgtaaaag cctgggggtgc ctaatgagtg      360
agctaactca cattaattgc gttgcgctca ctgcccgcct tccagtcggg aaacctgtcg      420
tgccagctgc attaatgaat cggccaacgc gcggggagag gcggtttgcg tattgggagc      480
tcttcgcgtt cctcgtctac tgactcgtg cgctcggctc ntcggctgcg gcgagcggta      540
tcaagctcac tcaaaggcgg taatacgtt atccacagaa tcagggggat acgcangaaa      600
gaacatgtga gcaaat
                                                                                   616

```

<210> 1081

<211> 615

<212> DNA

<213> Unknown (H38g931 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(615)

<223> n = A,T,C or G

<400> 1081

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ngnnnnntna ntcnangccn ngngccctct agatgcatgc tcgagcggcc gccagtgtga      60
tggatatctg cagaattcgc ccttccaatg tatttacttc tcagccagct ctcccttatg      120
gacctgatgt acatctccac caccgtcccc aagatggcgt acaacttcct gtccggccag      180
aaaggcatct ccttctctgg atgtggtgtg caaagcttct tcttcttgac catggcgtgt      240
tctgaaggct tactctgac ctccatggcc tacgaccgtt atttgccat ctgccactct      300
ctctattatc ctatccgcat gagtaaaatg atgtgtgtga agatgattgg aggctcttgg      360
acactggggt ccatcaactc cttggcacac acagtctttg cccttcatat tccctactgc      420
aggtctaggg ctattgacca ttcttctctg gatgtcccag ccatgttget tcttgctgta      480
cagatacttg ggtctatgaa tatatggttt ttgtaaggac aaagcctctt tcttcttttn      540
cctttcattg gcatcacttc ttctgngggc cgagtectaa ttgctggcta tataatgcac      600
tcaaaggagg ggagg
                                                                                   615

```

<210> 1082

<211> 628

<212> DNA

<213> Unknown (H38g932 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(628)

<223> n = A,T,C or G

<400> 1082

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gnnnnnnnnat ttnatgcent tnttgattcc cnttnnnnnn ncaagcagng gtaacaacgc      60
agagtacgcc ccctatgtat ttcttcttaa gatccaaata ttaaaataaa agacagtcac      120
cccaccacta actaaagtag tgtttcccac acttctctat taagaagcat gtgagatact      180
tggtacaacac ataacatcct ggtcccaccc caaagccact caatcaaata ctccagggaa      240
gggatctagg aattcgtagg tttaacgagt gccccaaaat gattattacc tggtggagaa      300
tctaggcaac aatgaattaa ggaaagctct ctaccatttg gtactggtag cagggtttgag      360
gatcacaggg aagagggtaa gcatatcaga ctagcagagc tgccagaact cgggctttca      420
aaagagaggt gccaccctct ccatgtcca tgtaagtagc aaacaaccct ctcatgtaca      480

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ctctgaggaa	caagggggcg	tacttctgtc	gtcttgagcg	tactgatggt	accagcttt	540
tgtcccttta	gtgagggtta	attgcgcgct	tggcgtaatc	atgggtcatag	ctgtttcctg	600
tgtgaaattg	ttatccgctc	acaattct				628

<210> 1083

<211> 613

<212> DNA

<213> Unknown (H38g933 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(613)

<223> n = A,T,C or G

<400> 1083

annncntng	gagctccaaa	gcagtggtaa	caacgcagag	tacgccccct	atgtacttac	60
ttttgttaag	tccaacctcc	atcctccttg	gccttttgat	tcaattgac	actccttcct	120
cctcaaaaaca	ccttggtcac	tcatectttc	tcagttcctc	ttgtggattc	ttcctcattt	180
atttgacctc	ttgctggtga	accctttcat	atacactctc	cgtaacaaag	agggcggtact	240
tctgtcgtct	tgagcgnact	gatggnaccc	agcttttggt	cccttttagtg	agggntaatt	300
gcgcgcttgg	cgnaatcatg	gncatagctg	nttctgngn	gaaantgnta	tttcgntnac	360
aattncacac	aacatacnag	ccgggagcat	aaaggggnnaa	gncctggggn	gcctaattgag	420
ggagcttact	cacaataatt	ggggtgngcc	cactggcccc	ttttcaggcg	ggaaaacctn	480
gcggggccag	ctggaataaa	tgaatcgggc	cacgcgccgg	ggaggagggc	gggttnngga	540
attgggcgct	ttttccnttt	ctnggttaat	ggactnggtn	ggcnnngtcc	gttcgggttg	600
ggggancggn	nnt					613

<210> 1084

<211> 886

<212> DNA

<213> Unknown (H38g934 nucleotide)

<220>

<223> Synthetic construct

<221> misc_feature

<222> (1)...(886)

<223> n = A,T,C or G

<400> 1084

ggtcccntcg	ngtatncntt	naccctctga	tgctgctcga	gcggccggca	gggtgatgga	60
tatctgcaga	attcgccctt	ctgttacgca	ggaatatata	aaggggttac	tgagggaataa	120
ataaatgggt	tactgaggaa	taaataaatg	ggttactgag	gaacaaatac	ataggggtga	180
aagaactgta	aaatagaaaa	aggaccttnt	gctgctctc	aggatggcgg	nacttagggg	240
ccatgtacat	gacgatgng	ctgccnntna	agagtccac	tnctcancng	cctcagcccc	300
nccttttntc	caennncnt	ntttntctnc	cctcttnnnc	tttttntctc	ctattccccc	360
cccttcnct	cctccctttt	gcntnaccat	tgncctnat	ccctttaatt	cnntcnntcn	420
tctccctct	attccttcnn	tnctegnet	cantctctnc	ctctttctcc	cccnctttct	480
ctentctnet	cttctctng	tcatectngt	tcnttctctt	ncctantcc	ctctancctt	540
ntcttattnc	tcctctatnc	cctctcatct	caentctent	cctctentcn	tacttnnctc	600
nnctctecn	ctcctctnc	cnctttctct	tcntnacgcc	acccctcnnn	cntnctctct	660
ntctentct	cactctctcc	tctccctncn	cntcactntt	ctcncctct	acntcctatn	720
ctcnctttct	nncttnactt	tgtaacgctc	tcctctctct	ctctaacgcac	nttttatctc	780
ttatctcnnc	catncctc	nnctctncac	netattnact	cttttctcnc	atactntatn	840
ctcctntcnn	cttanatcnc	ctcccttctn	tnancnntc	actgcn		886

<210> 1085

<211> 125

<212> PRT

<213> Unknown (H38g1 protein)

<220>

<223> Synthetic construct

<400> 1085

```

Leu Ala Cys Ala Asp Thr Ser Leu Ala Gln Arg Val Ser Phe Pro Asp
 1           5           10           15
Val Gly Leu Ile Ser Leu Val Cys Phe Leu Leu Ile Leu Leu Ser Tyr
          20           25           30
Thr Arg Ile Thr Ile Ser Ile Leu Ser Ile Arg Thr Thr Glu Gly Arg
          35           40           45
Arg Arg Ala Phe Ser Thr Cys Ser Ala His Leu Ile Ala Ile Leu Cys
          50           55           60
Ala Tyr Gly Pro Ile Ile Thr Val Tyr Leu Gln Pro Thr Pro Asn Pro
65           70           75           80
Met Leu Gly Thr Val Val Gln Ile Leu Met Asn Leu Val Gly Pro Met
          85           90           95
Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn Lys Glu Val Lys Thr Ala
          100          105          110
Leu Lys Thr Ile Leu His Arg Thr Gly His Val Pro Glu
          115          120          125

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<210> 1086

<211> 322

<212> PRT

<213> Unknown (H38g2 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(322)

<223> Xaa = Any Amino Acid

<400> 1086

```

His Thr Glu Pro Arg Asn Leu Thr Asp Val Xaa Glu Phe Leu Leu Leu
 1           5           10           15
Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Leu Leu Ser
          20           25           30
Leu Ser Leu Ser Met Tyr Leu Val Thr Val Met Arg Asn Leu Leu Ser
          35           40           45
Ile Leu Thr Val Ser Ser Val Ser Pro Leu His Thr Pro Met Tyr Phe
          50           55           60
Phe Leu Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Thr
65           70           75           80
Val Pro Thr Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Pro
          85           90           95
His Ala Gly Cys Leu Thr Gln Met Tyr Phe Leu Val Phe Phe Ala Cys
          100          105          110
Ile Glu Gly Met Leu Leu Thr Val Met Ala Tyr Asp Cys Phe Val Ala
          115          120          125
Ile Cys Arg Pro Leu His Tyr Pro Val Ile Val Asn Pro His Leu Cys
          130          135          140
Val Phe Phe Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln
145          150          155          160
Leu His Ser Xaa Ile Val Leu Gln Phe Asn Ile Ile Lys Asn Val Glu
          165          170          175
Ile Ser Asn Phe Val Cys Asp Pro Ser Gln Leu Leu Lys Leu Ala Cys
          180          185          190
Ser Asp Ser Val Ile Asn Ile Ile Phe Ile Tyr Phe Asp Ser Thr Met

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	195		200		205										
Phe	Ala	Phe	Leu	Pro	Ile	Ser	Gly	Ile	Leu	Trp	Ser	Tyr	Tyr	Lys	Ile
210					215						220				
Val	Pro	Ser	Ile	Leu	Arg	Ile	Ser	Ser	Ser	Asp	Gly	Lys	Tyr	Lys	Ser
225					230					235					240
Phe	Ser	Thr	Cys	Ala	Ser	His	Leu	Ala	Val	Val	Cys	Xaa	Phe	Asp	Gly
			245						250					255	
Thr	Gly	Ile	Gly	Met	Tyr	Leu	Thr	Ser	Ala	Val	Ser	Pro	Pro	Pro	Arg
			260					265					270		
Asn	Gly	Val	Val	Ala	Ser	Val	Met	Tyr	Ala	Val	Val	Thr	Pro	Met	Leu
		275					280					285			
Asn	Leu	Phe	Ile	Tyr	Ser	Leu	Arg	Asn	Arg	Asn	Ile	Gln	Ser	Ala	Leu
	290					295					300				
Arg	Arg	Leu	Arg	Ser	Arg	Thr	Val	Glu	Ser	His	Asp	Leu	Phe	His	Arg
305					310					315					320
Phe	Ser														

<210> 1087

<211> 312

<212> PRT

<213> Unknown (H38g3 protein)

<220>

<223> Synthetic construct

<400> 1087

Met	Asp	Gly	Asp	Asn	Gln	Ser	Glu	Asn	Ser	Gln	Phe	Leu	Leu	Leu	Gly
1				5				10						15	
Ile	Ser	Glu	Ser	Pro	Glu	Gln	Gln	Arg	Ile	Leu	Phe	Trp	Met	Phe	Leu
			20					25					30		
Ser	Met	Tyr	Leu	Val	Thr	Val	Leu	Gly	Asn	Val	Leu	Ile	Ile	Leu	Ala
		35					40				45				
Ile	Ser	Ser	Asp	Ser	His	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Ala
	50				55					60					
Asn	Leu	Ser	Phe	Thr	Asp	Leu	Phe	Phe	Val	Thr	Asn	Thr	Ile	Pro	Lys
65					70					75					80
Met	Leu	Val	Asn	Phe	Gln	Ser	Gln	Asn	Lys	Ala	Ile	Ser	Tyr	Ala	Gly
			85					90						95	
Cys	Leu	Thr	Gln	Leu	Tyr	Phe	Leu	Val	Ser	Leu	Val	Thr	Leu	Asp	Asn
			100					105					110		
Leu	Ile	Leu	Ala	Val	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Thr	Cys	Cys
			115					120					125		
Pro	Leu	His	Tyr	Val	Thr	Ala	Met	Ser	Pro	Gly	Leu	Cys	Val	Leu	Leu
	130					135				140					
Leu	Ser	Leu	Cys	Trp	Gly	Leu	Ser	Val	Leu	Tyr	Gly	Leu	Leu	Leu	Thr
145					150					155					160
Phe	Leu	Leu	Thr	Arg	Val	Thr	Phe	Cys	Gly	Pro	Arg	Glu	Ile	His	Tyr
			165						170					175	
Leu	Phe	Cys	Asp	Met	Tyr	Ile	Leu	Leu	Trp	Leu	Ala	Cys	Ser	Asn	Thr
			180					185					190		
His	Ile	Ile	His	Thr	Ala	Leu	Ile	Ala	Thr	Gly	Cys	Phe	Ile	Phe	Leu
	195						200					205			
Thr	Pro	Leu	Gly	Phe	Met	Thr	Thr	Ser	Tyr	Val	Arg	Ile	Val	Arg	Thr
	210					215					220				
Ile	Leu	Gln	Met	Pro	Ser	Ala	Ser	Lys	Lys	Tyr	Lys	Thr	Phe	Ser	Thr
225					230					235					240
Cys	Ala	Ser	His	Leu	Gly	Val	Val	Ser	Leu	Phe	Tyr	Gly	Thr	Leu	Ala
				245					250					255	
Met	Val	Tyr	Leu	Gln	Pro	Leu	His	Thr	Tyr	Ser	Met	Lys	Asp	Ser	Val
			260					265					270		

Ala Thr Val Met Tyr Ala Val Leu Thr Pro Met Met Asn Pro Phe Ile
 275 280 285
 Tyr Arg Leu Arg Asn Lys Asp Met His Gly Ala Pro Gly Arg Val Leu
 290 295 300
 Trp Arg Pro Phe Gln Arg Pro Lys
 305 310

<210> 1088

<211> 305

<212> PRT

<213> Unknown (H38g4 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(305)

<223> Xaa = Any Amino Acid

<400> 1088

Met Arg Asn His Thr Leu Leu Asn Glu Phe Ile Leu Arg Gly Ile Pro
 1 5 10 15
 Gln Thr Glu Gly Leu Glu Ala Val Leu Cys Ala Val Phe Ser Phe Ile
 20 25 30
 Tyr Leu Phe Thr Leu Leu Gly Asn Leu Leu Ile Leu Ile Ala Ile Phe
 35 40 45
 Leu His Thr Pro Met Tyr Phe Phe Leu Gly Arg Leu Ser Thr Phe Asp
 50 55 60
 Ile Leu Phe Pro Ser Val Thr Cys Pro Lys Met Leu Leu Tyr Leu Ser
 65 70 75 80
 Gly Gln Ser Pro Val Ile Ser Phe Lys Gly Cys Ala Ser Gln Leu Phe
 85 90 95
 Phe Tyr Gln Leu Leu Gly Ser Ala Glu Gly Cys Leu Tyr Ser Val Met
 100 105 110
 Ser Tyr Asp Arg Phe Val Ala Ile His His Thr Leu Arg Tyr Met Leu
 115 120 125
 Ile Met Lys Pro Gly Val Cys Val Gly Leu Val Val Val Pro Trp Leu
 130 135 140
 Val Gly Cys Leu His Ala Thr Ile Leu Thr Ser Phe Thr Phe Gln Leu
 145 150 155 160
 Ser Tyr Cys Gly Pro Asn Gln Val Asp Tyr Phe Phe Cys Asp Ile Pro
 165 170 175
 Ala Val Leu Pro Leu Ala Cys Thr Asp Ser Ala Leu Ala Gln Arg Val
 180 185 190
 Gly Ser Ile Asn Val Gly Phe Leu Ala Leu Thr Leu Leu Ile Ser Val
 195 200 205
 Cys Val Cys Tyr Thr Ser Ile Gly Ile Ala Ile Leu Arg Ile Arg Ser
 210 215 220
 Ser Glu Gly Arg Gln Lys Ala Phe Ser Thr Cys Ser Ala His Leu Val
 225 230 235 240
 Ala Ile Leu Cys Ala Tyr Gly Pro Val Ile Ile Tyr Leu Lys Ser
 245 250 255
 Thr Pro Asn Pro Leu Leu Gly Gly Gln Val Gln Ile Leu Asn Asn Val
 260 265 270
 Val Ser Pro Met Leu Asn Ser Leu Ile Tyr Ser Leu Arg Asn Lys Glu
 275 280 285
 Val Lys Arg Ser Leu Lys Arg Val Phe Xaa Asn Val Leu Leu Thr Val
 290 295 300
 Cys
 305

<210> 1089
 <211> 317
 <212> PRT
 <213> Unknown (H38g5 protein)

<220>
 <223> Synthetic construct

<400> 1089
 Met Gly Thr Asp Asn Gln Thr Trp Val Ser Glu Phe Ile Leu Leu Gly
 1 5 10 15
 Leu Ser Ser Asp Trp Asp Thr Arg Val Ser Leu Phe Val Leu Phe Leu
 20 25 30
 Val Met Tyr Val Val Thr Val Leu Gly Asn Cys Leu Ile Val Leu Leu
 35 40 45
 Ile Arg Leu Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Thr
 50 55 60
 Asn Leu Ser Leu Val Asp Val Ser Tyr Ala Thr Ser Val Val Pro Gln
 65 70 75 80
 Leu Leu Ala His Phe Leu Ala Glu His Lys Ala Ile Pro Phe Gln Ser
 85 90 95
 Cys Ala Ala Gln Leu Phe Phe Ser Leu Ala Leu Gly Gly Ile Glu Phe
 100 105 110
 Val Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Val Cys Asp
 115 120 125
 Ala Leu Arg Tyr Ser Ala Ile Met His Gly Gly Leu Cys Ala Arg Leu
 130 135 140
 Ala Ile Thr Ser Trp Val Ser Gly Phe Ile Ser Ser Pro Val Gln Thr
 145 150 155 160
 Ala Ile Thr Phe Gln Leu Pro Met Cys Arg Asn Lys Phe Ile Asp His
 165 170 175
 Ile Ser Cys Glu Leu Leu Ala Val Val Arg Leu Ala Cys Val Asp Thr
 180 185 190
 Ser Ser Asn Glu Val Thr Ile Met Val Ser Ser Ile Val Leu Leu Met
 195 200 205
 Thr Pro Phe Cys Leu Val Leu Leu Ser Tyr Ile Gln Ile Ile Ser Thr
 210 215 220
 Ile Leu Lys Ile Gln Ser Arg Glu Gly Arg Lys Lys Ala Phe His Thr
 225 230 235 240
 Cys Ala Ser His Leu Thr Val Val Ala Leu Cys Tyr Gly Val Ala Ile
 245 250 255
 Phe Thr Tyr Ile Gln Pro His Ser Ser Pro Ser Val Leu Gln Glu Lys
 260 265 270
 Leu Phe Ser Val Phe Tyr Ala Ile Leu Thr Pro Met Leu Asn Pro Met
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Gly Ala Trp Gln Lys Leu
 290 295 300
 Leu Trp Lys Phe Ser Gly Leu Thr Ser Lys Leu Ala Thr
 305 310 315

<210> 1090
 <211> 342
 <212> PRT
 <213> Unknown (H38g6 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(342)
 <223> Xaa = Any Amino Acid

<400> 1090
 Asp Thr Asp Pro Gln Ser Leu Thr Asp Val Ser Ile Phe Leu Leu Leu
 1 5 10 15
 Glu Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Ile Ala Gly Leu Phe
 20 25 30
 Leu Ser Met Cys Leu Val Thr Val Leu Glu Lys Leu Leu Ile Ile Met
 35 40 45
 Ala Val Ser Pro Asp Phe His Leu His Thr Pro Met Tyr Phe Phe Leu
 50 55 60
 Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro
 65 70 75 80
 Lys Met Ile Val Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala
 85 90 95
 Gly Cys Leu Thr Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu
 100 105 110
 Glu Asn Met Leu Leu Ser Val Met Ala Tyr Asp Gln Phe Val Ala Ile
 115 120 125
 Cys His Pro Pro Tyr Arg Ser Ala Ile Leu Asn Pro Cys Phe Cys Gly
 130 135 140
 Phe Gln Asp Leu Leu Ser Leu Phe Phe Phe Ser Phe Phe Phe Phe
 145 150 155 160
 Leu Arg Leu Leu Asp Ser Gln Leu His Asn Leu Ile Ala Leu Gln Met
 165 170 175
 Thr Cys Phe Lys Asp Val Glu Ile Ser Asn Val Phe Trp Glu Pro Ser
 180 185 190
 Gln Leu Pro His Leu Ala Cys Cys Asp Thr Phe Thr Arg Asn Ile Asn
 195 200 205
 Leu Tyr Phe Pro Ala Ala Val Leu Gly Phe Leu Pro Ile Ser Gly Thr
 210 215 220
 Leu Phe Ser Tyr Cys Lys Ile Val Ser Ser Ile Leu Arg Val Ser Ser
 225 230 235 240
 Ser Gly Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser
 245 250 255
 Ala Val Cys Xaa Phe Tyr Gly Thr Gly Val Gly Gly Tyr Leu Gly Ser
 260 265 270
 Asp Val Ser Ser Pro Arg Lys Ser Ala Val Ala Ser Val Met Tyr
 275 280 285
 Thr Val Val Thr Pro Met Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn
 290 295 300
 Arg Asp Met Lys Ser Val Leu Arg Arg Pro His Ser Ser Thr Val Xaa
 305 310 315 320
 Ser Gln Tyr Leu Leu Ile Cys Ser Ile Pro Phe Val Gly Trp Val Lys
 325 330 335
 Lys Gly Ser Lys Val Lys
 340

<210> 1091

<211> 313

<212> PRT

<213> Unknown (H38g7 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(313)

<223> Xaa = Any Amino Acid

<400> 1091

Met Val Lys Gly Asn His Ser Thr Val Thr Glu Phe Asn Leu Ala Gly

```

1           5           10           15
Leu Thr Asp Lys Pro Glu Leu Gln Leu Pro Leu Phe Leu Leu Phe Leu
20           25           30
Gly Ile Tyr Val Val Thr Val Val Gly Asn Leu Ser Met Ile Thr Leu
35           40           45
Ile Gly Phe Ser Ser His Leu His Thr Pro Met Tyr His Phe Leu Ser
50           55           60
Ser Leu Ser Phe Ile Asp Leu Cys Gln Ser Ser Val Ile Thr Pro Lys
65           70           75           80
Met Leu Val Asn Phe Val Ser Glu Arg Asn Ile Ile Ser Tyr Pro Ala
85           90           95
Cys Met Thr Gln Leu Tyr Phe Phe Leu Val Leu Val Ile Ser Glu Cys
100          105          110
His Met Leu Ala Ala Met Ala Tyr Asp His Tyr Ile Ala Ile Cys Asn
115          120          125
Pro Leu Leu Tyr His Val Ala Met Ser Tyr Gln Val Cys Ser Trp Met
130          135          140
Val Val Glu Val Tyr Phe Met Gly Phe Ile Gly Ala Ser Ala His Thr
145          150          155          160
Val Cys Met Leu Arg Val Leu Phe Cys Lys Ala Asp Val Ile Asn His
165          170          175
Tyr Phe Cys Asp Leu Phe Pro Leu Leu Glu Leu Ser Arg Ser Ser Ile
180          185          190
Ser Ile Asn Glu Ile Val Val Cys Ala Cys Ser Ala Phe Asn Ile Leu
195          200          205
Phe Arg Ser Leu Thr Ile Leu Ser Ser Tyr Ile Phe Ile Val Ala Ser
210          215          220
Ile Leu Cys Ile Arg Ser Thr Glu Gly Arg Ser Lys Thr Phe Ser Thr
225          230          235          240
Cys Ser Ser His Ile Ser Ala Val Ser Val Phe Phe Gly Ser Ala Ala
245          250          255
Phe Met Tyr Leu Gln Pro Ser Ser Val Ser Ser Met Asp Gln Gly Lys
260          265          270
Val Ser Ser Val Phe Tyr Ala Thr Val Val Pro Met Leu Asn Pro Leu
275          280          285
Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Val Ala Leu Ile Lys Phe
290          295          300
Leu Glu Lys Arg Ser Phe Leu Xaa Lys
305          310

```

<210> 1092

<211> 328

<212> PRT

<213> Unknown (H38g8 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(328)

<223> Xaa = Any Amino Acid

<400> 1092

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Met Gly Gln Glu Asn Lys Asn Gln Thr Trp Val Ser Glu Phe Ile Leu
1           5           10           15
Leu Gly Ile Ser Ser Asp Trp Gly Ile Gln Val Ser Leu Phe Ala Leu
20           25           30
Ile Leu Ala Met Tyr Leu Val Thr Ile Leu Gly Asn Thr Leu Ile Leu
35           40           45
Leu Leu Ile Arg Leu Asp Asn Arg Leu His Thr Pro Met Tyr Phe Ser
50           55           60

```

Leu Ser Val Leu Ser Phe Val Asp Phe Cys Tyr Thr Lys Ser Ile Val
 65 70 75 80
 Pro Gln Met Leu Ser His Leu Leu Ser Ala Arg Lys Ser Ile Pro Phe
 85 90 95
 Tyr Ser Cys Val Leu Gln Leu Tyr Val Ser Leu Ala Leu Cys Gly Ser
 100 105 110
 Glu Phe Phe Leu Leu Gly Ala Met Ala Tyr Asp Arg Tyr Val Ala Val
 115 120 125
 Cys His Pro Leu His Tyr Thr Val Ile Met His Gly Gly Leu Cys Leu
 130 135 140
 Gly Leu Ala Ala Ser Arg Leu Val Ala Gly Phe Ser Asn Ser Leu Met
 145 150 155 160
 Glu Thr Ile Ile Thr Phe Gln Leu Pro Val Ser Arg Phe Ile Asn His
 165 170 175
 Phe Val Cys Glu Thr Leu Ala Val Leu Gln Leu Ala Cys Val Asp Val
 180 185 190
 Pro Phe Asn Lys Val Met Val Ala Ile Ser Gly Phe Leu Val Ile Leu
 195 200 205
 Leu Pro Cys Ser Leu Val Leu Phe Ser Tyr Ala Cys Ile Val Ala Thr
 210 215 220
 Ile Leu Cys Ile Arg Ser Thr Gln Val Arg Cys Lys Ala Phe Gly Thr
 225 230 235 240
 Cys Ala Ser His Leu Ile Val Val Cys Met Cys Phe Gly Ala Thr Ile
 245 250 255
 Cys Thr Tyr Leu Gly Pro Gln Leu Ala Ser Ser Ala Glu Glu Glu Lys
 260 265 270
 Met Ile Ala Leu Phe Tyr Gly Val Val Ser Pro Met Leu Asn Pro Leu
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Glu Val Thr Ala Ala Val Arg Lys Val
 290 295 300
 Leu Glu Arg Cys Arg Xaa Arg Val Lys Thr Leu Arg Thr Ser Cys Tyr
 305 310 315 320
 Leu Ser Ser Lys Pro Lys Arg Arg
 325

<210> 1093

<211> 318

<212> PRT

<213> Unknown (H38g9 protein)

<220>

<223> Synthetic construct

<400> 1093

Met Asp Gln Ser Asn Tyr Ser Ser Leu His Gly Phe Ile Leu Leu Gly
 1 5 10 15
 Phe Ser Asn His Pro Lys Met Glu Met Ile Leu Ser Gly Val Val Ala
 20 25 30
 Ile Phe Tyr Leu Ile Thr Leu Val Gly Asn Thr Ala Ile Ile Leu Ala
 35 40 45
 Ser Leu Leu Asp Ser Gln Leu His Thr Pro Met Tyr Phe Phe Leu Arg
 50 55 60
 Asn Leu Ser Phe Leu Asp Leu Cys Phe Thr Thr Ser Ile Ile Pro Gln
 65 70 75 80
 Met Leu Val Asn Leu Trp Gly Pro Asp Lys Thr Ile Ser Tyr Val Gly
 85 90 95
 Cys Ile Ile Gln Leu Tyr Val Tyr Met Trp Leu Gly Ser Val Glu Cys
 100 105 110
 Leu Leu Leu Ala Val Met Ser Tyr Asp Arg Phe Thr Ala Ile Cys Lys
 115 120 125
 Pro Leu His Tyr Phe Val Val Met Asn Pro His Leu Cys Leu Lys Met

130	135	140
Ile Ile Met Ile Trp Ser	Ile Ser Leu Ala Asn	Ser Val Val Leu Cys
145	150	155
Thr Leu Thr Leu Asn	Leu Pro Thr Cys Gly	Asn Asn Ile Leu Asp His
165	170	175
Phe Leu Cys Glu Leu Pro	Ala Leu Val Lys Ile	Ala Cys Val Asp Thr
180	185	190
Thr Thr Val Glu Met Ser	Val Phe Ala Leu Gly	Ile Ile Ile Val Leu
195	200	205
Thr Pro Leu Ile Leu Ile	Leu Ile Ser Tyr Gly	Tyr Ile Ala Lys Ala
210	215	220
Val Leu Arg Thr Lys Ser	Lys Ala Ser Gln Arg	Lys Ala Met Asn Thr
225	230	235
Cys Gly Ser His Leu Thr	Val Val Ser Met Phe	Tyr Gly Thr Ile Ile
245	250	255
Tyr Met Tyr Leu Gln Pro	Gly Asn Arg Ala Ser	Lys Asp Gln Gly Lys
260	265	270
Phe Leu Thr Leu Phe Tyr	Thr Val Ile Thr Pro	Ser Leu Asn Pro Leu
275	280	285
Ile Tyr Thr Leu Arg Asn	Lys Asp Met Lys Asp	Ala Leu Lys Lys Leu
290	295	300
Met Arg Phe His His Lys	Ser Thr Lys Ile Lys	Arg Asn Cys
305	310	315

<210> 1094

<211> 324

<212> PRT

<213> Unknown (H38g10 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(324)

<223> Xaa = Any Amino Acid

<400> 1094

His Thr Glu Pro Arg Asn	Leu Thr Gly Val Xaa	Glu Phe Leu Leu Leu
1	5	10
Gly Leu Ser Glu Asp Pro	Glu Leu Gln Ser Val	Leu Ala Leu Leu Ser
20	25	30
Leu Ser Leu Ser Thr Tyr	Leu Ala Thr Val Leu	Arg Asn Val Leu Asn
35	40	45
Ile Leu Ala Val Ser Ser	Asp Ser Pro Leu His	Thr Pro Met Tyr Phe
50	55	60
Phe Leu Ser Asn Leu Cys	Trp Ala Asp Ile Gly	Phe Thr Ser Ala Thr
65	70	75
Val Pro Lys Met Ile Val	Asp Met Gln Ser Tyr	Ser Arg Val Ile Ser
85	90	95
His Glu Gly Cys Leu Thr	Gln Met Ser Phe Leu	Val Leu Phe Ala Cys
100	105	110
Ile Glu Gly Met Ile Leu	Thr Val Met Ala Tyr	Asp Cys Phe Val Ala
115	120	125
Ile Cys Arg Pro Leu His	Tyr Pro Val Ile Val	Asn Pro His Leu Cys
130	135	140
Val Phe Phe Val Leu Val	Ser Phe Phe Leu Ser	Leu Leu Asp Ser Gln
145	150	155
Leu His Ser Xaa Ile Val	Leu Gln Phe Asn Ile	Ile Lys Asn Val Glu
165	170	175
Ile Ser Asn Phe Val Cys	Asp Pro Ser Gln Phe	Leu Lys Leu Ala Cys
180	185	190

Ser Asp Ser Val Ile Asn Ser Ile Phe Thr Tyr Phe His Ser Thr Met
 195 200 205
 Phe Gly Phe Leu Pro Ile Ser Gly Ile Leu Phe Ser Xaa Phe Lys Ile
 210 215 220
 Val Thr Phe Ile Leu Trp Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala
 225 230 235 240
 Phe Ser Thr Cys Asp Ser His Leu Ala Val Val Cys Xaa Phe Tyr Gly
 245 250 255
 Thr Gly Ile Gly Met Tyr Leu Thr Ser Ala Val Ser Pro Pro Pro Arg
 260 265 270
 Asn Gly Val Val Ala Ser Met Met Tyr Ala Val Val Thr Pro Met Leu
 275 280 285
 Asn Leu Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu
 290 295 300
 Arg Arg Leu Leu Ser Arg Thr Val Glu Ser Pro Xaa Ser Val Pro Ser
 305 310 315 320
 Phe Phe Leu Cys

<210> 1095

<211> 311

<212> PRT

<213> Unknown (H38g11 protein)

<220>

<223> Synthetic construct

<400> 1095

Met Glu Leu Glu Asn Gln Thr Arg Val Thr Lys Phe Ile Leu Val Gly
 1 5 10 15
 Phe Pro Gly Ser Leu Ser Met Arg Ala Ala Met Phe Leu Ile Phe Leu
 20 25 30
 Val Ala Tyr Ile Leu Thr Val Ala Glu Asn Val Ile Ile Ile Leu Leu
 35 40 45
 Val Leu Gln Asn Arg Pro Leu His Lys Pro Met Tyr Phe Phe Leu Ala
 50 55 60
 Asn Leu Ser Phe Leu Glu Thr Trp Tyr Ile Ser Val Thr Val Pro Lys
 65 70 75 80
 Leu Leu Phe Ser Phe Trp Ser Val Asn Asn Ser Ile Ser Phe Thr Leu
 85 90 95
 Cys Met Ile Gln Leu Tyr Phe Phe Ile Ala Leu Met Cys Thr Glu Cys
 100 105 110
 Val Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Arg
 115 120 125
 Pro Leu His Tyr Pro Thr Ile Met Ser His Gly Leu Cys Phe Arg Leu
 130 135 140
 Ala Leu Gly Ser Trp Ala Ile Gly Phe Gly Ile Ser Leu Ala Lys Ile
 145 150 155 160
 Tyr Phe Ile Ser Cys Leu Ser Phe Cys Gly Pro Asn Val Ile Asn His
 165 170 175
 Phe Phe Cys Asp Ile Ser Pro Val Leu Asn Leu Ser Cys Thr Asp Met
 180 185 190
 Ser Ile Thr Glu Leu Val Asp Phe Ile Leu Ala Leu Val Ile Phe Leu
 195 200 205
 Phe Pro Leu Phe Ile Thr Val Leu Ser Tyr Gly Cys Ile Leu Ala Thr
 210 215 220
 Ile Leu Cys Met Pro Thr Gly Lys Gln Lys Ala Phe Ser Thr Cys Ala
 225 230 235 240
 Ser His Leu Val Val Val Thr Ile Phe Tyr Ser Ala Ile Ile Phe Met
 245 250 255
 Tyr Ala Arg Pro Arg Val Ile His Ala Phe Asn Met Asn Lys Ile Ile

260 265 270
 Ser Ile Phe Tyr Ala Ile Val Thr Pro Ser Leu Asn Pro Phe Ile Tyr
 275 280 285
 Cys Leu Arg Asn Arg Glu Val Lys Glu Ala Leu Lys Lys Leu Ala Tyr
 290 295 300
 Cys Gln Ala Ser Arg Ser Asp
 305 310

<210> 1096

<211> 313

<212> PRT

<213> Unknown (H38g12 protein)

<220>

<223> Synthetic construct

<400> 1096

Met Glu Gln Val Asn Lys Thr Val Val Arg Glu Phe Val Val Leu Gly
 1 5 10 15
 Phe Ser Ser Leu Ala Arg Leu Gln Gln Leu Leu Phe Val Ile Phe Leu
 20 25 30
 Leu Leu Tyr Leu Phe Thr Leu Gly Thr Asn Ala Ile Ile Ile Ser Thr
 35 40 45
 Ile Val Leu Asp Arg Ala Leu His Thr Pro Met Tyr Phe Phe Leu Ala
 50 55 60
 Ile Leu Ser Cys Ser Glu Ile Cys Tyr Thr Phe Val Ile Val Pro Lys
 65 70 75 80
 Met Leu Val Asp Leu Leu Ser Gln Lys Lys Thr Ile Ser Phe Leu Gly
 85 90 95
 Cys Ala Ile Gln Met Phe Ser Phe Leu Phe Phe Gly Ser Ser His Ser
 100 105 110
 Phe Leu Leu Ala Ala Met Gly Tyr Asp Arg Tyr Met Ala Ile Cys Asn
 115 120 125
 Pro Leu Arg Tyr Ser Val Leu Met Gly His Gly Val Cys Met Gly Leu
 130 135 140
 Met Ala Ala Ala Cys Ala Cys Gly Phe Thr Val Ser Leu Val Thr Thr
 145 150 155 160
 Ser Leu Val Phe His Leu Pro Phe His Ser Ser Asn Gln Leu His His
 165 170 175
 Phe Phe Cys Asp Ile Ser Pro Val Leu Lys Leu Ala Ser Gln His Ser
 180 185 190
 Gly Phe Ser Gln Leu Val Ile Phe Met Leu Gly Val Phe Ala Leu Val
 195 200 205
 Ile Pro Leu Leu Leu Ile Leu Val Ser Tyr Ile Arg Ile Ile Ser Ala
 210 215 220
 Ile Leu Lys Ile Pro Ser Ser Val Gly Arg Tyr Lys Thr Phe Ser Thr
 225 230 235 240
 Cys Ala Ser His Leu Ile Val Val Thr Val His Tyr Ser Cys Ala Ser
 245 250 255
 Phe Ile Tyr Leu Arg Pro Lys Thr Asn Tyr Thr Ser Ser Gln Asp Thr
 260 265 270
 Leu Ile Ser Val Ser Tyr Thr Ile Leu Thr Pro Leu Phe Asn Pro Met
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Glu Phe Lys Ser Ala Leu Arg Arg Thr
 290 295 300
 Ile Gly Gln Thr Phe Tyr Pro Leu Ser
 305 310

<210> 1097

<211> 318

<212> PRT

<213> Unknown (H38g13 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(318)

<223> Xaa = Any Amino Acid

<400> 1097

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Cys Val Asp Ser Ser Leu Lys Xaa Glu Ile Thr Gln Xaa Cys Leu Ser
 1           5           10          15
Leu Leu Leu Xaa Met Ala Glu Gly Trp Arg Leu Tyr Phe Ile Ile Leu
          20          25          30
Ile Ile Ser Tyr Lys Phe Cys Thr Leu Leu Gly Asn Val Ile Phe Arg
          35          40          45
Thr Leu Val Cys Ser Leu Gly Phe His Thr Ser Cys Met Tyr Phe Phe
          50          55          60
Pro Xaa Lys Ile Ser Leu Xaa Leu Ala Xaa Val Cys His Ser Ile Ile
65          70          75          80
Ala Leu Pro Ser Thr Gln Lys Xaa Ala Ile Asn Val Gln Gly Ala Ala
          85          90          95
Val His Val Phe Ser Phe Pro Cys Leu Tyr Cys Pro Glu Ile Phe Leu
          100         105         110
His Ser Leu Thr Gln Cys His Pro Phe Ile Ala Ile Gly Tyr Pro Leu
          115         120         125
Gln Gly Met His Thr Ile Thr His Lys Leu Tyr Ile Leu Leu Thr Thr
          130         135         140
Gly Pro Trp Arg Gly Cys Xaa Leu His Val Asn Leu Leu Thr Ala Ile
145         150         155         160
Leu Gly Ser Tyr Pro Asn Pro Val Pro Thr Lys Leu Trp Leu Ser Phe
          165         170         175
Pro Ser Ile Pro Glu Val Lys Leu Xaa Pro Met Gln Ala Tyr Thr Lys
          180         185         190
Pro Tyr Ala Gly Leu Ser Leu Cys Leu Ser Leu Ser Leu Ser Leu Ser
          195         200         205
Phe Ser Leu Phe Ser Ile Ile Ser Ile Ser Tyr Ile Cys Asn Glu Ile
          210         215         220
Asp Ile Pro Lys Ile Ile Ser Ala Asp Ser Val His Gly Ala Phe Ser
225         230         235         240
Thr Cys Leu Ala His Leu Phe Ala Phe Ser Thr Cys Ile Ala Gln Pro
          245         250         255
Ala Val Cys Asn Ser Leu Trp Pro Trp Thr Glu Ala Gln Thr Glu Ser
          260         265         270
Ser Arg Asp Ser Val Ile Gln Arg Pro Asn Leu Cys Val Thr Ile Ser
          275         280         285
Leu Asn Ser Leu Ile Ser Ser Leu Arg Asn Glu Ser Val Lys Gln Ala
          290         295         300
Ser His Lys Ile Phe Lys Glu Gln Thr Leu Phe Met Lys Ile
305         310         315

```

<210> 1098

<211> 333

<212> PRT

<213> Unknown (H38g14 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(333)

<223> Xaa = Any Amino Acid

<400> 1098

```

Met Asp Gly Glu Asn His Ser Val Val Ser Glu Phe Leu Phe Leu Gly
 1           5           10           15
Leu Thr His Ser Trp Glu Ile Gln Leu Leu Leu Leu Val Phe Ser Ser
          20           25           30
Val Leu Tyr Val Ala Ser Ile Thr Gly Asn Ile Leu Ile Val Phe Ser
          35           40           45
Val Thr Thr Asp Pro His Leu His Ser Pro Met Tyr Phe Leu Leu Ala
          50           55           60
Ser Leu Ser Phe Ile Asp Leu Gly Ala Cys Ser Val Thr Ser Pro Lys
          65           70           75           80
Met Ile Tyr Asp Leu Phe Arg Lys Arg Lys Val Ile Ser Phe Gly Gly
          85           90           95
Cys Ile Ala Gln Ile Phe Phe Ile His Val Ile Gly Gly Val Glu Met
          100          105          110
Val Leu Leu Ile Ala Met Ala Phe Asp Ser Tyr Val Ala Leu Cys Lys
          115          120          125
Pro Leu His Tyr Leu Thr Ile Met Ser Pro Arg Met Cys Leu Ser Phe
          130          135          140
Leu Ala Val Ala Trp Thr Leu Gly Val Ser His Ser Leu Phe Gln Leu
          145          150          155          160
Ala Phe Leu Val Asn Leu Pro Phe Cys Gly Pro Asn Val Leu Asp Ser
          165          170          175
Phe Tyr Cys Asp Leu Pro Gln Leu Leu Arg Leu Ala Cys Thr Asp Thr
          180          185          190
Tyr Arg Leu Gln Phe Met Val Thr Val Asn Ser Gly Phe Ile Cys Val
          195          200          205
Gly Thr Phe Phe Ile Leu Leu Ile Ser Tyr Ile Phe Ile Leu Phe Thr
          210          215          220
Val Trp Lys His Ser Ser Gly Gly Ser Ser Lys Ala Leu Ser Thr Leu
          225          230          235          240
Ser Ala His Ser Thr Ala Val Leu Leu Phe Phe Gly Pro Pro Met Phe
          245          250          255
Val Tyr Thr Trp Pro His Pro Asn Ser Gln Met Asp Lys Phe Leu Ala
          260          265          270
Ile Phe Asp Ala Val Leu Thr Pro Phe Leu Asn Pro Val Val Tyr Thr
          275          280          285
Phe Arg Asn Lys Glu Met Lys Ala Ala Ile Lys Arg Val Cys Lys Gln
          290          295          300
Leu Val Ile Tyr Lys Lys Ile Ser Xaa Met Ile Gln Xaa Ala Leu Leu
          305          310          315          320
Val Lys His Asp Met Ala Leu Cys Phe Phe Leu Xaa Tyr
          325          330

```

<210> 1099

<211> 322

<212> PRT

<213> Unknown (H38g15 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(322)

<223> Xaa = Any Amino Acid

<400> 1099

```

His Thr Gly Pro Arg Asn Leu Thr Asp Val Xaa Glu Phe Leu Leu Leu
 1           5           10           15

```

Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Leu Leu Thr Leu Leu Ser
 20 25 30
 Leu Ser Leu Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ser
 35 40 45
 Ile Leu Ala Val Ser Ser Asp Ser Pro Leu His Thr Pro Met Tyr Phe
 50 55 60
 Phe Leu Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr Xaa Ala Thr
 65 70 75 80
 Val Pro Lys Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser
 85 90 95
 His Ala Val Cys Leu Ile Gln Met Ser Leu Leu Val Leu Phe Ala Cys
 100 105 110
 Ile Glu Gly Met Leu Leu Thr Val Met Ala Tyr Asp Cys Phe Val Ala
 115 120 125
 Ile Cys Cys Pro Leu His Tyr Pro Val Ile Val Asn Pro His Leu Cys
 130 135 140
 Val Phe Phe Val Leu Val Ser Phe Leu Leu Ser Leu Leu Asp Ser Gln
 145 150 155 160
 Leu His Ser Trp Ile Val Leu Gln Phe Thr Ile Ile Lys Asn Val Glu
 165 170 175
 Ile Ser Asn Ser Val Cys Asp Pro Ser His Leu Leu Lys Leu Ala Cys
 180 185 190
 Ser Asp Ser Val Ile Asn Ser Ile Phe Ile Tyr Phe Asp Ser Thr Met
 195 200 205
 Phe Gly Phe Leu Pro Ile Ser Gly Ile Leu Trp Ser Tyr Tyr Lys Ile
 210 215 220
 Val Pro Ser Ile Leu Arg Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala
 225 230 235 240
 Phe Ser Thr Cys Ala Ser His Leu Ala Val Val Cys Xaa Phe Tyr Gly
 245 250 255
 Thr Gly Ile Gly Met Tyr Leu Thr Ser Ala Val Ser Pro Pro Pro Arg
 260 265 270
 Asn Gly Val Val Ala Ser Val Met Tyr Ala Val Val Thr Pro Met Leu
 275 280 285
 Asn Leu Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu
 290 295 300
 Arg Arg Leu Arg Ser Arg Thr Val Glu Ser His Asp Leu Phe His Arg
 305 310 315 320
 Phe Ser

<210> 1100

<211> 279

<212> PRT

<213> Unknown (H38g16 protein)

<220>

<223> Synthetic construct

<400> 1100

Met Tyr Leu Ala Thr Val Leu Gly Asn Leu Leu Ile Ile Leu Ala Ile
 1 5 10 15
 Ser Ile Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser Asn
 20 25 30
 Met Ser Phe Val Asp Asn Cys Phe Ser Thr Thr Val Pro Lys Met Leu
 35 40 45
 Ala Asn His Ile Leu Arg Thr Gln Thr Ile Ser Phe Ser Gly Cys Leu
 50 55 60
 Met Gln Met Tyr Phe Ile Ser Glu Leu Ala Asp Met Asp Asn Phe Leu
 65 70 75 80
 Leu Ala Val Met Ala Tyr Asp Arg Phe Val Ala Val Cys Arg Pro Leu

```

      85      90      95
His Tyr Thr Ala Lys Met Thr His Gln Leu Cys Ala Leu Leu Val Thr
      100      105      110
Gly Ser Trp Val Val Ala Asn Ser Asn Ala Leu Leu His Thr Leu Leu
      115      120      125
Met Ala Arg Leu Ser Phe Cys Ala Asp Asn Thr Ile Pro His Ile Phe
      130      135      140
Cys Asp Val Thr Pro Leu Leu Lys Leu Ser Cys Ser Asp Thr His Leu
      145      150      155      160
Ser Glu Val Met Ile Leu Thr Glu Ala Ala Leu Val Thr Ile Thr Pro
      165      170      175
Phe Leu Cys Leu Leu Ala Ser Tyr Met His Ile Thr Cys Val Val Leu
      180      185      190
Arg Val Pro Ser Thr Lys Gly Arg Trp Lys Ala Phe Ser Thr Cys Gly
      195      200      205
Ser His Leu Ala Val Val Leu Leu Phe Tyr Gly Thr Ile Met Ser Pro
      210      215      220
Tyr Phe Arg Thr Ser Ser Ser His Ser Ala Gln Arg Asp Ile Ala Ala
      225      230      235      240
Ala Val Arg Phe Thr Val Val Thr Pro Val Met Asn Pro Leu Ile Tyr
      245      250      255
Ser Leu Arg Asn Lys Asp Ile Lys Gly Ala Leu Val Lys Val Val Ala
      260      265      270
Val Lys Phe Phe Ser Val Gln
      275

```

<210> 1101

<211> 257

<212> PRT

<213> Unknown (H38g17 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(257)

<223> Xaa = Any Amino Acid

<400> 1101

```

Phe Ile Leu Trp Gly Phe Phe Asp His Pro Xaa Pro Glu Met Phe Leu
  1           5           10           15
Phe Ile Met Gly Leu Val Gly Leu Ser Leu His Thr Gly Gly Gln His
      20           25           30
Leu Asn Tyr Cys Gly Thr Gln Gly Ile Phe Xaa Gly Ser Thr Lys Cys
      35           40           45
Ile Ile Leu Ala Val Thr Ser Leu Asp Pro Tyr Ile Ala Ile Cys Lys
      50           55           60
His Leu Arg Tyr Pro Ala Ile Met His Gln Gln Leu Cys Val Leu Leu
      65           70           75           80
Val Ala Met Ala Trp Leu Ser Ser Leu Ala Asn Ser Leu Gln Ser Ser
      85           90           95
Leu Ala Val Gln Leu Pro Leu Gly Gly Asn Lys Val Asp Asp Phe Leu
      100          105          110
Cys Glu Val Ser Ala Met Ile Lys Ile Ser Arg Phe Asp Thr Thr Phe
      115          120          125
Asn Val Ser Met Leu Ser Ile Val Arg Ile Phe Xaa Ser Leu Val Leu
      130          135          140
Xaa Ser Ile Ile Phe Ala Tyr Cys Gly Phe Ile Val Ala Thr Val Leu
      145          150          155          160
Arg Ile Gln Ser Ser Gly Gly Lys Lys Glu Val Phe Asn Thr Cys Gly
      165          170          175

```

Ser His Ile Val Ser Leu Leu Tyr Gly Pro Val Ile Ser Met Tyr Val
 180 185 190
 Gln Pro Ser Ala Asn Ser Gln Asp Lys Asn Lys Phe Met Ser Leu Phe
 195 200 205
 Tyr Ser Leu Val Thr Pro Met Leu Asn Pro Phe Ile Tyr Thr Leu Ser
 210 215 220
 Asn Arg Asp Ile Lys Gly Ala Met Arg Arg Leu Leu Val Phe Leu Tyr
 225 230 235 240
 His Gln Glu Glu Asn Lys Ser Asn Tyr Cys Leu Tyr Ser Thr Phe Phe
 245 250 255
 Ile

<210> 1102

<211> 334

<212> PRT

<213> Unknown (H38g18 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(334)

<223> Xaa = Any Amino Acid

<400> 1102

Ser Thr Asp Pro Gln Asn Val Thr Asp Val Ser Arg Phe Leu Leu Leu
 1 5 10 15
 Lys Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Gly Leu Phe
 20 25 30
 Leu Ser Met Cys Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu
 35 40 45
 Ala Val Ser Pro Asp Ser His Leu His Thr Ser Met Tyr Phe Phe Leu
 50 55 60
 Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Pro Ser Pro Thr Val Pro
 65 70 75 80
 Lys Met Val Val Asp Ile Gln Ser His Arg Val Ile Ser Tyr Ala Gly
 85 90 95
 Cys Leu Thr Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu Glu
 100 105 110
 Asn Met Leu Leu Asn Val Met Ala Tyr Val Arg Phe Val Ala Ile Cys
 115 120 125
 His Pro Leu Tyr His Ser Ala Ile Met Asn Pro Cys Phe Cys Gly Phe
 130 135 140
 Leu Leu Leu Leu Ser Phe Phe Leu Gly Leu Leu Asp Ala Gln Leu
 145 150 155 160
 His Asn Met Ile Ala Leu Gln Met Thr Cys Phe Lys Asp Val Glu Ile
 165 170 175
 Pro Asn Phe Phe Trp Asp Pro Ser Gln Leu Pro His Leu Ala Cys Cys
 180 185 190
 Asp Thr Phe Thr Asn Asn Ile Ile Met Tyr Phe Pro Ala Ala Val Phe
 195 200 205
 Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser Tyr Ser Lys Ile Val
 210 215 220
 Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Lys Tyr Lys Pro Cys
 225 230 235 240
 Ser Thr Cys Gly Ser His Leu Ser Val Phe Cys Xaa Phe Tyr Gly Thr
 245 250 255
 Gly Ile Gly Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser Leu Arg Lys
 260 265 270
 Ala Ala Val Ala Ser Leu Met Tyr Lys Met Val Thr Pro Met Leu Asn

```

      275              280              285
Pro Ser Ile Tyr Ser Leu Arg Asn Arg Asp Ile Lys Ser Val Leu Arg
  290              295              300
Gln Pro His Gly Ser Thr Val Xaa Ser Gln Asp Leu Leu Ile Cys Ser
  305              310              315              320
Ile Pro Phe Val Val Trp Val Lys Lys Gly Ser Lys Val Lys
      325              330

```

<210> 1103

<211> 333

<212> PRT

<213> Unknown (H38g19 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(333)

<223> Xaa = Any Amino Acid

<400> 1103

```

Met Asp Gly Glu Asn His Ser Val Val Ser Glu Phe Leu Phe Leu Gly
  1              5              10              15
Leu Thr His Ser Trp Glu Ile Gln Leu Leu Leu Val Phe Ser Ser
      20              25              30
Val Leu Tyr Val Ala Ser Ile Thr Gly Asn Ile Leu Ile Val Phe Ser
      35              40              45
Val Thr Thr Asp Pro His Leu His Ser Pro Met Tyr Phe Leu Leu Ala
      50              55              60
Ser Leu Ser Phe Ile Asp Leu Gly Ala Cys Ser Val Thr Ser Pro Lys
      65              70              75              80
Met Ile Tyr Asp Leu Phe Arg Lys Arg Lys Val Ile Ser Phe Gly Gly
      85              90              95
Cys Ile Ala Gln Ile Phe Phe Ile His Val Ile Gly Gly Val Glu Met
      100              105              110
Val Leu Leu Ile Ala Met Ala Phe Asp Ser Tyr Val Ala Leu Cys Lys
      115              120              125
Pro Leu His Tyr Leu Thr Ile Met Ser Pro Arg Met Cys Leu Ser Phe
      130              135              140
Leu Ala Val Ala Trp Thr Leu Gly Val Ser His Ser Leu Phe Gln Leu
      145              150              155              160
Ala Phe Leu Val Asn Leu Pro Phe Cys Gly Pro Asn Val Leu Asp Ser
      165              170              175
Phe Tyr Cys Asp Leu Pro Arg Leu Leu Arg Leu Ala Cys Thr Asp Thr
      180              185              190
Tyr Arg Leu Gln Phe Met Val Thr Val Asn Ser Gly Phe Ile Cys Val
      195              200              205
Gly Thr Phe Phe Ile Leu Val Ile Ser Tyr Ile Phe Ile Leu Phe Thr
      210              215              220
Val Trp Lys His Ser Ser Gly Gly Ser Ser Lys Ala Leu Ser Thr Leu
      225              230              235              240
Ser Ala His Ser Thr Ala Val Leu Leu Phe Gly Pro Pro Met Phe
      245              250              255
Val Tyr Thr Trp Pro His Pro Asn Ser Gln Met Asp Lys Phe Leu Ala
      260              265              270
Ile Phe Asp Ala Val Leu Thr Pro Phe Leu Asn Pro Val Val Tyr Thr
      275              280              285
Phe Arg Asn Lys Glu Met Lys Ala Ala Ile Lys Arg Val Cys Lys Gln
      290              295              300
Leu Val Ile Tyr Lys Lys Ile Ser Xaa Met Ile Gln Xaa Ala Leu Leu
      305              310              315              320

```

Val Lys His Asp Met Ala Leu Cys Phe Phe Leu Xaa Tyr
 325 330

<210> 1104

<211> 339

<212> PRT

<213> Unknown (H38g20 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(339)

<223> Xaa = Any Amino Acid

<400> 1104

Asp Thr Asp Pro Gln Ser Leu Thr Asp Val Ser Ile Phe Leu Leu Leu
 1 5 10 15
 Glu Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Gly Leu Phe
 20 25 30
 Leu Ser Met Cys Leu Val Thr Val Leu Arg Asn Leu Leu Ile Ile Leu
 35 40 45
 Ala Ile Ser Pro Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu
 50 55 60
 Ser Asn Leu Ser Phe Pro Asp Ser Arg Phe Thr Ser Thr Thr Val Pro
 65 70 75 80
 Lys Met Ile Val Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala
 85 90 95
 Gly Cys Leu Thr Gln Met Ser Leu Phe Ala Ile Phe Gly Asp Met Glu
 100 105 110
 Glu Asn Met Phe Leu Ser Val Val Ala Tyr Asp Arg Phe Val Ala Ile
 115 120 125
 Cys His Pro Leu Tyr Arg Ser Ala Ile Leu Asn Pro Cys Phe Cys Gly
 130 135 140
 Phe Leu Asp Ser Leu Ser Leu Phe Phe Phe Phe Phe Phe Leu Ser Leu
 145 150 155 160
 Leu Asp Ser Gln Leu His Asn Leu Ile Ala Leu Gln Met Thr Cys Phe
 165 170 175
 Lys Asp Val Glu Ile Pro Asn Phe Phe Trp Glu Pro Ser Gln Leu Pro
 180 185 190
 His Leu Ala Cys Cys Asp Ile Phe Thr Arg Asn Ile Asn Leu Tyr Phe
 195 200 205
 Pro Ala Ala Ile Phe Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser
 210 215 220
 Tyr Tyr Lys Ile Val Ser Phe Ile Leu Arg Val Ser Ser Ser Gly Gly
 225 230 235 240
 Lys Tyr Lys Ala Phe Ser Ala Cys Gly Ser His Leu Ser Val Val Tyr
 245 250 255
 Xaa Val Tyr Gly Thr Gly Phe Gly Gly Tyr Leu Ser Ser Asp Val Ser
 260 265 270
 Ser Ser Pro Arg Lys Gly Ala Val Ala Ser Val Met Tyr Thr Val Val
 275 280 285
 Thr Pro Met Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Gly Asp Ile
 290 295 300
 Lys Ser Val Leu Arg Gln Pro His Gly Ser Thr Val Xaa Ser Gln Tyr
 305 310 315 320
 Leu Leu Ile Cys Ser Ile Pro Phe Val Val Trp Val Lys Lys Gly Ser
 325 330 335
 Lys Val Lys

<210> 1105
 <211> 314
 <212> PRT
 <213> Unknown (H38g21 protein)

<220>
 <223> Synthetic construct

<400> 1105
 Met Glu Thr Arg Lys Tyr Ser Ala Met Thr Glu Phe Phe Leu Val Gly
 1 5 10 15
 Leu Ser Gln Tyr Pro Glu Leu Gln Leu Phe Leu Phe Leu Cys Leu
 20 25 30
 Ile Met Tyr Met Ile Ile Leu Leu Gly Asn Ser Leu Leu Ile Ile Ile
 35 40 45
 Thr Ile Leu Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Gly
 50 55 60
 Asn Leu Ser Phe Leu Asp Ile Cys Tyr Thr Ser Ser Ile Pro Pro
 65 70 75 80
 Met Leu Ile Ile Phe Met Ser Glu Arg Lys Ser Ile Ser Phe Ile Gly
 85 90 95
 Cys Ala Leu Gln Met Val Val Ser Leu Gly Leu Gly Ser Thr Glu Cys
 100 105 110
 Val Leu Leu Ala Val Met Ala Tyr Asp His Tyr Val Ala Ile Cys Asn
 115 120 125
 Pro Leu Arg Tyr Ser Ile Ile Met Asn Gly Val Leu Tyr Val Gln Met
 130 135 140
 Ala Ala Trp Ser Trp Ile Ile Gly Cys Leu Thr Ser Leu Leu Gln Thr
 145 150 155 160
 Val Leu Thr Met Met Leu Pro Phe Cys Gly Asn Asn Val Ile Asp His
 165 170 175
 Ile Thr Cys Glu Ile Leu Ala Leu Leu Lys Leu Val Cys Ser Asp Ile
 180 185 190
 Thr Ile Asn Val Leu Ile Met Thr Val Thr Asn Ile Val Ser Leu Val
 195 200 205
 Ile Leu Leu Leu Leu Ile Phe Ile Ser Tyr Val Phe Ile Leu Ser Ser
 210 215 220
 Ile Leu Arg Ile Asn Cys Ala Glu Gly Arg Lys Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Ser Ala His Ser Ile Val Val Ile Leu Phe Tyr Gly Ser Ala Leu
 245 250 255
 Phe Met Tyr Met Lys Pro Lys Ser Lys Asn Thr Asn Thr Ser Asp Glu
 260 265 270
 Ile Ile Gly Leu Ser Tyr Gly Val Val Ser Pro Met Leu Asn Pro Ile
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Glu Ala Val Lys Lys Val
 290 295 300
 Leu Ser Arg His Leu His Leu Leu Lys Met
 305 310

<210> 1106
 <211> 319
 <212> PRT
 <213> Unknown (H38g22 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(319)
 <223> Xaa = Any Amino Acid

<400> 1106
 Met Lys Asn Lys Arg Asn Val Thr Glu Phe Val Leu Thr Gly Leu Thr
 1 5 10 15
 Gln Asn Pro Lys Met Glu Lys Val Met Phe Ala Val Phe Leu Val Leu
 20 25 30
 Tyr Met Ile Thr Leu Ser Gly Asn Leu Leu Val Val Thr Ile Thr
 35 40 45
 Thr Ser Gln Ala Leu Ser Ser Pro Met Tyr Phe Phe Leu Ser His Leu
 50 55 60
 Ser Leu Ile Asp Thr Val Tyr Ser Ser Ser Ala Pro Lys Leu Ile
 65 70 75 80
 Val Asp Ser Leu His Glu Lys Lys Ile Ile Ser Phe Asn Gly Cys Met
 85 90 95
 Ala Gln Ala Tyr Glu Glu His Ile Phe Gly Ala Thr Glu Ile Ile Leu
 100 105 110
 Leu Thr Val Met Ala Cys Asp Asn Tyr Val Ala Ile Cys Lys Pro Leu
 115 120 125
 His Tyr Thr Thr Ile Met Ser His Ser Leu Cys Ile Leu Leu Val Val
 130 135 140
 Val Ala Trp Ile Gly Gly Phe Leu His Ala Asn Ile Gln Ile Leu Phe
 145 150 155 160
 Thr Val Trp Leu Pro Phe Cys Gly Pro Asn Val Ile Asp His Phe Met
 165 170 175
 Cys Asp Leu Cys Pro Leu Leu Lys Leu Val Cys Leu Asp Thr His Thr
 180 185 190
 Leu Gly Leu Phe Val Ala Ala Asn Ser Gly Phe Ile Cys Leu Leu Asn
 195 200 205
 Phe Leu Leu Xaa Val Val Ser Tyr Val Ile Ile Leu Arg Cys Leu Lys
 210 215 220
 Asn Tyr Ile Leu Glu Gly Arg Gly Lys Ala Leu Ser Thr Cys Ile Ser
 225 230 235 240
 His Ile Ile Ile Val Val Leu Phe Phe Val Pro Cys Ile Phe Val Tyr
 245 250 255
 Leu His Pro Val Thr Thr Leu Pro Ile Asp Lys Ala Ala Ala Val Phe
 260 265 270
 Tyr Thr Met Val Val Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg
 275 280 285
 Asn Ala Glu Val Lys Ser Ala Ile Arg Lys Leu Trp Arg Lys Lys Val
 290 295 300
 Ile Ser Asp Asn Asp Xaa Ile Arg Pro Leu Ser Thr His His Arg
 305 310 315

<210> 1107

<211> 311

<212> PRT

<213> Unknown (H38g23 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(311)

<223> Xaa = Any Amino Acid

<400> 1107

Met Arg Asn Phe Ser Val Val Ser Glu Phe Ile Leu Leu Gly Ile Pro
 1 5 10 15
 His Thr Glu Gly Leu Glu Thr Ile Leu Leu Val Leu Phe Leu Ser Phe
 20 25 30
 Tyr Ile Phe Thr Leu Met Gly Asn Leu Leu Ile Leu Leu Ala Ile Val

35	40	45
Ser Ser Ala Arg Leu His Thr Pro Met Tyr Phe Phe Leu Cys Lys Leu		
50	55	60
Ser Val Phe Asp Leu Phe Phe Pro Ser Val Ser Ser Pro Lys Met Leu		
65	70	75
Cys Tyr Leu Ser Gly Asn Ser Arg Ala Ile Ser Tyr Ala Gly Cys Ala		
85	90	95
Ser Gln Leu Phe Phe Tyr His Phe Leu Gly Cys Thr Glu Cys Phe Leu		
100	105	110
Tyr Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu		
115	120	125
Arg Tyr Thr Ile Ile Met Ser His Arg Ala Cys Ile Ile Leu Ala Met		
130	135	140
Gly Thr Ser Phe Phe Gly Cys Ile Gln Ala Thr Phe Leu Thr Thr Leu		
145	150	155
Thr Phe Gln Leu Pro Tyr Cys Val Pro Asn Glu Val Asp Tyr Tyr Phe		
165	170	175
Cys Asp Ile Pro Val Met Leu Lys Leu Ala Cys Ala Asp Thr Ser Ala		
180	185	190
Leu Glu Met Val Gly Phe Ile Ser Val Gly Leu Met Pro Leu Ser Cys		
195	200	205
Phe Leu Leu Ile Leu Thr Ser Tyr Ser Gly Ile Val Phe Ser Ile Leu		
210	215	220
Xaa Ile Cys Ser Ala Glu Gly Arg Arg Arg Ala Phe Ser Thr Cys Ser		
225	230	235
Ala His Leu Thr Ala Ile Leu Leu Phe Tyr Met Pro Val Val Leu Ile		
245	250	255
Tyr Leu Arg Pro Thr His Ser Leu Trp Leu Asp Ala Thr Val Gln Ile		
260	265	270
Leu Asn Asn Leu Val Thr Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu		
275	280	285
Arg Asn Lys Glu Val Lys Leu Ser Leu Arg Lys Val Leu Tyr Gln Leu		
290	295	300
Gly Phe Leu Pro Glu Gln Leu		
305	310	

<210> 1108

<211> 302

<212> PRT

<213> Unknown (H38g24 protein)

<220>

<223> Synthetic construct

<400> 1108

Met Asp Ile Pro Gln Asn Ile Thr Glu Phe Phe Met Leu Gly Leu Ser	
1	5
Gln Asn Ser Glu Val Gln Arg Val Leu Phe Val Val Phe Leu Leu Ile	
20	25
Tyr Val Val Thr Val Cys Gly Asn Met Leu Ile Val Val Thr Ile Thr	
35	40
Ser Ser Pro Thr Leu Ala Ser Pro Val Tyr Phe Phe Leu Ala Asn Leu	
50	55
Ser Phe Ile Asp Thr Phe Tyr Ser Ser Ser Met Ala Pro Lys Leu Ile	
65	70
Ala Asp Ser Leu Tyr Glu Gly Arg Thr Ile Ser Tyr Glu Cys Cys Met	
85	90
Ala Gln Leu Phe Gly Ala His Phe Leu Gly Gly Val Glu Ile Ile Leu	
100	105
Leu Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu	
115	120
	125

```

His Asn Thr Thr Ile Met Thr Arg His Leu Cys Ala Met Leu Val Gly
  130                135                140
Val Ala Trp Leu Gly Gly Phe Leu His Ser Leu Val Gln Leu Leu Leu
 145                150                155                160
Val Leu Trp Leu Pro Phe Cys Gly Pro Asn Val Ile Asn His Phe Ala
                165                170                175
Cys Asp Leu Tyr Pro Leu Leu Glu Val Ala Cys Thr Asn Thr Tyr Val
                180                185                190
Ile Gly Leu Leu Val Val Ala Asn Ser Gly Leu Ile Cys Leu Leu Asn
                195                200                205
Phe Leu Met Leu Ala Ala Ser Tyr Ile Val Ile Leu Tyr Ser Leu Arg
                210                215                220
Ser His Ser Ala Asp Gly Arg Cys Lys Ala Leu Ser Thr Cys Gly Ala
 225                230                235                240
His Phe Ile Val Val Ala Leu Phe Phe Val Pro Cys Ile Phe Thr Tyr
                245                250                255
Val His Pro Phe Ser Thr Leu Pro Ile Asp Lys Asn Met Ala Leu Phe
                260                265                270
Tyr Gly Ile Leu Thr Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg
                275                280                285
Asn Glu Glu Val Lys Asn Ala Met Arg Lys Leu Phe Thr Trp
 290                295                300

```

<210> 1109

<211> 266

<212> PRT

<213> Unknown (H38g25 protein)

<220>

<223> Synthetic construct

<400> 1109

```

Met Ile Thr Leu Ile Gly Leu Ser Ser His Leu His Thr Pro Met Tyr
  1                5                10                15
Tyr Phe Leu Ser Leu Ser Phe Ile Asp Phe Cys His Ser Thr Val
                20                25                30
Ile Thr Pro Lys Met Leu Val Asn Phe Ala Thr Glu Lys Asn Ile Ile
  35                40                45
Ser Tyr Pro Glu Cys Met Ala Gln Leu Tyr Leu Phe Ser Ile Phe Ala
  50                55                60
Ile Ala Glu Cys His Met Leu Ala Ala Met Ala Tyr Asp Cys Tyr Val
  65                70                75                80
Ala Ile Cys Ser Pro Leu Leu Tyr Asn Val Ile Met Ser Tyr His His
                85                90                95
Cys Phe Trp Leu Thr Val Gly Val Tyr Ile Leu Gly Ile Leu Gly Ser
 100                105                110
Thr Ile His Thr Ser Phe Met Leu Arg Leu Phe Leu Cys Lys Thr Asn
 115                120                125
Val Ile Asn His Tyr Phe Cys Asp Leu Phe Pro Leu Leu Gly Leu Ser
 130                135                140
Cys Ser Ser Thr Tyr Ile Asn Glu Leu Leu Val Leu Val Leu Ser Ala
 145                150                155                160
Phe Asn Ile Leu Met Pro Ala Leu Thr Ile Leu Ala Ser Tyr Ile Phe
                165                170                175
Ile Ile Ala Ser Ile Leu Arg Ile His Ser Thr Glu Gly Arg Ser Lys
 180                185                190
Ala Phe Ser Thr Cys Ser Ser His Ile Leu Ala Val Ala Val Phe Phe
 195                200                205
Gly Ser Ala Ala Phe Met Tyr Leu Gln Pro Ser Ser Val Ser Ser Met
 210                215                220
Asp Gln Arg Lys Val Ser Ser Val Phe Tyr Thr Thr Ile Val Pro Met

```

225 230 235 240
 Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Leu Ala
 245 250 255
 Val Lys Lys Ile Leu His Gln Thr Ala Cys
 260 265

<210> 1110
 <211> 318
 <212> PRT
 <213> Unknown (H38g26 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(318)
 <223> Xaa = Any Amino Acid

<400> 1110
 Met Gly Asn Ser Asn Gln Ser Phe Met Thr Glu Phe Val Leu Leu Gly
 1 5 10 15
 Leu Ser Gly Tyr Pro Glu Leu Glu Ala Ile Tyr Phe Val Leu Val Leu
 20 25 30
 Cys Met Tyr Leu Val Ile Leu Leu Gly Asn Gly Val Ile Ile Ile Val
 35 40 45
 Ser Val Tyr Asp Thr His Leu His Thr Pro Met Tyr Phe Phe Leu Ser
 50 55 60
 Asn Leu Ser Phe Leu Asp Ile Cys Tyr Thr Ser Ser Ser Ile Pro Leu
 65 70 75 80
 Phe Leu Ser Ser Phe Leu Thr Ser Lys Lys Thr Ile Ser Phe Ser Gly
 85 90 95
 Cys Gly Val Gln Met Phe Leu Ser Phe Ala Met Gly Ala Thr Glu Cys
 100 105 110
 Val Leu Leu Ser Met Met Ala Phe Asp Cys Tyr Val Ala Ile Cys Asn
 115 120 125
 Pro Leu Xaa Tyr Pro Ile Ile Met Ser Lys Ala Ser Tyr Met Ser Met
 130 135 140
 Ala Ala Gly Ser Trp Ile Gly Gly Gly Ile Asn Ser Val Leu Gln Thr
 145 150 155 160
 Ser Leu Ala Met Arg Leu Pro Phe Cys Gly Asp Asn Val Ile Asn His
 165 170 175
 Phe Thr Cys Glu Ile Leu Ala Val Leu Lys Leu Ala Cys Ala Asn Ile
 180 185 190
 Ser Ile Asn Ile Ile Ser Met Val Val Ala Ser Met Ile Phe Leu Val
 195 200 205
 Gly Pro Val Leu Phe Ile Phe Val Thr Tyr Val Phe Ile Leu Ser Thr
 210 215 220
 Ile Leu Arg Ile Pro Ser Ala Glu Gly Arg His Lys Ala Ser Ser Thr
 225 230 235 240
 Cys Ser Ala His Leu Thr Val Val Ile Ile Phe Tyr Arg Thr Ile Leu
 245 250 255
 Phe Met Tyr Ala Lys Pro Lys Ala Lys Asp Ser Ser Gly Ala Asp Lys
 260 265 270
 Glu Gln Val Thr Asp Lys Ile Ile Ser Leu Phe Tyr Gly Val Val Thr
 275 280 285
 Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys
 290 295 300
 Ala Ala Val Lys Ser Ile Leu Xaa Gln Lys Cys Phe Leu Glu
 305 310 315

<210> 1111

<211> 329
 <212> PRT
 <213> Unknown (H38g27 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(329)
 <223> Xaa = Any Amino Acid

<400> 1111
 Lys Ser Met Lys Lys Met Asn Asn Val Ile Glu Phe Ile Leu Leu Gly
 1 5 10 15
 Leu Thr His Asn Pro Glu Leu Gln Lys Phe Leu Phe Val Met Phe Leu
 20 25 30
 Ile Thr Tyr Leu Ile Thr Leu Ala Gly Asn Leu Phe Ile Ser Val Ile
 35 40 45
 Ile Phe Ile Ser Pro Ala Leu Gly Ser Pro Met Tyr Ser Phe Pro Ser
 50 55 60
 Tyr Leu Phe Ile Ile Asp Ile Phe Cys Ser Ser Ser Ile Ala Pro Lys
 65 70 75 80
 Met Asn Phe Asp Leu Ile Ser Glu Lys Asn Thr Ile Ser Phe Asn Gly
 85 90 95
 Cys Met Thr Gln Leu Phe Thr Glu His Phe Phe Thr Glu His Phe Phe
 100 105 110
 Glu Ala Ala Glu Ile Ile Leu Leu Ser Val Met Ala Tyr Asp His Tyr
 115 120 125
 Val Ala Ile Arg Lys Pro Leu His Tyr Ala Thr Ile Met Ser Gln Pro
 130 135 140
 Met Cys Gly Phe Leu Met Val Val Ala Gly Ile Leu Gly Phe Val His
 145 150 155 160
 Gly Gly Ile Gln Thr Leu Phe Ile Ala Gln Leu Pro Phe Cys Gly Pro
 165 170 175
 Asn Val Ile Asn His Phe Met Cys Asp Leu Val Pro Leu Leu Glu Leu
 180 185 190
 Ala Cys Thr Asp Thr His Thr Leu Gly Pro Leu Ile Ala Ala Asn Ser
 195 200 205
 Gly Ser Leu Cys Phe Leu Ile Phe Ser Met Leu Val Ala Ser Tyr Val
 210 215 220
 Ile Ile Leu Cys Phe Leu Arg Thr His Ser Ser Glu Gly Arg Arg Lys
 225 230 235 240
 Ala Leu Ser Ser Cys Ala Ser His Ile Phe Ile Val Ile Leu Phe Phe
 245 250 255
 Val Pro Phe Ser Tyr Leu Tyr Leu Arg Pro Ile His Ser Phe Pro Thr
 260 265 270
 Asp Lys Ala Val Thr Val Phe Cys Thr Leu Phe Thr Pro Met Leu Asn
 275 280 285
 Pro Leu Ile Tyr Thr Leu Lys Asn Lys Glu Val Lys Asn Val Ile Lys
 290 295 300
 Lys Leu Trp Lys Gln Ile Met Thr Thr Asp Asp Lys Xaa Val Leu Xaa
 305 310 315 320
 His Lys His Leu Gly Lys Asn Ile Trp
 325

<210> 1112
 <211> 318
 <212> PRT
 <213> Unknown (H38g28 protein)

<220>

<223> Synthetic construct

<400> 1112

```

Met Glu Trp Glu Asn His Thr Ile Leu Val Glu Phe Phe Leu Lys Gly
 1           5           10           15
Leu Ser Gly His Pro Arg Leu Glu Leu Leu Phe Phe Val Leu Ile Phe
 20           25           30
Ile Met Tyr Val Val Ile Leu Leu Gly Asn Gly Thr Leu Ile Leu Ile
 35           40           45
Ser Ile Leu Asp Pro His Leu His Thr Pro Met Tyr Phe Phe Leu Gly
 50           55           60
Asn Leu Ser Phe Leu Asp Ile Cys Tyr Thr Thr Thr Ser Ile Pro Ser
 65           70           75           80
Thr Leu Val Ser Phe Leu Ser Glu Arg Lys Thr Ile Ser Leu Ser Gly
 85           90           95
Cys Ala Val Gln Met Phe Leu Gly Leu Ala Met Gly Thr Thr Glu Cys
 100          105          110
Val Leu Leu Gly Met Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Asn
 115          120          125
Pro Leu Arg Tyr Pro Ile Ile Met Ser Lys Asp Ala Tyr Val Pro Met
 130          135          140
Ala Ala Gly Ser Trp Ile Ile Gly Ala Val Asn Ser Ala Val Gln Ser
 145          150          155          160
Val Phe Val Val Gln Leu Pro Phe Cys Arg Asn Asn Ile Ile Asn His
 165          170          175
Phe Thr Cys Glu Ile Leu Ala Val Met Lys Leu Ala Cys Ala Asp Ile
 180          185          190
Ser Asp Asn Glu Phe Ile Met Leu Val Ala Thr Thr Leu Phe Ile Leu
 195          200          205
Thr Pro Leu Leu Leu Ile Ile Val Ser Tyr Thr Leu Ile Ile Val Ser
 210          215          220
Ile Phe Lys Ile Ser Ser Ser Glu Gly Arg Ser Lys Ala Ser Ser Thr
 225          230          235          240
Cys Ser Ala His Leu Thr Val Val Ile Ile Phe Tyr Gly Thr Ile Leu
 245          250          255
Phe Met Tyr Met Lys Pro Lys Ser Lys Glu Thr Leu Asn Ser Asp Asp
 260          265          270
Leu Asp Ala Thr Asp Lys Ile Ile Ser Met Phe Tyr Gly Val Met Thr
 275          280          285
Pro Met Met Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys
 290          295          300
Glu Ala Val Lys His Leu Leu Asn Arg Arg Phe Phe Ser Lys
 305          310          315

```

<210> 1113

<211> 264

<212> PRT

<213> Unknown (H38g29 protein)

<220>

<223> Synthetic construct

<400> 1113

```

Met Val Asp Asn Leu Ile Ile Val Val Thr Ile Thr Thr Ser Pro Ala
 1           5           10           15
Leu Asp Ser Pro Val Tyr Phe Phe Leu Ser Phe Phe Ser Phe Ile Asp
 20           25           30
Gly Cys Ser Ser Ser Thr Met Ala Pro Lys Met Ile Phe Asp Leu Leu
 35           40           45
Thr Glu Lys Lys Thr Ile Ser Phe Ser Gly Cys Met Thr Gln Leu Phe
 50           55           60

```

Val Glu His Phe Phe Gly Gly Val Glu Ile Ile Leu Leu Val Val Met
 65 70 75 80
 Ala Tyr Asp Cys Tyr Val Ala Ile Cys Lys Pro Leu Tyr Tyr Leu Ile
 85 90 95
 Thr Met Asn Arg Gln Val Cys Gly Leu Leu Val Ala Met Ala Trp Val
 100 105 110
 Gly Gly Phe Leu His Ala Leu Ile Gln Met Leu Leu Ile Val Trp Leu
 115 120 125
 Pro Phe Cys Gly Pro Asn Val Ile Asp His Phe Ile Cys Asp Leu Phe
 130 135 140
 Pro Leu Leu Lys Leu Ser Cys Thr Asp Thr His Val Phe Gly Leu Phe
 145 150 155 160
 Val Ala Ala Asn Ser Gly Leu Met Cys Met Leu Ile Phe Ser Ile Leu
 165 170 175
 Ile Thr Ser Tyr Val Leu Ile Leu Cys Ser Gln Arg Lys Ala Leu Ser
 180 185 190
 Thr Cys Ala Phe His Ile Thr Val Val Leu Phe Phe Val Pro Cys
 195 200 205
 Ile Leu Val Tyr Leu Arg Pro Met Ile Thr Phe Pro Ile Asp Lys Ala
 210 215 220
 Val Ser Val Phe Tyr Thr Val Val Thr Pro Met Leu Asn Pro Leu Ile
 225 230 235 240
 Tyr Thr Leu Arg Asn Thr Glu Val Lys Asn Ala Met Lys Gln Leu Trp
 245 250 255
 Ser Gln Ile Ile Trp Gly Asn Asn
 260

<210> 1114

<211> 312

<212> PRT

<213> Unknown (H38g30 protein)

<220>

<223> Synthetic construct

<400> 1114

Met Trp Pro Asn Ile Thr Ala Ala Pro Phe Leu Leu Thr Gly Phe Pro
 1 5 10 15
 Gly Leu Glu Ala Ala His His Trp Ile Ser Ile Pro Phe Phe Ala Val
 20 25 30
 Tyr Val Cys Ile Leu Leu Gly Asn Gly Met Leu Leu Tyr Leu Ile Lys
 35 40 45
 His Asp His Ser Leu His Glu Pro Met Tyr Tyr Phe Leu Thr Met Leu
 50 55 60
 Ala Gly Thr Asp Leu Met Val Thr Leu Thr Thr Met Pro Thr Val Met
 65 70 75 80
 Gly Ile Leu Trp Val Asn His Arg Glu Ile Ser Ser Val Gly Cys Phe
 85 90 95
 Leu Gln Ala Tyr Phe Ile His Ser Leu Ser Val Val Glu Ser Gly Ser
 100 105 110
 Leu Leu Ala Met Ala Tyr Asp Arg Phe Ile Ala Ile Arg Asn Pro Leu
 115 120 125
 Arg Tyr Ala Ser Ile Phe Thr Asn Thr Arg Val Ile Ala Leu Gly Val
 130 135 140
 Gly Val Phe Leu Arg Gly Phe Val Ser Ile Leu Pro Val Ile Leu Arg
 145 150 155 160
 Leu Phe Ser Phe Ser Tyr Cys Lys Ser His Val Ile Thr Arg Ala Phe
 165 170 175
 Cys Leu His Gln Glu Ile Met Arg Leu Ala Cys Ala Asp Ile Thr Phe
 180 185 190
 Asn Arg Leu Tyr Pro Val Ile Leu Ile Ser Leu Thr Ile Phe Leu Asp

```

      195              200              205
Ser Leu Ile Ile Leu Phe Ser Tyr Ile Leu Ile Leu Asn Thr Val Ile
  210              215              220
Gly Ile Ala Ser Gly Glu Glu Arg Ala Lys Ala Leu Asn Thr Cys Ile
  225              230              235              240
Ser His Ile Ser Cys Val Leu Ile Phe Tyr Val Thr Val Met Gly Leu
      245              250              255
Thr Phe Ile Tyr Arg Phe Gly Lys Asn Val Pro Glu Val Val His Ile
      260              265              270
Ile Met Ser Tyr Ile Tyr Phe Leu Phe Pro Pro Leu Met Asn Pro Val
      275              280              285
Ile Tyr Ser Ile Lys Thr Lys Gln Ile Gln Tyr Gly Ile Ile Arg Leu
      290              295              300
Leu Ser Lys His Arg Phe Ser Arg
  305              310

```

<210> 1115

<211> 285

<212> PRT

<213> Unknown (H38g31 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(285)

<223> Xaa = Any Amino Acid

<400> 1115

```

Asp Thr Glu Pro Gln Asn Leu Thr Ala Val Ser Glu Phe Leu Leu Leu
  1              5              10              15
Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Ile Leu Ala Gly Leu Phe
      20              25              30
Leu Ser Met Tyr Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu
      35              40              45
Ala Ile Gly Ser Asp Ser His Leu Asp Thr Pro Met Tyr Phe Phe Leu
      50              55              60
Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Ala Thr Val Pro
      65              70              75              80
Lys Met Ile Glu Glu Met Gln Ser His Ser Arg Val Ile Tyr His Gly
      85              90              95
Asp Cys Leu Thr Gln Met Ser Phe Phe Val Leu Phe Ala Cys Lys Asp
      100              105              110
Asp Met Ile Leu Thr Val Met Ala Tyr Asp Trp Phe Val Ala Ile Cys
      115              120              125
His Pro Leu Asn Tyr Pro Gly Ile Met Asn Pro His Leu Cys Val Leu
      130              135              140
Leu Val Leu Val Pro Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His
      145              150              155              160
Asn Leu Ile Val Leu Gln Phe Ile Cys Phe Lys Asn Val Glu Ile Ser
      165              170              175
Asn Phe Phe Cys Asp Pro Phe Gln Arg Leu Asn Leu Ala Cys Ser Asp
      180              185              190
Ser Asp Ile Asn Asn Ile Tyr Ile Tyr Leu Asp Ser Thr Ile Phe Gly
      195              200              205
Phe Leu Arg Ile Ser Gly Ile Leu Leu Cys Tyr Tyr Thr Val Val Phe
      210              215              220
Pro Ile Leu Arg Ile Pro Ser Ser Asp Gly Asn Tyr Lys Ala Phe Ser
      225              230              235              240
Thr Xaa Gly Ser Arg Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Gly
      245              250              255

```

Ile Gly Val Tyr Leu Thr Ser Ala Val Ser Ser Ser Pro Arg Asn Asp
 260 265 270
 Val Val Ala Ser Val Met Tyr Ala Val Val Val Thr Pro
 275 280 285

<210> 1116
 <211> 317
 <212> PRT
 <213> Unknown (H38g32 protein)

<220>
 <223> Synthetic construct

<400> 1116
 Met Gly Glu Ile Asn Gln Thr Leu Val Ser Glu Phe Leu Leu Leu Gly
 1 5 10 15
 Leu Ser Gly Tyr Pro Lys Ile Glu Ile Val Tyr Phe Ala Leu Ile Leu
 20 25 30
 Val Met Tyr Leu Val Ile Leu Ile Gly Asn Gly Val Leu Ile Ile Ala
 35 40 45
 Ser Ile Phe Asp Ser His Phe His Thr Pro Met Tyr Phe Phe Leu Gly
 50 55 60
 Asn Leu Ser Phe Leu Asp Ile Cys Tyr Thr Ser Ser Val Pro Ser
 65 70 75 80
 Thr Leu Val Ser Leu Ile Ser Lys Lys Arg Asn Ile Ser Phe Ser Gly
 85 90 95
 Cys Ala Val Gln Met Phe Phe Gly Phe Ala Met Gly Ser Thr Glu Cys
 100 105 110
 Leu Leu Leu Gly Met Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Asn
 115 120 125
 Pro Leu Arg Tyr Pro Ile Ile Leu Ser Lys Val Ala Tyr Val Leu Met
 130 135 140
 Ala Ser Val Ser Trp Leu Ser Gly Gly Ile Asn Ser Ala Val Gln Thr
 145 150 155 160
 Leu Leu Ala Met Arg Leu Pro Phe Cys Gly Asn Asn Ile Ile Asn His
 165 170 175
 Phe Ala Cys Glu Ile Leu Ala Val Leu Lys Leu Ala Cys Ala Asp Ile
 180 185 190
 Ser Leu Asn Ile Ile Thr Met Val Ile Ser Asn Met Ala Phe Leu Val
 195 200 205
 Leu Pro Leu Met Val Ile Phe Phe Ser Tyr Met Phe Ile Leu Tyr Thr
 210 215 220
 Ile Leu Gln Met Asn Ser Ala Thr Gly Arg Arg Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Ser Ala His Leu Thr Val Val Ile Ile Phe Tyr Gly Thr Ile Phe
 245 250 255
 Phe Met Tyr Ala Lys Pro Lys Ser Gln Asp Leu Ile Gly Glu Glu Lys
 260 265 270
 Leu Gln Ala Leu Asp Lys Leu Ile Ser Leu Phe Tyr Gly Val Val Thr
 275 280 285
 Pro Met Leu Asn Pro Ile Leu Tyr Ser Leu Arg Asn Lys Asp Val Lys
 290 295 300
 Ala Ala Val Lys Tyr Leu Leu Asn Lys Lys Pro Ile His
 305 310 315

<210> 1117
 <211> 309
 <212> PRT
 <213> Unknown (H38g33 protein)

<220>

<223> Synthetic construct

<400> 1117

```

Met Gly Ala Lys Asn Asn Val Thr Glu Phe Val Leu Phe Gly Leu Phe
 1           5           10           15
Glu Ser Arg Glu Met Gln His Thr Cys Phe Val Val Phe Phe Leu Phe
 20           25           30
His Val Leu Thr Val Leu Gly Asn Leu Leu Val Ile Ile Thr Ile Asn
 35           40           45
Ala Arg Lys Thr Leu Lys Ser Pro Met Tyr Phe Phe Leu Ser Gln Leu
 50           55           60
Ser Phe Ala Asp Ile Cys Tyr Pro Ser Thr Thr Ile Pro Lys Met Ile
 65           70           75           80
Ala Asp Thr Phe Val Glu His Lys Ile Ile Ser Phe Asn Gly Cys Met
 85           90           95
Thr Gln Leu Phe Ser Ala His Phe Phe Gly Gly Thr Glu Ile Phe Leu
 100          105          110
Leu Thr Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Arg Pro Leu
 115          120          125
His Tyr Thr Ala Ile Met Asp Cys Arg Lys Cys Gly Leu Leu Ala Gly
 130          135          140
Ala Ser Trp Leu Ala Gly Phe Leu His Ser Ile Leu Gln Thr Leu Leu
 145          150          155          160
Thr Val Gln Leu Pro Phe Cys Gly Pro Asn Glu Ile Asp Asn Phe Phe
 165          170          175
Cys Asp Val His Pro Leu Leu Lys Leu Ala Cys Ala Asp Thr Tyr Met
 180          185          190
Val Gly Leu Ile Val Val Ala Asn Ser Gly Met Ile Ser Leu Ala Ser
 195          200          205
Phe Phe Ile Leu Ile Ile Ser Tyr Val Ile Ile Leu Leu Asn Leu Arg
 210          215          220
Ser Gln Ser Ser Glu Asp Arg Arg Lys Ala Val Ser Thr Cys Gly Ser
 225          230          235          240
His Val Ile Thr Val Leu Leu Val Leu Met Pro Pro Met Phe Met Tyr
 245          250          255
Ile Arg Pro Ser Thr Thr Leu Ala Ala Asp Lys Leu Ile Ile Leu Phe
 260          265          270
Asn Ile Val Met Pro Pro Leu Leu Asn Pro Leu Ile Tyr Thr Leu Arg
 275          280          285
Asn Asn Asp Val Lys Asn Ala Met Arg Lys Leu Phe Arg Val Lys Arg
 290          295          300
Ser Leu Gly Glu Lys
305

```

<210> 1118

<211> 329

<212> PRT

<213> Unknown (H38g34 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(329)

<223> Xaa = Any Amino Acid

<400> 1118

```

Ala Thr Cys His Leu Xaa Thr His Asn Ala Ala Pro Phe Leu Leu Pro
 1           5           10           15
Gly Phe Ser Val Leu Glu Ala Thr Tyr His Ser Ile Ser Ile Pro Phe
 20           25           30

```

Phe Ala Val Tyr Val Cys Val Leu Leu Gly Asn Gly Lys Leu Leu Tyr
 35 40 45
 Leu Ile Lys His Asp His Ser Leu His Glu Pro Met Tyr Cys Phe Leu
 50 55 60
 Ala Thr Leu Arg Gln Asp Leu Met Val Lys Leu Thr Met Met Pro Thr
 65 70 75 80
 Val Met Gly Val Leu Trp Met Asn His Lys Glu Val Ile His Gly Ala
 85 90 95
 Cys Phe Leu Gln Val Tyr Ile Ile His Ser His Tyr Pro Leu Ala Glu
 100 105 110
 Ser Gly Ile Leu Leu Ser Met Ala Tyr Asp Arg Phe Ile Ile Ile His
 115 120 125
 Met Leu Leu Arg Tyr Asn Ser Ile Ser Thr Lys Ser Trp Val Lys Ile
 130 135 140
 Glu Leu Trp Leu Phe Met Arg Asp Phe Leu Ser Leu Val Pro Pro Ile
 145 150 155 160
 Leu Pro Leu His Cys Phe Pro Tyr Cys His Ser His Val Leu Phe His
 165 170 175
 Thr Phe Phe Leu His Gln Asp Val Leu Lys Leu Ala Cys Ala Asp Ile
 180 185 190
 Thr Phe Asn His Leu Tyr Pro Ala Ile Leu Val Ala Leu Ile Phe Phe
 195 200 205
 Leu Asp Ala Leu Ile Ile Val Phe Ser Tyr Ile Leu Ile Leu Lys Thr
 210 215 220
 Val Ile Gly Ile Ala Ser Arg Lys Glu Gln Ala Lys Ala Leu Asn Met
 225 230 235 240
 Cys Val Ser His Ile Ser Cys Val Leu Val Phe His Ile Thr Val Ile
 245 250 255
 Ser Glu Thr Phe Ile His Arg Phe Gly Lys His Ala Pro His Val Val
 260 265 270
 His Ile Thr Val Ser Tyr Asp Ser Phe Leu Phe Pro Pro Phe Met Asn
 275 280 285
 Pro Ile Ile Tyr Ser Ile Lys Thr Lys Gln Ile Gln Arg Ser Ile Val
 290 295 300
 Arg Leu Phe Ser Gly His Arg Met Ala Xaa Ala Leu Phe Ser Glu Phe
 305 310 315 320
 Cys Asp Leu His Asp Phe Trp Ala Phe
 325

<210> 1119

<211> 296

<212> PRT

<213> Unknown (H38g35 protein)

<220>

<223> Synthetic construct

<400> 1119

Leu Leu Leu Val Leu Leu Leu Pro Thr Phe Leu Leu Ser Leu Met
 1 5 10 15
 Gly Asn Met Leu Ile Ile Ser Thr Val Leu Ser Cys Ser Arg Leu His
 20 25 30
 Thr Pro Met Tyr Phe Phe Leu Cys Asn Leu Ser Ile Leu Asp Ile Leu
 35 40 45
 Phe Thr Ser Val Ile Ser Pro Lys Val Leu Ala Asn Leu Gly Ser Arg
 50 55 60
 Asp Lys Thr Ile Ser Phe Ala Gly Cys Ile Thr Gln Cys Tyr Phe Tyr
 65 70 75 80
 Phe Phe Leu Gly Thr Val Glu Phe Leu Leu Leu Thr Val Met Ser Tyr
 85 90 95
 Asp Cys Tyr Ala Ala Ile Cys Cys Pro Leu Arg Tyr Thr Thr Ile Met

```

      100      105      110
Arg Pro Tyr Val Cys Ile Gly Thr Val Val Phe Ser Trp Val Gly Gly
      115      120      125
Phe Leu Ser Val Leu Phe Pro Thr Ile Leu Ile Ser Gln Leu Pro Phe
      130      135      140
Cys Gly Ser Asn Ile Ile Asn His Phe Phe Cys Asp Ser Gly Pro Leu
      145      150      155      160
Leu Ala Leu Ala Cys Ala Asp Thr Thr Ala Ile Glu Leu Met Asp Phe
      165      170      175
Met Leu Ser Ser Met Val Ile Leu Cys Cys Ile Val Leu Val Ala Tyr
      180      185      190
Ser Tyr Thr Tyr Ile Ile Leu Thr Ile Met Arg Ile Pro Ser Ala Ser
      195      200      205
Gly Arg Lys Lys Ala Phe Asn Thr Cys Ala Ser His Leu Thr Ile Val
      210      215      220
Ile Ile Ser Ser Gly Ile Thr Val Phe Ile Tyr Val Thr Pro Ser Gln
      225      230      235      240
Lys Glu Tyr Leu Glu Ile Asn Lys Ile Pro Ser Val Leu Ser Ser Leu
      245      250      255
Val Thr Pro Phe Leu Asn Pro Phe Ile Tyr Thr Leu Arg Asn Asp Thr
      260      265      270
Val Gln Gly Val Leu Arg Asp Val Trp Val Arg Val Arg Gly Val Phe
      275      280      285
Glu Lys Arg Met Arg Ala Val Leu
      290      295

```

<210> 1120

<211> 310

<212> PRT

<213> Unknown (H38g36 protein)

<220>

<223> Synthetic construct

<400> 1120

```

Met Trp Tyr Asn Asn Ser Ala Gly Pro Phe Leu Leu Thr Gly Phe Leu
  1      5      10      15
Gly Ser Glu Ala Val His Tyr Arg Ile Ser Met Ser Phe Phe Val Ile
      20      25      30
Tyr Phe Ser Val Leu Phe Gly Asn Gly Thr Leu Leu Val Leu Ile Trp
      35      40      45
Asn Asp His Ser Leu His Glu Pro Met Tyr Tyr Phe Leu Ala Met Leu
      50      55      60
Ala Asp Thr Asp Leu Gly Met Thr Phe Thr Thr Met Pro Thr Val Leu
      65      70      75      80
Gly Val Leu Leu Leu Asp Gln Arg Glu Ile Ala His Ala Ala Cys Phe
      85      90      95
Thr Gln Ser Phe Ile His Ser Leu Ala Ile Val Glu Ser Gly Ile Leu
      100      105      110
Leu Val Leu Ala Tyr Asp Cys Phe Ile Ala Ile Arg Thr Pro Leu Arg
      115      120      125
Tyr Asn Cys Ile Leu Thr Asn Ser Arg Val Met Asn Ile Gly Leu Gly
      130      135      140
Val Leu Met Arg Gly Phe Met Ser Ile Leu Pro Ile Ile Leu Ser Leu
      145      150      155      160
Tyr Cys Tyr Pro Tyr Cys Gly Ser Arg Ala Leu Leu His Thr Phe Cys
      165      170      175
Leu His Gln Asp Val Ile Lys Leu Ala Cys Ala Asp Ile Thr Phe Asn
      180      185      190
His Ile Tyr Pro Ile Ile Gln Thr Ser Leu Thr Val Phe Leu Asp Ala
      195      200      205

```

Leu Ile Ile Ile Phe Ser Tyr Ile Leu Ile Leu Lys Thr Val Met Gly
 210 215 220
 Ile Ala Ser Gly Gln Glu Glu Ala Lys Ser Leu Asn Thr Cys Val Ser
 225 230 235 240
 His Ile Ser Cys Val Leu Val Phe His Ile Thr Val Met Gly Leu Ser
 245 250 255
 Phe Ile His Arg Phe Gly Lys His Ala Pro His Val Val Pro Ile Thr
 260 265 270
 Met Ser Tyr Val His Phe Leu Phe Pro Pro Phe Val Asn Pro Ile Ile
 275 280 285
 Tyr Ser Ile Lys Thr Lys Gln Ile Gln Arg Ser Ile Ile Arg Leu Phe
 290 295 300
 Ser Gly Gln Ser Arg Ala
 305 310

<210> 1121
 <211> 332
 <212> PRT
 <213> Unknown (H38g37 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(332)
 <223> Xaa = Any Amino Acid

<400> 1121
 His Thr Glu Pro Arg Asn Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu
 1 5 10 15
 Gly Leu Pro Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Leu Leu Ser
 20 25 30
 Leu Ser Leu Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ile
 35 40 45
 Ile Leu Ala Val Ser Ser Val Ser Pro Leu His Thr Pro Met Tyr Phe
 50 55 60
 Phe Leu Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Thr
 65 70 75 80
 Val Pro Lys Met Ile Val Asp Met Gln Ser His Ser Arg Ala Ile Ser
 85 90 95
 His Ala Gly Cys Leu Thr Gln Met Ser Phe Leu Phe Leu Phe Ala Cys
 100 105 110
 Ile Glu Gly Met Leu Leu Thr Val Met Ala Tyr Asp Cys Phe Val Ala
 115 120 125
 Ile Cys Arg Pro Leu His Tyr Pro Val Ile Val Asn Pro His Phe Cys
 130 135 140
 Val Phe Phe Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln
 145 150 155 160
 Leu His Ser Trp Ile Val Leu Gln Phe Thr Ile Phe Lys Asn Val Glu
 165 170 175
 Ile Ser Asn Phe Val Cys Asp Pro Ser Gln Leu Leu Lys Leu Ala Cys
 180 185 190
 Ser Asp Gly Val Ile Asn Ser Ile Phe Ile Tyr Phe Asp Ser Thr Met
 195 200 205
 Phe Gly Phe Leu Pro Ile Ser Gly Ile Leu Trp Ser Tyr Tyr Lys Ile
 210 215 220
 Val Pro Ser Ile Leu Arg Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala
 225 230 235 240
 Phe Ser Thr Cys Gly Ser His Gln Ala Val Val Cys Xaa Phe Tyr Arg
 245 250 255
 Thr Gly Ile Gly Met Tyr Leu Thr Ser Ala Val Ser Pro Pro Pro Arg

```

      260      265      270
Asn Gly Val Val Ala Ser Leu Ile Tyr Ala Val Val Thr Pro Met Leu
      275      280      285
Asn Leu Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu
      290      295      300
Arg Arg Leu Leu Ser Arg Thr Val Glu Ser His Asp Leu Phe His Pro
      305      310      315      320
Phe Ser Trp Trp Val Arg Lys Gly Asn His Ile Lys
      325      330

```

<210> 1122

<211> 310

<212> PRT

<213> Unknown (H38g38 protein)

<220>

<223> Synthetic construct

<400> 1122

```

Met Gly Asp Asn Ile Thr Ser Ile Arg Glu Phe Leu Leu Leu Gly Phe
 1      5      10      15
Pro Val Gly Pro Arg Ile Gln Met Leu Leu Phe Gly Leu Phe Ser Leu
      20      25      30
Phe Tyr Val Phe Thr Leu Leu Gly Asn Gly Thr Ile Leu Gly Leu Ile
      35      40      45
Ser Leu Asp Ser Arg Leu His Ala Pro Met Tyr Phe Phe Leu Ser His
      50      55      60
Leu Ala Val Val Asp Ile Ala Tyr Ala Cys Asn Thr Val Pro Arg Met
      65      70      75      80
Leu Val Asn Leu Leu His Pro Ala Lys Pro Ile Ser Phe Ala Gly Arg
      85      90      95
Met Met Gln Thr Phe Leu Phe Ser Thr Phe Ala Val Thr Glu Cys Leu
      100      105      110
Leu Leu Val Val Met Ser Tyr Asp Leu Tyr Val Ala Ile Cys His Pro
      115      120      125
Leu Arg Tyr Leu Ala Ile Met Thr Trp Arg Val Cys Ile Thr Leu Ala
      130      135      140
Val Thr Ser Trp Thr Thr Gly Val Leu Leu Ser Leu Ile His Leu Val
      145      150      155      160
Leu Leu Leu Pro Leu Pro Phe Cys Arg Pro Gln Lys Ile Tyr His Phe
      165      170      175
Phe Cys Glu Ile Leu Ala Val Leu Lys Leu Ala Cys Ala Asp Thr His
      180      185      190
Ile Asn Glu Asn Met Val Leu Ala Gly Ala Ile Ser Gly Leu Val Gly
      195      200      205
Pro Leu Ser Thr Ile Val Val Ser Tyr Met Cys Ile Leu Cys Ala Ile
      210      215      220
Leu Gln Ile Gln Ser Arg Glu Val Gln Arg Lys Ala Phe Arg Thr Cys
      225      230      235      240
Phe Ser His Leu Cys Val Ile Gly Leu Val Tyr Gly Thr Ala Ile Ile
      245      250      255
Met Tyr Val Gly Pro Arg Tyr Gly Asn Pro Lys Glu Gln Lys Lys Tyr
      260      265      270
Leu Leu Leu Phe His Ser Leu Phe Asn Pro Met Leu Asn Pro Leu Ile
      275      280      285
Cys Ser Leu Arg Asn Ser Glu Val Lys Asn Thr Leu Lys Arg Val Leu
      290      295      300
Gly Val Glu Arg Ala Leu
      305      310

```

<210> 1123

<211> 323
 <212> PRT
 <213> Unknown (H38g39 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(323)
 <223> Xaa = Any Amino Acid

<400> 1123
 His Thr Glu Pro Arg Asn Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu
 1 5 10 15
 Gly Ile Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Gly Leu Thr
 20 25 30
 Leu Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ile Ile Leu
 35 40 45
 Ala Val Ser Ser Asp Ser His Leu His Thr Ser Met Tyr Phe Val Leu
 50 55 60
 Ser Asn Leu Arg Trp Val Asp Ile Gly Phe Thr Ser Ala Thr Val Pro
 65 70 75 80
 Lys Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser Tyr Ala
 85 90 95
 Gly Cys Leu Thr Gln Met Ser Phe Leu Val Phe Phe Ala Cys Ile Glu
 100 105 110
 Asp Met Leu Leu Thr Val Met Ser Tyr Asp Gln Phe Leu Ala Ile Cys
 115 120 125
 His Pro Leu His Tyr Pro Val Ile Val Asn Pro His Phe Cys Val Phe
 130 135 140
 Leu Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His
 145 150 155 160
 Arg Trp Ile Val Leu Gln Phe Thr Phe Phe Lys Asn Val Glu Ile Ser
 165 170 175
 Asn Phe Val Cys Glu Pro Ser Gln Leu Leu Asn Leu Ala Cys Ser Asp
 180 185 190
 Ser Val Ile Asn Ile Ile Phe Ile Tyr Leu Asp Ser Thr Met Phe Gly
 195 200 205
 Phe Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys Ile Val Pro
 210 215 220
 Ser Ile Leu Arg Met Ser Leu Ser Asp Val Lys Tyr Lys Ala Phe Ser
 225 230 235 240
 Thr Cys Gly Ser His Leu Ala Val Phe Cys Leu Phe Tyr Gly Ala Gly
 245 250 255
 Ile Gly Val Tyr Leu Thr Ser Ala Val Ser Pro Pro Ser Gly Asn Gly
 260 265 270
 Val Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro
 275 280 285
 Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Pro Trp Arg
 290 295 300
 Leu Arg Ser Thr Thr Val Glu Ser Pro Xaa Ser Leu Pro Ser Phe Phe
 305 310 315 320
 Leu Cys Leu

<210> 1124
 <211> 320
 <212> PRT
 <213> Unknown (H38g40 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(320)

<223> Xaa = Any Amino Acid

<400> 1124

His	Thr	Glu	Pro	Gln	Asn	Leu	Thr	Gly	Val	Xaa	Glu	Phe	Leu	Leu	Leu
1				5					10					15	
Gly	Leu	Ser	Glu	Asp	Pro	Glu	Leu	Gln	Pro	Ile	Leu	Ala	Gly	Leu	Ser
			20					25					30		
Leu	Ser	Met	Tyr	Leu	Val	Thr	Val	Leu	Arg	Asn	Leu	Leu	Ile	Ile	Leu
		35					40					45			
Ala	Val	Ser	Ser	Asp	Pro	His	Leu	His	Thr	Pro	Met	Cys	Phe	Phe	Leu
	50					55					60				
Ser	Asn	Leu	Cys	Trp	Ala	Asp	Ile	Gly	Phe	Thr	Leu	Ala	Thr	Val	Pro
	65				70					75					80
Lys	Met	Ile	Val	Asp	Met	Gln	Ser	His	Thr	Arg	Val	Ile	Ser	Tyr	Glu
				85					90					95	
Gly	Cys	Leu	Thr	Arg	Ile	Ser	Phe	Leu	Val	Leu	Phe	Ala	Cys	Ile	Glu
			100					105					110		
Asp	Met	Leu	Leu	Thr	Val	Met	Ala	Tyr	Asp	Cys	Phe	Val	Ala	Ile	Cys
		115					120					125			
Arg	Pro	Leu	His	Tyr	Pro	Val	Ile	Val	Asn	Pro	His	Leu	Cys	Val	Phe
	130					135					140				
Phe	Leu	Leu	Val	Tyr	Phe	Phe	Leu	Ser	Leu	Leu	Asp	Ser	Gln	Leu	His
	145				150					155					160
Ser	Trp	Ile	Val	Leu	Gln	Phe	Thr	Ile	Ile	Lys	Asn	Val	Glu	Ile	Ser
			165					170						175	
Asn	Phe	Val	Cys	Asp	Pro	Ser	Gln	Leu	Leu	Lys	Leu	Ala	Cys	Ser	Asp
		180						185					190		
Ser	Val	Ile	Asn	Ser	Ile	Phe	Met	Tyr	Phe	His	Ser	Thr	Met	Phe	Gly
		195					200					205			
Phe	Leu	Pro	Ile	Ser	Gly	Ile	Leu	Leu	Ser	Tyr	Tyr	Lys	Ile	Val	Pro
	210				215						220				
Ser	Ile	Leu	Arg	Ile	Ser	Ser	Ser	Asp	Gly	Lys	Tyr	Lys	Ala	Phe	Ser
	225				230					235					240
Thr	Cys	Gly	Ser	His	Leu	Ala	Val	Val	Cys	Xaa	Phe	Tyr	Gly	Thr	Gly
			245						250					255	
Ile	Gly	Val	Tyr	Leu	Thr	Ser	Ala	Val	Ser	Pro	Pro	Pro	Arg	Asn	Gly
		260						265					270		
Val	Val	Ala	Ser	Val	Met	Tyr	Ala	Val	Val	Thr	Pro	Met	Leu	Asn	Leu
		275					280					285			
Phe	Ile	Tyr	Ser	Leu	Arg	Asn	Arg	Asp	Ile	Gln	Ser	Ala	Leu	Arg	Arg
	290					295					300				
Leu	Leu	Ser	Arg	Thr	Val	Glu	Ser	His	Asp	Leu	Phe	His	Pro	Phe	Ser
	305				310					315					320

<210> 1125

<211> 327

<212> PRT

<213> Unknown (H38g41 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(327)

<223> Xaa = Any Amino Acid

<400> 1125

Ser Thr Asp Xaa Gln Ser Leu Thr Gly Val Ser Ile Phe Leu Leu Leu
 1 5 10 15
 Glu Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Gly Leu Phe
 20 25 30
 Leu Ser Met Cys Leu Val Lys Val Leu Gly Asn Leu Leu Ile Ile Leu
 35 40 45
 Ala Ile Ser Pro Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu
 50 55 60
 Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Thr Met Val Pro
 65 70 75 80
 Lys Met Ile Val Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala
 85 90 95
 Gly Cys Leu Thr Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu
 100 105 110
 Glu Asn Met Leu Leu Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile
 115 120 125
 Cys His Pro Leu Tyr His Ser Ala Ile Met Asn Pro Cys Phe Cys Gly
 130 135 140
 Phe Leu Val Leu Leu Ser Phe Phe Leu Ser Phe Ser Gln Leu His Asn
 145 150 155 160
 Leu Ile Ala Leu Lys Met Thr Cys Phe Lys Asn Val Gly Ile Pro Asn
 165 170 175
 Phe Leu Cys Asp Pro Ser Gln Leu Pro His Leu Thr Cys Cys Asp Thr
 180 185 190
 Phe Thr Asn His Ile Ile Met Tyr Phe Pro Ala Ala Ile Phe Gly Phe
 195 200 205
 Leu Pro Ile Ser Gly Thr Leu Phe Ser Tyr His Val Ile Val Ser Ser
 210 215 220
 Ile Leu Arg Val Ser Ser Arg Gly Arg Cys Lys Ala Phe Ser His
 225 230 235 240
 Leu Xaa Val Val Cys Xaa Tyr Tyr Gly Thr Gly Phe Gly Gly Tyr Leu
 245 250 255
 Ser Ser Asp Val Ser Ser Ser Leu Arg Lys Ala Ala Val Ala Ser Val
 260 265 270
 Met Tyr Met Val Val Thr Pro Met Leu Asn Pro Phe Ile Tyr Ser Leu
 275 280 285
 Arg Asn Arg Asp Ile Lys Ser Val Val Gln Arg Pro His Gly Ser Thr
 290 295 300
 Val Xaa Ser Gln Tyr Leu Leu Ile Cys Ser Ile Pro Phe Val Val Trp
 305 310 315 320
 Val Lys Lys Gly Ser Lys Val
 325

<210> 1126

<211> 313

<212> PRT

<213> Unknown (H38g42 protein)

<220>

<223> Synthetic construct

<400> 1126

Met Gly Asn Trp Ser Thr Val Thr Glu Ile Thr Leu Ile Ala Phe Pro
 1 5 10 15
 Ala Leu Leu Glu Ile Arg Ile Ser Leu Phe Val Val Leu Val Val Thr
 20 25 30
 Tyr Thr Leu Thr Ala Thr Gly Asn Ile Thr Ile Ile Ser Leu Ile Trp
 35 40 45
 Ile Asp His Arg Leu Gln Thr Pro Met Tyr Phe Phe Leu Ser Asn Leu
 50 55 60
 Ser Phe Leu Asp Ile Leu Tyr Thr Thr Val Ile Thr Pro Lys Leu Leu

```

65          70          75          80
Ala Cys Leu Leu Gly Glu Glu Lys Thr Ile Ser Phe Ala Gly Cys Met
      85          90          95
Ile Gln Thr Tyr Phe Tyr Phe Phe Leu Gly Thr Val Glu Phe Ile Leu
      100        105        110
Leu Ala Val Met Ser Phe Asp Arg Tyr Met Ala Ile Cys Asp Pro Leu
      115        120        125
His Tyr Thr Val Ile Met Asn Ser Arg Ala Cys Leu Leu Leu Val Leu
      130        135        140
Gly Cys Trp Val Gly Ala Phe Leu Ser Val Leu Phe Pro Thr Ile Val
      145        150        155        160
Val Thr Arg Leu Pro Tyr Cys Arg Lys Glu Ile Asn His Phe Phe Cys
      165        170        175
Asp Ile Ala Pro Leu Leu Gln Val Ala Cys Ile Asn Thr His Leu Ile
      180        185        190
Glu Lys Ile Asn Phe Leu Leu Ser Ala Leu Val Ile Leu Ser Ser Leu
      195        200        205
Ala Phe Thr Thr Gly Ser Tyr Val Tyr Ile Ile Ser Thr Ile Leu Arg
      210        215        220
Ile Pro Ser Thr Gln Gly Arg Gln Lys Ala Phe Ser Thr Cys Ala Ser
      225        230        235        240
His Ile Thr Val Val Ser Ile Ala His Gly Ser Asn Ile Phe Val Tyr
      245        250        255
Val Arg Pro Asn Gln Asn Ser Ser Leu Asp Tyr Asp Lys Val Ala Ala
      260        265        270
Val Leu Ile Thr Val Val Thr Pro Leu Leu Asn Pro Phe Ile Tyr Ser
      275        280        285
Leu Arg Asn Glu Lys Val Gln Glu Val Leu Arg Glu Thr Val Asn Arg
      290        295        300
Ile Met Thr Leu Ile Gln Arg Lys Thr
305          310

```

<210> 1127

<211> 247

<212> PRT

<213> Unknown (H38g43 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(247)

<223> Xaa = Any Amino Acid

<400> 1127

```

Met Gly Asn Ile Asn Ile Ser Leu Glu Asn Tyr Phe Ile Leu Leu Gly
  1          5          10          15
Leu Ser Asn Xaa Pro Pro Leu Glu Ile Val Ile Phe Val Val Leu Leu
      20        25        30
Ile Phe Cys Phe Met Thr Leu Ile Gly Lys Leu Phe Ser Ile Ile Leu
      35        40        45
Ser Tyr Leu Asp Ser His Pro His Thr Pro Arg Tyr Leu Phe Ser Phe
      50        55        60
Leu Asp Phe Cys Tyr Thr Ile Ser Ser Ile Phe Xaa Leu Gln Tyr Asn
      65        70        75        80
Leu Trp Gly Pro Gln Lys Asn Ile Ser Tyr Ala Ser Gly Met Ile Gln
      85        90        95
Ile Tyr Phe Val Leu Thr Leu Gly Thr Met Asp Cys Ala Leu Leu Val
      100       105       110
Val Met Ser Arg Thr Val Tyr Ala Ala Gly His Arg His Leu Pro Tyr
      115       120       125

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Thr Val Val Met Ala Val Ala Phe Trp Val Ser Ser Phe Thr Asn Ser
  130                      135                      140
Ala Phe Asp Ser Phe Phe Thr Phe Trp Val Thr Leu Cys Gly His His
145                      150                      155                      160
Tyr Tyr Ala Tyr Ile Phe Ile Phe Thr Ser Leu Leu Val Xaa Arg Trp
                      165                      170                      175
Phe Ile Asn Arg Lys Lys Gln Ser Val Phe Ser Leu Asn His Ala Ala
                      180                      185                      190
Leu Leu Thr Leu Ser Phe Pro Leu Xaa Asn Asp Cys Phe Gln Glu Ile
                      195                      200                      205
Glu Lys Asn Met Leu Arg Lys His Ser Ile Gly Glu Cys Xaa Lys His
                      210                      215                      220
Val Met Leu Val Gln Leu Asn Gln Val Ser Lys Thr Cys Ile Phe Met
225                      230                      235                      240
Arg Pro Ile Leu Gly Asn Ser
                      245

```

<210> 1128

<211> 316

<212> PRT

<213> Unknown (H38g44 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(316)

<223> Xaa = Any Amino Acid

<400> 1128

```

Asp Ile Gln Asn Gln Thr Thr Val Thr Glu Phe Thr Leu Thr Ala Phe
  1                      5                      10                      15
Pro Val Leu Gln Gln Leu Gln Ile Ser Leu Leu Ala Val Leu Trp Phe
                      20                      25                      30
Thr Tyr Met Leu Thr Leu Thr Gly Asn Val Ala Ile Ile Ser Leu Thr
                      35                      40                      45
Trp Ala Asn His Arg Leu Gln Thr Pro Met Tyr Phe Phe Leu Ser Asn
                      50                      55                      60
Trp Ser Ile Trp Asp Ile Phe Phe Thr Thr Ser Val Ile Pro Lys Leu
65                      70                      75                      80
Leu Ala Cys Leu Leu Gln Asp Lys Lys Thr Ile Ser Leu Ala Gly Cys
                      85                      90                      95
Ile Thr Gln Thr Tyr Phe Leu Gly Phe Leu Gly Thr Val Glu Phe Ile
                      100                      105                      110
Leu Trp Ala Val Met Ser Phe Asp Cys Tyr Val Ala Ile Cys Asp Pro
                      115                      120                      125
Leu His Tyr Thr Ile Ile Met Asn Ser Arg Ala Cys Leu Leu Leu Val
                      130                      135                      140
Leu Gly Cys Trp Val Gly Ala Phe Leu Ser Val Leu Cys Pro Thr Ile
145                      150                      155                      160
Val Val Ser Arg Leu Pro Phe Cys Tyr Lys Glu Ile Ser His Phe Phe
                      165                      170                      175
Cys Asp Ile Thr Pro Leu Leu His Val Ser Cys Ile Asp Thr His Phe
                      180                      185                      190
Ile Glu Met Ile Asn Phe Leu Leu Ser Ser Leu Ile Leu Leu Thr Ser
                      195                      200                      205
Leu Val Leu Thr Thr Val Ser Tyr Ile Tyr Ile Ile Ser Thr Ile Leu
210                      215                      220
His Ile Pro Ser Ala Gln Gly Arg Arg Lys Ala Phe Ser Thr Cys Ala
225                      230                      235                      240
Ser His Ile Thr Val Ile Ser Ile Ala Tyr Ile Ser Asn Ile Phe Arg

```

245 250 255
 Tyr Val Arg Pro Ser Gln Ser His Ser Met Gly Phe Asp Lys Val Thr
 260 265 270
 Ala Val Pro Thr Met Val Thr Pro Leu Leu Asn Pro Phe Thr Tyr Ser
 275 280 285
 Leu Arg Asn Glu Lys Val Lys Ala Val Leu Lys Glu Ala Val Ser Lys
 290 295 300
 Ile Met Ser Ser Trp His Arg Arg Thr Xaa Asn Phe
 305 310 315

<210> 1129

<211> 310

<212> PRT

<213> Unknown (H38g45 protein)

<220>

<223> Synthetic construct

<400> 1129

Met Glu Pro Gln Asn Thr Thr Gln Val Ser Met Phe Val Leu Leu Gly
 1 5 10 15
 Phe Ser Gln Thr Gln Glu Leu Gln Lys Phe Leu Phe Leu Leu Phe Leu
 20 25 30
 Leu Val Tyr Val Thr Thr Ile Val Gly Asn Leu Leu Ile Met Val Thr
 35 40 45
 Val Thr Phe Asp Cys Arg Leu His Thr Pro Met Tyr Phe Leu Leu Arg
 50 55 60
 Asn Leu Ala Leu Ile Asp Leu Cys Tyr Ser Thr Val Thr Ser Pro Lys
 65 70 75 80
 Met Leu Val Asp Phe Leu His Glu Thr Lys Thr Ile Ser Tyr Gln Gly
 85 90 95
 Cys Met Ala Gln Ile Phe Phe Phe His Leu Leu Gly Gly Gly Thr Val
 100 105 110
 Phe Phe Leu Ser Val Met Ala Tyr Asp Arg Tyr Ile Ala Ile Ser Gln
 115 120 125
 Pro Leu Arg Tyr Val Thr Ile Met Asn Thr Gln Leu Cys Val Gly Leu
 130 135 140
 Val Val Ala Ala Trp Val Gly Gly Phe Val His Ser Ile Val Gln Leu
 145 150 155 160
 Ala Leu Ile Leu Pro Leu Pro Phe Cys Asp Pro Asn Ile Ile Asp Asn
 165 170 175
 Phe Tyr Cys Asp Val Pro Gln Val Leu Arg Leu Ala Cys Thr Asp Thr
 180 185 190
 Ser Leu Leu Glu Phe Leu Met Ile Phe Asn Ser Gly Leu Leu Val Ile
 195 200 205
 Ile Trp Phe Leu Leu Leu Leu Ile Ser Tyr Thr Val Ile Leu Val Met
 210 215 220
 Leu Arg Ser His Ser Gly Lys Ala Arg Arg Lys Ala Ala Ser Thr Cys
 225 230 235 240
 Thr Thr His Ile Ile Val Val Ser Met Ile Phe Ile Pro Cys Ile Tyr
 245 250 255
 Ile Tyr Thr Trp Pro Phe Thr Pro Phe Leu Met Asp Lys Ala Val Ser
 260 265 270
 Ile Ser Tyr Thr Val Met Thr Pro Met Leu Asn Pro Met Ile Tyr Thr
 275 280 285
 Leu Arg Asn Gln Asp Met Lys Ala Ala Met Arg Arg Leu Gly Lys Cys
 290 295 300
 Leu Val Ile Cys Arg Glu
 305 310

<210> 1130

<211> 311
 <212> PRT
 <213> Unknown (H38g46 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(311)
 <223> Xaa = Any Amino Acid

<400> 1130
 Asp Gln Glu Asn Gln Thr Ser Glu Val Thr Phe Ile Leu Leu Gly Phe
 1 5 10 15
 Ser Glu Tyr Pro Asp Leu Gln Thr Pro Leu Phe Leu Val Phe Leu Thr
 20 25 30
 Ile Tyr Thr Val Thr Val Leu Gly Asn Leu Gly Met Ile Ile Val Ile
 35 40 45
 Arg Ile Ser Pro Lys Leu His Thr Pro Met Cys Phe Phe Leu Ser His
 50 55 60
 Leu Ser Phe Val Asp Phe Cys Tyr Ser Thr Thr Ile Thr Pro Lys Leu
 65 70 75 80
 Leu Glu Asn Leu Val Val Glu Asp Arg Thr Ile Ser Phe Thr Gly Cys
 85 90 95
 Thr Met Gln Leu Phe Phe Val Cys Ile Phe Val Val Thr Glu Thr Phe
 100 105 110
 Met Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Val Cys Asn Pro
 115 120 125
 Leu Leu Tyr Thr Val Ala Met Tyr Gln Arg Leu Cys Ser Leu Leu Val
 130 135 140
 Ala Thr Ser Tyr Cys Trp Gly Ile Val Cys Ser Leu Thr Leu Thr Xaa
 145 150 155 160
 Phe Leu Leu Glu Leu Ser Phe Arg Gly Asn Asn Ile Ile Asn Asn Phe
 165 170 175
 Val Cys Glu His Ala Ala Ile Val Ala Val Ser Cys Ser Asp Pro Cys
 180 185 190
 Val Ser Gln Glu Ile Thr Leu Val Ser Ala Thr Phe Asn Glu Ile Ser
 195 200 205
 Ser Leu Thr Ser Tyr Ala Phe Ile Phe Ile Thr Val Met Lys Thr Pro
 210 215 220
 Ser Thr Gly Gly Arg Lys Lys Ala Phe Ser Thr Ser Ala Ser His Leu
 225 230 235 240
 Thr Ala Ile Thr Ile Phe His Gly Thr Ile Leu Phe Leu Tyr Cys Val
 245 250 255
 Pro Asn Ser Lys Ser Ser Trp Leu Met Val Lys Val Ala Ser Val Phe
 260 265 270
 Tyr Thr Val Val Ile Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg
 275 280 285
 Asn Lys Asp Val Lys Glu Thr Val Arg Arg Leu Leu Ile Thr Lys Leu
 290 295 300
 Leu Cys Leu Ile Leu Xaa Asn
 305 310

<210> 1131
 <211> 334
 <212> PRT
 <213> Unknown (H38g47 protein)

<220>
 <223> Synthetic construct

<221> VARIANT

<222> (1)...(334)

<223> Xaa = Any Amino Acid

<400> 1131

```

Tyr Ala Asp Pro Gln Asn Leu Thr Asp Val Ser Ile Phe Leu Leu Leu
 1          5          10          15
Glu Val Ser Gly Asp Pro Glu Leu Gln Pro Val Leu Ala Gly Leu Phe
 20          25          30
Leu Ser Met Cys Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu
 35          40          45
Ala Ile Ser Pro Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu
 50          55          60
Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro
 65          70          75          80
Lys Met Ile Val Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala
 85          90          95
Gly Cys Leu Thr Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu
 100         105         110
Glu Asn Met Leu Leu Ser Val Met Ala Tyr Asp Trp Phe Val Ala Ile
 115         120         125
Cys His Pro Leu Tyr His Leu Thr Ile Met Asn Pro Cys Phe Cys Ala
 130         135         140
Phe Leu Val Leu Leu Ser Phe Phe Phe Ser Val Phe Xaa His Ser Gln
 145         150         155         160
Leu His Asn Leu Ile Ala Leu Gln Val Thr Cys Phe Lys Asp Val Glu
 165         170         175
Ile Pro Asn Phe Phe Cys Asp Pro Ser Gln Leu Ser His Leu Ala Cys
 180         185         190
Cys Asp Thr Phe Thr Ile Asn Ile Ile Met Tyr Phe Pro Ala Ala Ile
 195         200         205
Phe Gly Phe Leu Pro Ile Leu Gly Thr Leu Phe Ser Phe Ser Lys Ile
 210         215         220
Val Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Lys Tyr Lys Ala
 225         230         235         240
Leu Ser Thr Cys Gly Ser Arg Leu Ser Val Val Cys Xaa Val Tyr Gly
 245         250         255
Thr Gly Val Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser Pro Arg
 260         265         270
Lys Gly Ala Val Ala Ser Val Met Tyr Thr Leu Val Thr Pro Met Leu
 275         280         285
Thr Pro Phe Ile Tyr Ser Leu Arg Asn Arg Asp Met Lys Gly Val Leu
 290         295         300
Arg Gln Pro His Gly Ser Thr Val Xaa Ser Gln Tyr Leu Ile Cys Ser
 305         310         315         320
Ile Pro Phe Val Val Trp Val Gln Lys Gly Ser Lys Val Lys
 325         330

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<210> 1132

<211> 307

<212> PRT

<213> Unknown (H38g48 protein)

<220>

<223> Synthetic construct

<400> 1132

```

Met Glu Thr Gly Asn Leu Thr Trp Val Ser Asp Phe Val Phe Leu Gly
 1          5          10          15
Leu Ser Gln Thr Arg Glu Leu Gln Arg Phe Leu Phe Leu Met Phe Leu
 20          25          30

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Phe Val Tyr Ile Thr Thr Val Met Gly Asn Ile Leu Ile Ile Ile Thr
 35 40 45
 Val Thr Ser Asp Ser Gln Leu His Thr Pro Met Tyr Phe Leu Leu Arg
 50 55 60
 Asn Leu Ala Val Leu Asp Leu Cys Phe Ser Ser Val Thr Ala Pro Lys
 65 70 75 80
 Met Leu Val Asp Leu Leu Ser Glu Lys Lys Thr Ile Ser Tyr Gln Gly
 85 90 95
 Cys Met Gly Gln Ile Phe Phe Phe His Phe Leu Gly Gly Ala Met Val
 100 105 110
 Phe Phe Leu Ser Val Met Ala Phe Asp Arg Leu Ile Ala Ile Ser Arg
 115 120 125
 Pro Leu Arg Tyr Val Thr Val Met Asn Thr Gln Leu Trp Val Gly Leu
 130 135 140
 Val Val Ala Thr Trp Val Gly Gly Phe Val His Ser Ile Val Gln Leu
 145 150 155 160
 Ala Leu Met Leu Pro Leu Pro Phe Cys Gly Pro Asn Ile Leu Asp Asn
 165 170 175
 Phe Tyr Cys Asp Val Pro Gln Val Leu Arg Leu Ala Cys Thr Asp Thr
 180 185 190
 Ser Leu Leu Glu Phe Leu Lys Ile Ser Asn Ser Gly Leu Leu Asp Val
 195 200 205
 Val Trp Phe Phe Leu Leu Leu Met Ser Tyr Leu Phe Ile Leu Val Met
 210 215 220
 Leu Arg Ser His Pro Gly Glu Ala Arg Arg Lys Ala Ala Ser Thr Cys
 225 230 235 240
 Thr Thr His Ile Ile Val Val Ser Met Ile Phe Val Pro Ser Ile Tyr
 245 250 255
 Leu Tyr Ala Arg Pro Phe Thr Pro Phe Pro Met Asp Lys Leu Val Ser
 260 265 270
 Ile Gly His Thr Val Met Thr Pro Met Leu Asn Pro Met Ile Tyr Thr
 275 280 285
 Leu Arg Asn Gln Asp Met Gln Ala Ala Val Arg Arg Leu Gly Arg His
 290 295 300
 Arg Leu Val
 305

<210> 1133

<211> 316

<212> PRT

<213> Unknown (H38g49 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(316)

<223> Xaa = Any Amino Acid

<400> 1133

His Thr Glu Pro Gln Asn Leu Thr Asp Val Xaa Glu Phe Leu Leu Leu
 1 5 10 15
 Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Leu Leu Ser
 20 25 30
 Leu Ser Leu Ser Met Tyr Leu Val Met Val Leu Arg Asn Leu Leu Ser
 35 40 45
 Ile Leu Ala Val Ser Ser Val Ser Pro Leu His Thr Pro Asn Leu Cys
 50 55 60
 Trp Ala Asp Ile Gly Phe Thr Leu Ala Thr Val Pro Lys Met Ile Val
 65 70 75 80
 Asp Met Gln Ser His Ser Arg Val Ile Ser His Ala Gly Cys Leu Thr

			85					90					95				
Gln	Met	Ser	Phe	Phe	Ile	Leu	Phe	Ala	Cys	Ile	Glu	Gly	Met	Leu	Leu		
			100					105					110				
Thr	Val	Met	Ala	Tyr	Asp	Cys	Phe	Val	Ala	Ile	Cys	Arg	Pro	Leu	His		
			115					120					125				
Tyr	Pro	Val	Ile	Val	Asn	Pro	His	Leu	Cys	Val	Phe	Phe	Val	Leu	Val		
			130					135					140				
Ser	Phe	Phe	Leu	Ser	Leu	Leu	Asp	Ser	Gln	Leu	His	Ser	Xaa	Ile	Val		
145			150					155					160				
Leu	Gln	Phe	Thr	Ile	Ile	Lys	Asn	Val	Glu	Ile	Ser	His	Phe	Phe	Cys		
			165					170					175				
Asp	Pro	Ser	Gln	Leu	Leu	Lys	Leu	Ala	Cys	Ser	Asp	Ser	Val	Ile	Asn		
			180					185					190				
Ser	Ile	Phe	Ile	Tyr	Phe	Asp	Ser	Thr	Met	Phe	Gly	Phe	Leu	Pro	Ile		
			195					200					205				
Ser	Gly	Ile	Leu	Trp	Ser	Tyr	Tyr	Lys	Ile	Ile	Pro	Ser	Ile	Leu	Arg		
210			215					220					225				
Ile	Ser	Ser	Ser	Tyr	Gly	Lys	Tyr	Lys	Ala	Phe	Ser	Thr	Cys	Ala	Ser		
			230					235					240				
His	Leu	Ala	Val	Val	Cys	Xaa	Phe	Tyr	Val	Thr	Gly	Ile	Gly	Met	Tyr		
			245					250					255				
Leu	Thr	Ser	Ala	Val	Ser	Pro	Pro	Pro	Ser	Asn	Gly	Val	Val	Ala	Ser		
			260					265					270				
Val	Met	Tyr	Ala	Ala	Val	Thr	Pro	Met	Leu	Asn	Pro	Phe	Ile	Tyr	Ser		
			275					280					285				
Leu	Arg	Asn	Arg	Asp	Ile	Gln	Ser	Ala	Leu	Arg	Arg	Val	Leu	Ser	Arg		
290			295					300					305				
Thr	Val	Glu	Phe	His	Asp	Leu	Phe	His	Pro	Phe	Ser						
305			310					315									

<210> 1134

<211> 123

<212> PRT

<213> Unknown (H38q50 protein)

<220>

<223> Synthetic construct

<400> 1134

Met	Ser	Gly	Ser	Pro	Thr	Gln	Leu	Thr	Ala	Gly	Pro	Arg	Thr	Ala	Ser
1				5					10					15	
Gly	Cys	Val	Ile	Met	Ile	Cys	Phe	Ala	Leu	Thr	Val	Leu	Ser	Tyr	Ile
			20					25					30		
Arg	Ile	Leu	Ala	Thr	Val	Val	Gln	Ile	Arg	Ser	Ala	Ala	Ser	Arg	Arg
		35					40					45			
Lys	Ala	Phe	Ser	Thr	Cys	Ser	Ser	His	Leu	Gly	Met	Val	Leu	Leu	Phe
	50					55					60				
Tyr	Gly	Thr	Gly	Ser	Ser	Thr	Tyr	Met	Arg	Pro	Thr	Thr	Arg	Tyr	Ser
65					70					75					80
Pro	Leu	Glu	Gly	Arg	Leu	Ala	Ala	Val	Phe	Tyr	Ser	Ile	Leu	Ile	Pro
				85					90					95	
Thr	Leu	Asn	Pro	Leu	Ile	Tyr	Ser	Leu	Arg	Asn	Gln	Asp	Met	Lys	Arg
			100					105					110		
Ala	Leu	Trp	Lys	Leu	Tyr	Leu	Gln	Val	Pro	Tyr					
		115					120								

<210> 1135

<211> 356

<212> PRT

<213> Unknown (H38g51 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(356)

<223> Xaa = Any Amino Acid

<400> 1135

```

Met Ile Asn Asp Ser His Phe Ser Gly Phe Ile Leu Leu Gly Phe Thr
 1           5           10           15
Gly Gln Pro Gln Leu Gln Met Met Ile Ser Gly Val Val Phe Phe Phe
          20           25           30
Tyr Thr Ile Ala Phe Met Gly Asn Met Ala Ile Ile Leu Leu Ser Phe
          35           40           45
Leu Asp Asp His Leu Gln Val Pro Met Tyr Phe Phe Leu Arg Asn Leu
          50           55           60
Ala Ile Leu Asp Leu Cys Tyr Thr Thr Asn Ile Val Pro Gln Met Leu
65           70           75           80
Val Ser Ile Trp Gly Lys Asp Lys Arg Ile Thr Phe Gly Gly Cys Ala
          85           90           95
Phe Gln Leu Phe Ile Asp Val Ala Leu Tyr Ser Val Glu Cys Ile Leu
          100          105          110
Leu Ser Met Met Ser Tyr Asp Arg Leu Asn Ala Ile Cys Lys Pro Leu
          115          120          125
His His Met Thr Ile Met Asn Leu Gln Leu Cys Gln Gly Leu Val Val
          130          135          140
Ile Ser Trp Val Val Gly Val Ile Asn Cys Ile Ile Pro Ser Pro Tyr
145           150           155           160
Ala Thr Ser Leu Pro Arg Cys Arg Asn His His Leu Asp His Phe Phe
          165          170          175
Val Cys Val Lys Cys Leu Gln Xaa Ser Arg Phe Lys Ile Ala Cys Val
          180          185          190
Asp Thr Thr Ala Met Glu Val Thr Thr Phe Ala Met Cys Leu Ile Ile
          195          200          205
Val Leu Val Pro Leu Leu Leu Ile Leu Val Ser Tyr Gly Phe Ile Ala
          210          215          220
Val Ala Val Leu Lys Ile Lys Ser Ala Ala Gly Arg Gln Lys Ala Phe
225           230           235           240
Gly Thr Cys Ser Ser His Leu Val Val Val Ser Ile Phe Cys Gly Thr
          245          250          255
Val Thr Tyr Met Tyr Ile Gln Pro Gly Asn Ser Pro Asn Gln Asn Glu
          260          265          270
Gly Lys Leu Leu Ser Ile Phe Tyr Ser Ile Val Thr Pro Ser Leu Asn
          275          280          285
Pro Leu Ile Tyr Thr Val Arg Asn Lys Glu Phe Lys Gly Ala Met Lys
          290          295          300
Arg Leu Thr Gly Lys Glu Lys Asp Cys Met Glu Lys Arg Gly His Xaa
305           310           315           320
Phe Phe Leu Pro Ala Ile Ser Asn Met Ala Ile Asp Leu Pro Asn Leu
          325          330          335
Lys Cys Arg Gln Phe Ile Leu Xaa Ile Asn Cys Leu His Leu Arg Xaa
          340          345          350
Arg Xaa Tyr Pro
          355

```

<210> 1136

<211> 317

<212> PRT

<213> Unknown (H38g52 protein)

<220>

<223> Synthetic construct

<400> 1136

```

Met Ile Asn Asp Ser Tyr Phe Gly Trp Leu Met Leu Leu Gly Phe Pro
 1           5           10           15
Gly Lys Pro Gln Leu Glu Met Ile Ile Ser Gly Val Val Phe Phe Phe
 20           25           30
Tyr Ala Ile Ser Leu Met Gly Asn Met Val Leu Ile Leu Leu Pro Leu
 35           40           45
Leu Asp Lys His Leu Gln Thr Pro Ile Tyr Phe Phe Leu Arg Asn Leu
 50           55           60
Ala Ile Leu Asp Leu Cys Tyr Thr Thr Asn Ile Val Pro Gln Met Leu
 65           70           75           80
Val Asn Ala Trp Gly Lys Asp Lys Lys Ile Thr Phe Gly Gly Cys Ala
 85           90           95
Phe Gln Leu Phe Thr Asn Val Thr Leu Cys Thr Val Glu Cys Met Leu
100           105           110
Leu Ala Val Met Ser Tyr Asp Pro Phe Asn Ala Val Cys Lys Pro Leu
115           120           125
Asp Tyr Met Thr Ile Met Asn Pro Gln Leu Cys Gln Gly Leu Val Ala
130           135           140
Met Thr Trp Leu Ile Gly Val Thr Asn Cys Met Ile Leu Ser Pro Cys
145           150           155           160
Pro Val Ser Leu Pro Arg Cys Gly Asp His His Leu Asp His Tyr Phe
165           170           175
Cys Glu Ile Ser Ala Met Val Lys Ile Ala Cys Gly Ala Thr Thr Val
180           185           190
Met Glu Glu Lys Pro Tyr Leu His Cys Val Val Val Val Val Phe Ile
195           200           205
Phe Leu Ala Ser Leu Leu Leu Ile Leu Val Ser Tyr Gly Phe Ile Ala
210           215           220
Val Ala Val Leu Lys Ile Lys Ser Ala Ala Gly Arg Gln Lys Ala Phe
225           230           235           240
Gly Thr Cys Phe Ser His Leu Ile Val Val Ser Ile Phe Tyr Gly Thr
245           250           255
Val Arg Tyr Met Tyr Ile Glu Pro Gly Asn Ser Pro Ser Gln Asp Glu
260           265           270
Gly Lys Leu Leu His Ile Phe Tyr Ser Ile Val Thr Pro Thr Leu Asn
275           280           285
Pro Tyr Pro Leu Arg Asn Lys Glu Phe Lys Trp Ala Met Lys Arg Leu
290           295           300
Ile Gly Lys Glu Lys Gly Ser Gly Asp Thr Ile Gly His
305           310           315

```

<210> 1137

<211> 312

<212> PRT

<213> Unknown (H38g53 protein)

<220>

<223> Synthetic construct

<400> 1137

```

Met Val Asn Gln Ser Ser Thr Pro Gly Phe Leu Leu Leu Gly Phe Ser
 1           5           10           15
Glu His Pro Gly Leu Glu Arg Thr Leu Phe Val Val Val Phe Thr Ser
 20           25           30
Tyr Leu Leu Thr Leu Val Gly Asn Thr Leu Ile Ile Leu Leu Ser Ala
 35           40           45
Leu Asp Pro Lys Leu His Ser Pro Met Tyr Phe Phe Leu Ser Asn Leu
 50           55           60

```

Ser Phe Leu Asp Leu Cys Phe Thr Thr Ser Cys Val Pro Gln Met Leu
 65 70 75 80
 Val Asn Leu Trp Gly Pro Lys Lys Thr Ile Ser Phe Leu Asp Cys Ser
 85 90 95
 Val Gln Ile Phe Ile Phe Leu Ser Leu Gly Thr Thr Glu Cys Ile Leu
 100 105 110
 Leu Thr Val Met Ala Phe Asp Arg Tyr Val Ala Val Cys Gln Pro Leu
 115 120 125
 His Tyr Ala Thr Ile Ile His Pro Arg Leu Cys Trp Gln Leu Ala Ser
 130 135 140
 Val Ala Trp Val Ile Gly Leu Val Glu Ser Val Val Gln Thr Pro Ser
 145 150 155 160
 Thr Leu His Leu Pro Phe Cys Pro Asp Arg Gln Val Asp Asp Phe Val
 165 170 175
 Cys Glu Val Pro Ala Leu Ile Arg Leu Ser Cys Glu Asp Thr Ser Tyr
 180 185 190
 Asn Glu Ile Gln Val Ala Val Ala Ser Val Phe Ile Leu Val Val Pro
 195 200 205
 Leu Ser Leu Ile Leu Val Ser Tyr Gly Ala Ile Thr Trp Ala Val Leu
 210 215 220
 Arg Ile Asn Ser Ala Lys Gly Arg Arg Lys Ala Phe Gly Thr Cys Ser
 225 230 235 240
 Ser His Leu Thr Val Val Thr Leu Phe Tyr Ser Ser Val Ile Ala Val
 245 250 255
 Tyr Leu Gln Pro Lys Asn Pro Tyr Ala Gln Glu Arg Gly Lys Phe Phe
 260 265 270
 Gly Leu Phe Tyr Ala Val Gly Thr Pro Ser Leu Asn Pro Leu Ile Tyr
 275 280 285
 Thr Leu Arg Asn Lys Glu Val Thr Arg Ala Phe Arg Arg Leu Leu Gly
 290 295 300
 Lys Glu Met Gly Leu Thr Gln Ser
 305 310

<210> 1138

<211> 343

<212> PRT

<213> Unknown (H38g54 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(343)

<223> Xaa = Any Amino Acid

<400> 1138

Met Val Asn Gln Ser Ser Ala Pro Gly Phe Leu Leu Leu Gly Phe Ser
 1 5 10 15
 Glu His Pro Ala Leu Glu Arg Thr Leu Phe Val Val Val Phe Thr Ser
 20 25 30
 Tyr Leu Leu Thr Leu Gly Gly Leu Ile Ile Leu Leu Ser Val Leu Asp
 35 40 45
 Pro Arg Leu His Ser Pro Met Tyr Phe Phe Leu Ser Asn Leu Ser Phe
 50 55 60
 Leu Asp Leu Cys Phe Thr Ile Ser Cys Val Pro Gly Met Leu Val Asn
 65 70 75 80
 Leu Trp Glu Pro Lys Lys Thr Ile Ile Leu Leu Gly Cys Ser Val Gln
 85 90 95
 Phe Phe Ile Phe Leu Ser Leu Gly Thr Thr Glu Cys Ile Leu Leu Thr
 100 105 110
 Val Met Ala Phe Asp Arg Tyr Met Ala Ile Phe Lys Pro Leu Arg His

```

      115              120              125
Ala Thr Ile Val His Leu Cys Leu Cys Trp Gln Leu Ala Ser Val Ala
  130              135              140
Trp Val Ile Gly Leu Val Glu Ser Val Val Gln Thr Pro Ser Thr Leu
  145              150              155              160
Arg Leu Pro Phe Cys Pro His Gln Gln Val Asp Asp Phe Val Cys Glu
      165              170              175
Val Pro Ala Leu Ile Arg Leu Ser Cys Glu Asp Thr Ser Tyr Asn Glu
      180              185              190
Ile Gln Met Ala Val Ala Ser Val Phe Ile Leu Ala Val Pro Ser Leu
      195              200              205
Ile Leu Val Ser Tyr Gly Ala Ile Ala Trp Ala Val Leu Arg Ile Thr
      210              215              220
Ala Lys Gly Gln Arg Lys Ala Phe Gly Thr Cys Ser Ser His Leu Thr
  225              230              235              240
Val Val Thr Leu Phe Tyr Ser Ser Val Ile Ala Val Tyr Leu Gln Pro
      245              250              255
Lys Asn Pro Tyr Ala Gln Glu Arg Gly Lys Phe Phe Gly Leu Phe Tyr
      260              265              270
Ala Val Gly Thr Pro Ser Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn
      275              280              285
Lys Glu Val Thr Arg Ala Phe Arg Arg Leu Leu Ala Lys Glu Met Gly
  290              295              300
Leu Ile Gln Ser Xaa Gly Arg Ala Val Xaa Cys Ala Phe Xaa Ile Lys
  305              310              315              320
Lys Lys Leu Phe Ile Leu Leu Xaa Thr Ser Leu Ser Ser Gln Val Tyr
      325              330              335
Tyr Leu Ser Tyr Thr His His
      340

```

<210> 1139

<211> 291

<212> PRT

<213> Unknown (H38g55 protein)

<220>

<223> Synthetic construct

<400> 1139

```

Met Phe Ala Ala Leu Val Leu Leu Cys Tyr Leu Leu Thr Leu Thr Gly
  1              5              10              15
Asn Ser Ala Leu Val Leu Leu Ala Val Arg Asp Pro Arg Leu His Thr
      20              25              30
Pro Met Tyr Tyr Phe Leu Cys His Leu Ala Leu Val Asp Ala Gly Phe
      35              40              45
Thr Thr Ser Val Val Pro Pro Leu Leu Ala Asn Leu Arg Gly Pro Ala
      50              55              60
Leu Trp Leu Pro Arg Ser His Cys Thr Ala Gln Leu Cys Ala Ser Leu
  65              70              75              80
Ala Leu Gly Ser Ala Glu Cys Val Leu Leu Ala Val Met Ala Leu Asp
      85              90              95
Arg Ala Ala Lys Lys Val Lys Gly Ala Ala Arg Arg Leu Leu Arg Ser
      100              105              110
Leu Gly Arg Gly Gln Ala Gly Gln Ser Ala Ser Trp Leu Ser Gly Leu
      115              120              125
Thr Asn Ser Val Ala Gln Thr Ala Leu Leu Ala Glu Arg Pro Leu Cys
      130              135              140
Ala Pro Arg Leu Leu Asp His Phe Ile Cys Glu Leu Pro Ala Leu Leu
  145              150              155              160
Lys Leu Ala Cys Gly Gly Asp Gly Asp Thr Thr Glu Asn Gln Met Phe
      165              170              175

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Ala Ala Arg Val Val Ile Leu Leu Leu Pro Phe Ala Val Ile Leu Ala
 180 185 190
 Ser Tyr Gly Ala Val Ala Arg Ala Val Cys Cys Met Arg Phe Ser Gly
 195 200 205
 Gly Arg Arg Arg Ala Val Gly Thr Cys Gly Ser His Leu Thr Ala Val
 210 215 220
 Cys Leu Phe Tyr Gly Ser Ala Ile Tyr Thr Tyr Leu Gln Pro Ala Gln
 225 230 235 240
 Arg Tyr Asn Gln Ala Arg Gly Lys Phe Val Ser Leu Phe Tyr Thr Val
 245 250 255
 Val Thr Pro Ala Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn Lys Lys
 260 265 270
 Val Lys Gly Ala Ala Arg Arg Leu Leu Arg Ser Leu Gly Arg Gly Gln
 275 280 285
 Ala Gly Gln
 290

<210> 1140

<211> 307

<212> PRT

<213> Unknown (H38g56 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(307)

<223> Xaa = Any Amino Acid

<400> 1140

Glu Leu Ile Thr Asn Ser Ser Ser Val Pro Ser Cys Glu Arg Thr Ile
 1 5 10 15
 Gln Ile Phe Leu Phe Ser Leu Ile Thr Thr Ile Tyr Ala Leu Thr Ile
 20 25 30
 Thr Gly Asn Gly Ala Ile Ala Phe Ala Leu Trp Cys Asp Arg Arg Leu
 35 40 45
 His Thr Pro Met Tyr Met Phe Leu Gly Asp Phe Ser Phe Leu Glu Ile
 50 55 60
 Trp Tyr Val Phe Ser Thr Val Pro Lys Met Leu Val Asn Phe Leu Ser
 65 70 75 80
 Glu Lys Thr Asn Ile Ser Phe Ala Gly Cys Phe Leu Gln Ile Tyr Phe
 85 90 95
 Phe Phe Ser Leu Asn Thr Ser Glu Cys Leu Leu Leu Thr Val Met Ala
 100 105 110
 Phe Asp Gln Asn Leu Ala Ile Cys Arg Pro Leu His Tyr Pro Asn Ile
 115 120 125
 Met Thr Gly His Leu Cys Ala Lys Leu Ala Ile Leu Cys Trp Val Cys
 130 135 140
 Gly Phe Leu Trp Phe Leu Ile Pro Ile Val Leu Ile Ser Gln Met Pro
 145 150 155 160
 Phe Cys Gly Pro Asn Ile Ile Asp His Val Val Cys Asp Pro Gly Pro
 165 170 175
 Leu Phe Ala Leu Asp Cys Val Ser Ala Pro Arg Ile Gln Leu Phe Cys
 180 185 190
 Tyr Thr Leu Ser Ser Leu Val Ile Phe Gly Asn Phe Leu Phe Ile Ile
 195 200 205
 Gly Ser Tyr Thr Ile Val Leu Lys Val Val Leu Gly Thr Pro Ser Ser
 210 215 220
 Thr Gly Arg His Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ala Val
 225 230 235 240
 Val Ser Leu Cys Tyr Gly Ser Leu Met Val Met Tyr Val Ser Pro Gly

<400> 1142

Met Ala Lys Asn Asn Leu Thr Arg Val Thr Glu Phe Ile Leu Met Gly
 1 5 10 15
 Phe Met Asp His Pro Lys Leu Glu Ile Pro Leu Phe Leu Val Phe Leu
 20 25 30
 Ser Phe Tyr Leu Val Thr Leu Leu Gly Asn Val Gly Met Ile Met Leu
 35 40 45
 Ile Gln Val Asp Val Lys Leu Tyr Thr Pro Met Tyr Phe Phe Leu Ser
 50 55 60
 His Leu Ser Leu Leu Asp Ala Cys Tyr Thr Ser Val Ile Thr Pro Gln
 65 70 75 80
 Ile Leu Ala Thr Leu Ala Thr Gly Lys Thr Val Ile Ser Tyr Gly His
 85 90 95
 Cys Ala Ala Gln Phe Phe Leu Phe Thr Ile Cys Ala Gly Thr Glu Cys
 100 105 110
 Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Ala Ala Ile Arg Asn
 115 120 125
 Pro Leu Leu Tyr Thr Val Ala Met Asn Pro Arg Leu Cys Trp Ser Leu
 130 135 140
 Val Val Gly Ala Tyr Val Cys Gly Val Ser Gly Ala Ile Leu Arg Thr
 145 150 155 160
 Thr Cys Thr Phe Thr Leu Ser Phe Cys Lys Asp Asn Gln Ile Asn Phe
 165 170 175
 Phe Phe Cys Asp Leu Pro Pro Leu Leu Lys Leu Ala Cys Ser Asp Thr
 180 185 190
 Ala Asn Ile Glu Ile Val Ile Ile Phe Phe Gly Asn Phe Val Ile Leu
 195 200 205
 Ala Asn Ala Ser Val Ile Leu Ile Ser Tyr Leu Leu Ile Ile Lys Thr
 210 215 220
 Ile Leu Lys Val Lys Ser Ser Gly Gly Arg Ala Lys Thr Phe Ser Thr
 225 230 235 240
 Cys Ala Ser His Ile Thr Ala Val Ala Leu Phe Phe Gly Ala Leu Ile
 245 250 255
 Phe Met Tyr Leu Gln Ser Gly Ser Gly Lys Ser Leu Glu Glu Asp Lys
 260 265 270
 Val Val Ser Val Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro Leu
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Asp Ala Phe Arg Lys Val
 290 295 300
 Ala Arg Arg Leu Gln Val Ser Leu Ser Met
 305 310

<210> 1143

<211> 315

<212> PRT

<213> Unknown (H38g59 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(315)

<223> Xaa = Any Amino Acid

<400> 1143

Met Gly Gly Leu Lys Arg Asp Asn Ala Ser Glu Met Thr Glu Leu Ile
 1 5 10 15
 Leu Val Gly Phe Ala Gln His Pro Glu Ile Gln Thr Ala Phe Leu
 20 25 30
 Glu Leu Leu Phe Phe Tyr Xaa Ser Gln Leu Phe Glu Asn Ile Leu Ile
 35 40 45
 Val Ala Val Val Arg Xaa Asp Ser Arg Leu His Thr Pro Met Gly Phe

50		55		60	
Phe	Phe	Leu	Ser	Thr	Leu
65					70
Trp	Glu	Leu	Xaa	Val	Leu
		85			90
Ser	Tyr	Asn	Ser	Cys	Ser
		100			105
Thr	Ala	Gln	Cys	Leu	Leu
		115			120
Glu	Ile	Ser	Tyr	Leu	Leu
		130			135
Cys	Ile	Gln	Leu	Ala	Leu
145					150
Val	Thr	Leu	Ile	Ile	Ala
					165
Ile	Asn	His	Phe	Thr	Cys
					180
Ser	Asp	Thr	Leu	Val	Ser
		195			200
Thr	Leu	Pro	Leu	Pro	Phe
		210			215
Phe	Val	Arg	Ala	Val	Glu
225					230
Ser	His	Leu	Thr	Gly	Val
					245
Tyr	Leu	Lys	Pro	Gln	Ser
					260
Ser	Lys	Leu	Tyr	Gly	Ala
					275
Ile	Gln	Arg	Asn	Lys	Asp
					290
Gly	Asn	Glu	Lys	Ser	Xaa
305					310

<210> 1144

<211> 351

<212> PRT

<213> Unknown (H38g61 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(351)

<223> Xaa = Any Amino Acid

<400> 1144

Met	Asp	Ile	Leu	Val	Ile	Asp	Asn	Gly	Ser	Glu	Val	Thr	Glu	Phe	Ile
1				5				10						15	
Leu	Val	Gly	Leu	Tyr	Asn	His	Pro	Lys	Phe	Gln	Ile	Ala	Phe	Tyr	Arg
			20					25						30	
Thr	Met	Val	Val	Val	Tyr	Leu	Ile	Thr	Phe	Val	Gly	Ser	Ser	Leu	Ile
			35					40						45	
Ile	Val	Val	Val	Lys	Val	Asp	Gly	Trp	Leu	His	Thr	Pro	Met	Cys	Phe
			50				55				60				
Phe	Leu	Ser	Asn	Leu	Ser	Phe	Leu	Asp	Ile	Cys	Tyr	Ser	Ser	Asn	Ser
65							70				75				80
Val	Pro	Phe	Leu	Leu	Phe	Asn	Gly	Leu	Arg	Asp	Tyr	Pro	Thr	Ile	Ser
			85						90					95	
Tyr	Asn	Ser	Cys	Tyr	Ala	Gln	Met	Thr	Ser	Ala	Phe	Phe	Leu	Gly	Met
			100					105						110	

Thr Gly Cys Leu Leu Leu Ala Val Met Ala Tyr Glu Arg Phe Val Val
 115 120 125
 Ile Ser Asn Pro Leu Arg Tyr Ile Ile Ile Met Asn Asn Lys Val Cys
 130 135 140
 Ile Gln Leu Ala Met Val Thr Trp Ala Ser Ala Ser Pro Tyr Val Ile
 145 150 155 160
 Asn Thr Ile Ile Ala Ile Ile His Cys Asn Asn Thr Leu Ile Ala Met
 165 170 175
 Ile Ala Leu Ser Ile Pro Ala His Phe Cys Gly His Asn Val Ile Asn
 180 185 190
 His Phe Thr Cys Glu Val Gln Glu Leu Leu Lys Leu Val Cys Ser Asp
 195 200 205
 Ile Pro Gly Ser Leu Ile Leu Gly Leu Val Ile Gly Ile Phe Thr Leu
 210 215 220
 Ser Leu Pro Phe Thr Leu Pro Leu Pro Phe Thr Phe Ile Leu Phe Ala
 225 230 235 240
 Tyr Ala His Ile Val Val Ala Val Leu Arg Ile Asn Ser Ala Glu Ala
 245 250 255
 Arg Leu Lys Ala Phe Ser Thr Cys Gly Ser His Leu Thr Val Ile Ile
 260 265 270
 Ile Phe Tyr Gly Thr Ala Thr Tyr Met Tyr Leu Lys Pro Gln Ser Arg
 275 280 285
 Glu Ser Gln Asp Glu Gly Lys Val Ile Ser Val Phe Phe Leu Lys Val
 290 295 300
 Glu Lys Gln His Gln Asn Asp Ser Ile Ser Val Phe Tyr Gly Val Val
 305 310 315 320
 Thr Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asp Lys Asp Ala
 325 330 335
 Lys His Ala Leu Arg Lys Ile Ile Arg Lys Lys Glu Ser Xaa Lys
 340 345 350

<210> 1145

<211> 318

<212> PRT

<213> Unknown (H38g62 protein)

<220>

<223> Synthetic construct

<400> 1145

Met Asp Lys Ile Asn Gln Thr Phe Val Arg Glu Phe Ile Leu Leu Gly
 1 5 10 15
 Leu Ser Gly Tyr Pro Lys Leu Glu Ile Phe Phe Ala Leu Ile Leu
 20 25 30
 Val Met Tyr Val Val Ile Leu Ile Gly Asn Gly Val Leu Ile Ile Ala
 35 40 45
 Ser Ile Leu Asp Ser Arg Leu His Met Pro Met Tyr Phe Phe Leu Gly
 50 55 60
 Asn Leu Ser Phe Leu Asp Ile Cys Tyr Thr Thr Ser Ser Ile Pro Ser
 65 70 75 80
 Thr Leu Val Ser Leu Ile Ser Lys Lys Arg Asn Ile Ser Phe Ser Gly
 85 90 95
 Cys Ala Val Gln Met Phe Phe Gly Phe Ala Met Gly Ser Thr Glu Cys
 100 105 110
 Phe Leu Leu Gly Met Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Asn
 115 120 125
 Pro Leu Arg Tyr Pro Ile Ile Met Asn Lys Val Val Tyr Val Leu Leu
 130 135 140
 Thr Ser Val Ser Trp Leu Ser Gly Gly Ile Asn Ser Thr Val Gln Thr
 145 150 155 160
 Ser Leu Ala Met Arg Trp Pro Phe Cys Gly Asn Asn Ile Ile Asn His

```

      165      170      175
Phe Leu Cys Glu Ile Leu Ala Val Leu Lys Leu Ala Cys Ser Asp Ile
      180      185      190
Ser Val Asn Ile Val Thr Leu Ala Val Ser Asn Ile Ala Phe Leu Val
      195      200      205
Leu Pro Leu Leu Val Ile Phe Phe Ser Tyr Met Phe Ile Leu Tyr Thr
      210      215      220
Ile Leu Arg Thr Asn Ser Ala Thr Gly Arg His Lys Ala Phe Ser Thr
      225      230      235
Cys Ser Ala His Leu Thr Val Val Ile Ile Phe Tyr Gly Thr Ile Phe
      245      250      255
Phe Met Tyr Ala Lys Pro Lys Ser Gln Asp Leu Leu Gly Lys Asp Asn
      260      265      270
Leu Gln Ala Thr Glu Gly Leu Val Ser Met Phe Tyr Gly Val Val Thr
      275      280      285
Pro Met Leu Asn Pro Ile Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys
      290      295      300
Ala Ala Ile Lys Tyr Leu Leu Ser Arg Lys Ala Ile Asn Gln
      305      310      315

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<210> 1146

<211> 319

<212> PRT

<213> Unknown (H38g63 protein)

<220>

<223> Synthetic construct

<400> 1146

```

Met Phe Pro Ala Asn Trp Thr Ser Val Lys Val Phe Phe Phe Leu Gly
1      5      10      15
Phe Phe His Tyr Pro Lys Val Gln Val Ile Ile Phe Ala Val Cys Leu
      20      25      30
Leu Met Tyr Leu Ile Thr Leu Leu Gly Asn Ile Phe Leu Ile Ser Ile
      35      40      45
Thr Ile Leu Asp Ser His Leu His Thr Pro Met Tyr Leu Phe Leu Ser
      50      55      60
Asn Leu Ser Phe Leu Asp Ile Trp Tyr Ser Ser Ala Leu Ser Pro
      65      70      75      80
Met Leu Ala Asn Phe Val Ser Gly Arg Asn Thr Ile Ser Phe Ser Gly
      85      90      95
Cys Ala Thr Gln Met Tyr Leu Ser Leu Ala Met Gly Ser Thr Glu Cys
      100      105      110
Val Leu Leu Pro Met Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn
      115      120      125
Pro Leu Arg Tyr Pro Val Ile Met Asn Arg Arg Thr Cys Val Gln Ile
      130      135      140
Ala Ala Gly Ser Trp Met Thr Gly Cys Leu Thr Ala Met Val Glu Met
      145      150      155      160
Met Ser Val Leu Pro Leu Ser Leu Cys Gly Asn Ser Ile Ile Asn His
      165      170      175
Phe Thr Cys Glu Ile Leu Ala Ile Leu Lys Leu Val Cys Val Asp Thr
      180      185      190
Ser Leu Val Gln Leu Ile Met Leu Val Ile Ser Val Leu Leu Leu Pro
      195      200      205
Met Pro Met Leu Leu Ile Cys Ile Ser Tyr Ala Phe Ile Leu Ala Ser
      210      215      220
Ile Leu Arg Ile Ser Ser Val Glu Gly Arg Ser Lys Ala Phe Ser Thr
      225      230      235
Cys Thr Ala His Leu Met Val Val Val Leu Phe Tyr Gly Thr Ala Leu
      245      250      255

```

Ser Met His Leu Lys Pro Ser Ala Val Asp Ser Gln Glu Ile Asp Lys
 260 265 270
 Phe Met Ala Leu Val Tyr Ala Gly Gln Thr Pro Met Leu Asn Pro Ile
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Val Ala Leu Lys Lys Leu
 290 295 300
 Leu Ile Arg Asn His Phe Asn Thr Ala Phe Ile Ser Ile Leu Lys
 305 310 315

<210> 1147

<211> 310

<212> PRT

<213> Unknown (H38g64 protein)

<220>

<223> Synthetic construct

<400> 1147

Met Ala Glu Met Asn Leu Thr Leu Val Thr Glu Phe Leu Leu Ile Ala
 1 5 10 15
 Phe Thr Glu Tyr Pro Glu Trp Ala Leu Pro Leu Phe Leu Leu Phe Leu
 20 25 30
 Phe Met Tyr Leu Ile Thr Val Leu Gly Asn Leu Glu Met Ile Ile Leu
 35 40 45
 Ile Leu Met Asp His Gln Leu His Ala Pro Met Tyr Phe Leu Leu Ser
 50 55 60
 His Leu Ala Phe Met Asp Val Cys Tyr Ser Ser Ile Thr Val Pro Gln
 65 70 75 80
 Met Leu Ala Val Leu Leu Glu His Gly Ala Ala Leu Ser Tyr Thr Arg
 85 90 95
 Cys Ala Ala Gln Phe Phe Leu Phe Thr Phe Phe Gly Ser Ile Asp Cys
 100 105 110
 Tyr Leu Leu Ala Leu Met Ala Tyr Asp Arg Tyr Leu Ala Val Cys Gln
 115 120 125
 Pro Leu Leu Tyr Val Thr Ile Leu Thr Gln Gln Ala Arg Leu Ser Leu
 130 135 140
 Val Ala Gly Ala Tyr Val Ala Gly Leu Ile Ser Ala Leu Val Arg Thr
 145 150 155 160
 Val Ser Ala Phe Thr Leu Ser Phe Cys Gly Thr Ser Glu Ile Asp Phe
 165 170 175
 Ile Phe Cys Asp Leu Pro Pro Leu Leu Lys Leu Thr Cys Gly Glu Ser
 180 185 190
 Tyr Thr Gln Glu Val Leu Ile Ile Met Phe Ala Ile Phe Val Ile Pro
 195 200 205
 Ala Ser Met Val Val Ile Leu Val Ser Tyr Leu Phe Ile Ile Val Ala
 210 215 220
 Ile Met Gly Ile Pro Ala Gly Ser Gln Ala Lys Thr Phe Ser Thr Cys
 225 230 235 240
 Thr Ser His Leu Thr Ala Val Ser Leu Phe Phe Gly Thr Leu Ile Phe
 245 250 255
 Met Tyr Leu Arg Gly Asn Ser Asp Gln Ser Ser Glu Lys Asn Arg Val
 260 265 270
 Val Ser Val Leu Tyr Thr Glu Val Ile Pro Met Leu Asn Pro Leu Ile
 275 280 285
 Tyr Ser Leu Arg Asn Lys Glu Val Lys Glu Ala Leu Arg Lys Ile Leu
 290 295 300
 Asn Arg Ala Lys Leu Ser
 305 310

<210> 1148

<211> 321

<212> PRT

<213> Unknown (H38g65 protein)

<220>

<223> Synthetic construct

<400> 1148

```

Met Gly Met Glu Gly Leu Leu Gln Asn Ser Thr Asn Phe Val Leu Thr
 1          5          10          15
Gly Leu Ile Thr His Pro Ala Phe Pro Gly Leu Leu Phe Ala Ile Val
 20          25          30
Phe Ser Ile Phe Val Val Ala Ile Thr Ala Asn Leu Val Met Ile Leu
 35          40          45
Leu Ile His Met Asp Ser Arg Leu His Thr Pro Met Tyr Phe Leu Leu
 50          55          60
Ser Gln Leu Ser Ile Met Asp Thr Ile Tyr Ile Cys Ile Thr Val Pro
 65          70          75          80
Lys Met Leu Gln Asp Leu Leu Ser Lys Asp Lys Thr Ile Ser Phe Leu
 85          90          95
Gly Cys Ala Val Gln Ile Phe Leu Tyr Leu Thr Leu Ile Gly Gly Glu
100          105          110
Phe Phe Leu Leu Gly Leu Met Ala Tyr Asp Arg Tyr Val Ala Val Cys
115          120          125
Asn Pro Leu Arg Tyr Pro Leu Leu Met Asn Arg Arg Val Cys Leu Phe
130          135          140
Met Val Val Gly Ser Trp Val Gly Gly Ser Leu Asp Gly Phe Met Leu
145          150          155          160
Thr Pro Val Thr Met Ser Phe Pro Phe Cys Arg Ser Arg Glu Ile Asn
165          170          175
His Phe Phe Cys Glu Ile Pro Ala Val Leu Lys Leu Ser Cys Thr Asp
180          185          190
Thr Ser Leu Tyr Glu Thr Leu Met Tyr Ala Cys Cys Val Leu Met Leu
195          200          205
Leu Ile Pro Leu Ser Val Ile Ser Val Ser Tyr Thr His Ile Leu Leu
210          215          220
Thr Val His Arg Met Asn Ser Ala Glu Gly Arg Arg Lys Ala Phe Ala
225          230          235          240
Thr Cys Ser Ser His Ile Met Ala Val Ser Val Phe Tyr Gly Ala Ala
245          250          255
Phe Tyr Thr Asn Val Leu Pro His Ser Tyr His Thr Pro Glu Lys Asp
260          265          270
Lys Val Val Ser Ala Phe Tyr Thr Ile Leu Thr Pro Met Leu Asn Pro
275          280          285
Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Ala Ala Ala Leu Arg Lys
290          295          300
Val Leu Gly Arg Cys Gly Ser Ser Gln Ser Ile Arg Val Ala Thr Val
305          310          315          320
Ile

```

<210> 1149

<211> 311

<212> PRT

<213> Unknown (H38g66 protein)

<220>

<223> Synthetic construct

<400> 1149

```

Met Ala His Thr Asn Glu Ser Met Val Ser Glu Phe Val Leu Leu Gly
 1          5          10          15

```

Leu Ser Asn Ser Trp Gly Leu Gln Leu Phe Phe Phe Ala Ile Phe Ser
 20 25 30
 Ile Val Tyr Val Thr Ser Val Leu Gly Asn Val Leu Ile Ile Val Ile
 35 40 45
 Ile Ser Phe Asp Ser His Leu Asn Ser Pro Met Tyr Phe Leu Leu Ser
 50 55 60
 Asn Leu Ser Phe Ile Asp Ile Cys Gln Ser Asn Phe Ala Thr Pro Lys
 65 70 75 80
 Met Leu Val Asp Phe Phe Ile Glu Arg Lys Thr Ile Ser Phe Glu Gly
 85 90 95
 Cys Met Ala Gln Ile Phe Val Leu His Ser Phe Val Gly Ser Glu Met
 100 105 110
 Met Leu Leu Val Ala Met Ala Tyr Asp Arg Phe Ile Ala Ile Cys Lys
 115 120 125
 Pro Leu His Tyr Ser Thr Ile Met Asn Arg Arg Leu Cys Val Ile Phe
 130 135 140
 Val Ser Ile Ser Trp Ala Val Gly Val Leu His Ser Val Ser His Leu
 145 150 155 160
 Ala Phe Thr Val Asp Leu Pro Phe Cys Gly Pro Asn Glu Val Asp Ser
 165 170 175
 Phe Phe Cys Asp Leu Pro Leu Val Ile Glu Leu Ala Cys Met Asp Thr
 180 185 190
 Tyr Glu Met Glu Ile Met Thr Leu Thr Asn Ser Gly Leu Ile Ser Leu
 195 200 205
 Ser Cys Phe Leu Ala Leu Ile Ile Ser Tyr Thr Ile Ile Leu Ile Gly
 210 215 220
 Val Arg Cys Arg Ser Ser Ser Gly Ser Ser Lys Ala Leu Ser Thr Leu
 225 230 235 240
 Thr Ala His Ile Thr Val Val Ile Leu Phe Phe Gly Pro Cys Ile Tyr
 245 250 255
 Phe Tyr Ile Trp Pro Phe Ser Arg Leu Pro Val Asp Lys Phe Leu Ser
 260 265 270
 Val Phe Tyr Thr Val Cys Thr Pro Leu Leu Asn Pro Ile Ile Tyr Ser
 275 280 285
 Leu Arg Asn Glu Asp Val Lys Ala Ala Met Trp Lys Leu Arg Asn Arg
 290 295 300
 His Val Asn Ser Trp Lys Asn
 305 310

<210> 1150

<211> 312

<212> PRT

<213> Unknown (H38g67 protein)

<220>

<223> Synthetic construct

<400> 1150

Met Asp Gln Lys Asn Gly Ser Ser Phe Thr Gly Phe Ile Leu Leu Gly
 1 5 10 15
 Phe Ser Asp Arg Pro Gln Leu Glu Leu Val Leu Phe Val Val Leu Leu
 20 25 30
 Ile Phe Tyr Ile Phe Thr Leu Leu Gly Asn Lys Thr Ile Ile Val Leu
 35 40 45
 Ser His Leu Asp Pro His Leu His Thr Pro Met Tyr Phe Phe Phe Ser
 50 55 60
 Asn Leu Ser Phe Leu Asp Leu Cys Tyr Thr Thr Gly Ile Val Pro Gln
 65 70 75 80
 Leu Leu Val Asn Leu Arg Gly Ala Asp Lys Ser Ile Ser Tyr Gly Gly
 85 90 95
 Cys Val Val Gln Leu Tyr Ile Ser Leu Gly Leu Gly Ser Thr Glu Cys

```

      100      105      110
Val Leu Leu Gly Val Met Val Phe Asp Arg Tyr Ala Ala Val Cys Arg
      115      120      125
Pro Leu His Tyr Thr Val Val Met His Pro Cys Leu Tyr Val Leu Met
      130      135      140
Ala Ser Thr Ser Trp Val Ile Gly Phe Ala Asn Ser Leu Leu Gln Thr
      145      150      155      160
Val Leu Ile Leu Leu Thr Leu Cys Gly Arg Asn Lys Leu Glu His
      165      170      175
Phe Leu Cys Glu Val Pro Pro Leu Leu Lys Leu Ala Cys Val Asp Thr
      180      185      190
Thr Met Asn Glu Ser Glu Leu Phe Phe Val Ser Val Ile Ile Leu Leu
      195      200      205
Val Pro Val Ala Leu Ile Ile Phe Ser Tyr Ser Gln Ile Val Arg Ala
      210      215      220
Val Met Arg Ile Lys Leu Ala Thr Gly Gln Arg Lys Val Phe Gly Thr
      225      230      235      240
Cys Gly Ser His Leu Thr Val Val Ser Leu Phe Tyr Gly Thr Ala Ile
      245      250      255
Tyr Ala Tyr Leu Gln Pro Gly Asn Asn Tyr Ser Gln Asp Gln Gly Lys
      260      265      270
Phe Ile Ser Leu Phe Tyr Thr Ile Ile Thr Pro Met Ile Asn Pro Leu
      275      280      285
Ile Tyr Thr Leu Arg Asn Lys Asp Val Lys Gly Ala Leu Lys Lys Val
      290      295      300
Leu Trp Lys Asn Tyr Asp Ser Arg
305      310

```

<210> 1151

<211> 313

<212> PRT

<213> Unknown (H38g68 protein)

<220>

<223> Synthetic construct

<400> 1151

```

Met Cys Ser Gly Asn Gln Thr Ser Gln Asn Gln Thr Ala Ser Thr Asp
  1      5      10      15
Phe Thr Leu Thr Gly Leu Phe Ala Glu Ser Lys His Ala Ala Leu Leu
      20      25      30
Tyr Thr Val Thr Phe Leu Leu Phe Leu Met Ala Leu Thr Gly Asn Ala
      35      40      45
Leu Leu Ile Leu Leu Ile His Ser Glu Pro Arg Leu His Thr Pro Met
      50      55      60
Tyr Phe Phe Ile Ser Gln Leu Ala Leu Met Asp Leu Met Tyr Leu Cys
      65      70      75      80
Val Thr Val Pro Lys Met Leu Val Gly Gln Val Thr Gly Asp Asp Thr
      85      90      95
Ile Ser Pro Ser Gly Cys Gly Ile Gln Met Phe Phe His Leu Thr Leu
      100      105      110
Ala Gly Ala Glu Val Phe Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr
      115      120      125
Ala Ala Val Cys Arg Pro Leu His Tyr Pro Leu Leu Met Asn Gln Arg
      130      135      140
Val Cys Gln Leu Leu Val Ser Ala Cys Trp Val Leu Gly Met Val Asp
      145      150      155      160
Gly Leu Leu Leu Thr Pro Ile Thr Met Ser Phe Pro Phe Cys Gln Ser
      165      170      175
Arg Lys Ile Leu Ser Phe Phe Cys Glu Thr Pro Ala Leu Leu Lys Leu
      180      185      190

```

Ser Cys Ser Asp Val Ser Leu Tyr Lys Met Leu Thr Tyr Leu Cys Cys
 195 200 205
 Ile Leu Met Leu Leu Thr Pro Ile Met Val Ile Ser Ser Ser Tyr Thr
 210 215 220
 Leu Ile Leu His Leu Ile His Arg Met Asn Ser Ala Ala Gly Arg Arg
 225 230 235 240
 Lys Ala Leu Ala Thr Cys Ser Ser His Met Ile Ile Val Leu Leu Leu
 245 250 255
 Phe Gly Ala Ser Phe Tyr Thr Tyr Met Leu Pro Ser Ser Tyr His Thr
 260 265 270
 Ala Glu Gln Asp Met Met Val Ser Ala Phe Tyr Thr Ile Phe Thr Pro
 275 280 285
 Val Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Thr Arg
 290 295 300
 Ala Met Arg Ser Met Met Gln Ser Arg
 305 310

<210> 1152

<211> 314

<212> PRT

<213> Unknown (H38g69 protein)

<220>

<223> Synthetic construct

<400> 1152

Met Asp Val Gly Asn Lys Ser Thr Met Ser Glu Phe Val Leu Leu Gly
 1 5 10 15
 Leu Ser Asn Ser Trp Glu Leu Gln Met Phe Phe Phe Met Val Phe Ser
 20 25 30
 Leu Leu Tyr Val Ala Thr Met Val Gly Asn Ser Leu Ile Val Ile Thr
 35 40 45
 Val Ile Val Asp Pro His Leu His Ser Pro Met Tyr Phe Leu Leu Thr
 50 55 60
 Asn Leu Ser Ile Ile Asp Met Ser Leu Ala Ser Phe Ala Thr Pro Lys
 65 70 75 80
 Met Ile Thr Asp Tyr Leu Thr Gly His Lys Thr Ile Ser Phe Asp Gly
 85 90 95
 Cys Leu Thr Gln Ile Phe Phe Leu His Leu Phe Thr Gly Thr Glu Ile
 100 105 110
 Ile Leu Leu Met Ala Met Ser Phe Asp Arg Tyr Ile Ala Ile Cys Lys
 115 120 125
 Pro Leu His Tyr Ala Ser Val Ile Ser Pro Gln Val Cys Val Ala Leu
 130 135 140
 Val Val Ala Ser Trp Ile Met Gly Val Met His Ser Met Ser Gln Val
 145 150 155 160
 Ile Phe Ala Leu Thr Leu Pro Phe Cys Gly Pro Tyr Glu Val Asp Ser
 165 170 175
 Phe Phe Cys Asp Leu Pro Val Val Phe Gln Leu Ala Cys Val Asp Thr
 180 185 190
 Tyr Val Leu Gly Leu Phe Met Ile Ser Thr Ser Gly Ile Ile Ala Leu
 195 200 205
 Ser Cys Phe Ile Val Leu Phe Asn Ser Tyr Val Ile Val Leu Val Thr
 210 215 220
 Val Lys His His Ser Ser Arg Gly Ser Ser Lys Ala Leu Ser Thr Cys
 225 230 235 240
 Thr Ala His Phe Ile Val Val Phe Leu Phe Phe Gly Pro Cys Ile Phe
 245 250 255
 Ile Tyr Met Trp Pro Leu Ser Ser Phe Leu Thr Asp Lys Ile Leu Ser
 260 265 270
 Val Phe Tyr Thr Ile Phe Thr Pro Thr Leu Asn Pro Ile Ile Tyr Thr

275 280 285
 Leu Arg Asn Gln Glu Val Lys Ile Ala Met Arg Lys Leu Lys Asn Arg
 290 295 300
 Phe Leu Asn Phe Asn Lys Ala Met Pro Ser
 305 310

<210> 1153

<211> 310

<212> PRT

<213> Unknown (H38g70 protein)

<220>

<223> Synthetic construct

<400> 1153

Met Gly Asp Asn Ile Thr Ser Ile Arg Glu Phe Leu Leu Leu Gly Phe
 1 5 10 15
 Pro Val Gly Pro Arg Ile Gln Met Leu Leu Phe Gly Leu Phe Ser Leu
 20 25 30
 Phe Tyr Val Phe Thr Leu Leu Gly Asn Gly Thr Ile Leu Gly Leu Ile
 35 40 45
 Ser Leu Asp Ser Arg Leu His Ala Pro Met Tyr Phe Phe Leu Ser His
 50 55 60
 Leu Ala Val Val Asp Ile Ala Tyr Ala Cys Asn Thr Val Pro Arg Met
 65 70 75 80
 Leu Val Asn Leu Leu His Pro Ala Lys Pro Ile Ser Phe Ala Gly Arg
 85 90 95
 Met Met Gln Thr Phe Leu Phe Ser Thr Phe Ala Val Thr Glu Cys Leu
 100 105 110
 Leu Leu Val Val Met Ser Tyr Asp Leu Tyr Val Ala Ile Cys His Pro
 115 120 125
 Leu Arg Tyr Leu Ala Ile Met Thr Trp Arg Val Cys Ile Thr Leu Ala
 130 135 140
 Val Thr Ser Trp Thr Thr Gly Val Leu Leu Ser Leu Ile His Leu Val
 145 150 155 160
 Leu Leu Leu Pro Leu Pro Phe Cys Arg Pro Gln Lys Ile Tyr His Phe
 165 170 175
 Phe Cys Glu Ile Leu Ala Val Leu Lys Leu Ala Cys Ala Asp Thr His
 180 185 190
 Ile Asn Glu Asn Met Val Leu Ala Gly Ala Ile Ser Gly Leu Val Gly
 195 200 205
 Pro Leu Ser Thr Ile Val Val Ser Tyr Met Cys Ile Leu Cys Ala Ile
 210 215 220
 Leu Gln Ile Gln Ser Arg Glu Val Gln Arg Lys Ala Phe Arg Thr Cys
 225 230 235 240
 Phe Ser His Leu Cys Val Ile Gly Leu Val Tyr Gly Thr Ala Ile Ile
 245 250 255
 Met Tyr Val Gly Pro Arg Tyr Gly Asn Pro Lys Glu Gln Lys Lys Tyr
 260 265 270
 Leu Leu Leu Phe His Ser Leu Phe Asn Pro Met Leu Asn Pro Leu Ile
 275 280 285
 Cys Ser Leu Arg Asn Ser Glu Val Lys Asn Thr Leu Lys Arg Val Leu
 290 295 300
 Gly Val Glu Arg Ala Leu
 305 310

<210> 1154

<211> 323

<212> PRT

<213> Unknown (H38g71 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(323)

<223> Xaa = Any Amino Acid

<400> 1154

```

His Thr Glu Pro Arg Asn Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu
 1           5           10           15
Gly Leu Ser Glu Asp Pro Glu Leu Leu Pro Val Leu Ala Leu Leu Ser
          20           25           30
Leu Ser Leu Ser Met Tyr Leu Val Met Val Leu Arg Asn Leu Leu Ser
          35           40           45
Ile Leu Ala Val Ser Ser Asp Ser Pro His Thr Pro Val Tyr Phe Phe
          50           55           60
Leu Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Pro Thr Val
65          70          75          80
Pro Lys Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser His
          85          90          95
Ala Gly Cys Leu Ala Gln Met Ser Phe Leu Val Leu Phe Ala Cys Ile
          100         105         110
Glu Asp Met Leu Leu Thr Val Met Ala Tyr Asp Ser Phe Val Ala Ile
          115         120         125
Cys His Pro Leu His Tyr Pro Val Ile Met Asn Pro His Leu Cys Val
          130         135         140
Phe Phe Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu
145         150         155         160
His Gly Trp Ile Val Leu Gln Phe Thr Ile Ile Lys Asn Val Glu Ile
          165         170         175
Ser Asn Phe Leu Cys Asp Pro Ser Gln Leu Leu Lys Leu Ala Cys Ser
          180         185         190
Asp Ser Val Thr Asn Ser Ile Phe Ile Tyr Phe Asp Ser Thr Met Phe
          195         200         205
Gly Phe Leu Pro Ile Ser Gly Ile Leu Leu Ser Xaa Tyr Lys Ile Val
          210         215         220
Pro Ser Ile Leu Arg Met Ser Ser Ser Asp Gly Lys Tyr Lys Ala Phe
225         230         235         240
Thr Thr Cys Gly Ser His Leu Ala Val Val Cys Xaa Phe Asp Gly Thr
          245         250         255
Gly Ile Gly Met Tyr Leu Thr Ser Ala Leu Ser Pro Pro Pro Arg Asn
          260         265         270
Gly Val Ala Ala Ser Val Met Tyr Ala Val Val Thr Pro Met Leu Asn
          275         280         285
Leu Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu Arg
          290         295         300
Arg Leu Arg Ser Arg Thr Val Glu Ser Pro Xaa Ser Val Pro Ser Phe
305         310         315         320
Phe Leu Cys

```

<210> 1155

<211> 315

<212> PRT

<213> Unknown (H38g72 protein)

<220>

<223> Synthetic construct

<400> 1155

Met Ala Trp Ser Asn Gln Ser Ala Val Thr Glu Phe Ile Leu Arg Gly

1		5		10		15
Leu	Ser	Ser	Ser	Leu	Glu	Leu
		20				
Ile	Val	Tyr	Ala	Ala	Thr	Val
	35					
Ile	Ala	Ser	Glu	Pro	His	Leu
	50					
Asn	Leu	Ser	Phe	Ile	Asp	Met
	65					
Met	Ile	Ala	Asp	Phe	Leu	Arg
Cys	Met	Thr	Gln	Met	Phe	Phe
Val	Leu	Leu	Ile	Ser	Met	Ser
	115					
Pro	Leu	His	Tyr	Leu	Thr	Ile
	130					
Val	Ile	Leu	Ser	Trp	Ile	Val
	145					
Ala	Phe	Thr	Val	Asn	Leu	Pro
Phe	Phe	Cys	Asp	Leu	Pro	Leu
Tyr	Ile	Leu	Gly	Val	Phe	Met
	195					
Val	Cys	Phe	Ile	Leu	Leu	Val
	210					
Val	Arg	Gln	Arg	Ser	Ser	Gly
	225					
Ser	Ala	His	Phe	Thr	Val	Val
Ile	Tyr	Val	Trp	Pro	Phe	Thr
Val	Phe	Tyr	Thr	Ile	Tyr	Thr
	275					
Val	Arg	Asn	Lys	Asp	Val	Lys
	290					
Ile	Phe	Lys	Ser	Arg	Lys	Thr
	305					

<210> 1156

<211> 321

<212> PRT

<213> Unknown (H38g73 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(321)

<223> Xaa = Any Amino Acid

<400> 1156

Met	Lys	Lys	Tyr	Met	Glu	Arg	Thr	Asn	Xaa	Thr	Thr	Glu	Phe	Glu	Leu
1				5				10						15	
Ile	Leu	Ile	Ser	Leu	Xaa	Val	Leu	Ile	Ser	Xaa	Gln	Lys	Leu	Leu	Phe
				20				25						30	
Val	Thr	Cys	Leu	Val	Val	Tyr	Leu	Val	Thr	Leu	Leu	Gly	Asn	Arg	Ile
				35				40						45	
Gln	Ile	Ile	Pro	Thr	Leu	Leu	Val	Ser	His	Leu	Tyr	Leu	Cys	His	Gly
	50							55						60	

```

Asn Pro Ser Phe Leu Asp Ile Gly Leu Thr Ser Ser Phe Thr Pro Ser
65          70          75          80
Ile Leu Ile Asn Phe Leu Ser Glu Gly Lys Lys Leu Ser Phe Thr Asp
      85          90          95
Cys Ile Ile Gln Met Ser Ile Phe Tyr Ser Met Gly Ser Thr Glu Cys
      100        105        110
Val Leu Leu Ala Val Met Ala Tyr Asp Asn Cys Val Val Ile Ser Lys
      115        120        125
Phe Leu Arg Tyr Pro Leu Ile Asn Lys Val Asn Lys Ile Lys Lys
      130        135        140
Val Leu Cys Val Phe Met Ala Thr Val Ser Tyr Glu Leu Gly Phe Leu
145          150        155        160
Asn Arg Gln Asn Val Leu Ile Val Thr Tyr Ala Met His Phe Cys Gly
      165        170        175
Lys His Ile Ile Asn His Phe Tyr Lys Ile Leu Gln Leu Met Ala Leu
      180        185        190
Ala Cys Ile Asp Ile Ser Leu Asn Glu Asn Ile Ile Ile Leu Gly Lys
      195        200        205
Val Asn Phe Ser Phe Thr Leu Leu Leu Pro Phe Gln Phe Phe Ile Phe
      210        215        220
Ser Phe Leu Tyr Phe His His Leu Cys Cys Ile Glu Ile Asn Ser Ala
225          230        235        240
Glu Gly Arg Lys Lys Val Ser Ser Thr Cys Ser Ala His Ile Thr Val
      245        250        255
Val Ile Val Phe His Arg Thr Ile Leu Phe Met Tyr Ile Lys Ser Thr
      260        265        270
Ser Asn Gly Thr Thr Ser Glu Lys Leu Val Asp Leu Phe Cys Gly Val
      275        280        285
Val Met Leu Met Leu Asn Leu Ile Ile Tyr Ser Leu Gly Asn Met Glu
      290        295        300
Val Leu Gly Val Met Lys Lys Leu Ile Ser Met Ser Arg Pro Trp Cys
305          310        315        320
Trp

```

<210> 1157

<211> 325

<212> PRT

<213> Unknown (H38g74 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(325)

<223> Xaa = Any Amino Acid

<400> 1157

```

His Thr Glu Pro Arg Asn Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu
1          5          10          15
Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Leu Leu Ser
      20          25          30
Leu Ser Leu Ser Met Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu
      35          40          45
Leu Ser Ile Leu Ala Val Ser Ser Asp Ser Gln Leu His Thr Pro Met
      50          55          60
Tyr Phe Phe Leu Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser
65          70          75          80
Pro Met Val Pro Lys Met Ile Met Asp Met Gln Ser His Ser Arg Val
      85          90          95
Ile Ser His Ala Gly Cys Leu Thr Arg Met Ser Phe Leu Val Leu Phe

```

100	105	110
Ala Cys Ile Glu Asp Met Leu Leu Thr Val Met Ala Tyr Asp Cys Phe		
115	120	125
Val Ala Ile Cys Arg Pro Leu His Tyr Pro Val Ile Met Asn Pro His		
130	135	140
Leu Cys Val Phe Phe Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp		
145	150	155
Ser Gln Leu His Ser Xaa Ile Val Leu Gln Phe Thr Phe Phe Asn Asn		
165	170	175
Val Glu Ile Ala Asn Phe Val Tyr Glu Pro Ser Gln Leu Leu Asn Leu		
180	185	190
Asp Cys Ser Asp Thr Val Ile Asn Ser Val Phe Ile Tyr Phe Asp Ser		
195	200	205
Met Phe Gly Phe Leu Pro Ile Ser Gly Ile Leu Leu Ser Xaa Tyr Lys		
210	215	220
Ile Val Pro Ser Ile Leu Arg Met Ser Ser Ser Asp Gly Lys Tyr Lys		
225	230	235
Ala Phe Ala Thr Cys Gly Ser His Leu Ala Val Val Cys Xaa Phe Asp		
245	250	255
Gly Thr Gly Ile Gly Met Tyr Leu Thr Ser Ala Val Ser Pro Pro Pro		
260	265	270
Arg Asn Gly Val Ala Ala Ser Val Met Tyr Ala Val Val Thr Pro Met		
275	280	285
Leu Asn Leu Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala		
290	295	300
Leu Gln Arg Leu Ser Ser Arg Thr Val Glu Ser Pro Xaa Ser Val Pro		
305	310	315
Ser Phe Phe Leu Cys		320
325		

<210> 1158

<211> 319

<212> PRT

<213> Unknown (H38g75 protein)

<220>

<223> Synthetic construct

<400> 1158

Met Gly Asn Trp Thr Ala Ala Val Thr Glu Phe Val Leu Leu Gly Phe	
1 5 10 15	
Ser Leu Ser Arg Glu Val Glu Leu Leu Leu Val Leu Leu Leu Pro	
20 25 30	
Thr Phe Leu Leu Thr Leu Leu Gly Asn Leu Leu Ile Ile Ser Thr Val	
35 40 45	
Leu Ser Cys Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Cys Asn	
50 55 60	
Leu Ser Ile Leu Asp Ile Leu Phe Thr Ser Val Ile Ser Pro Lys Val	
65 70 75 80	
Leu Ala Asn Leu Gly Ser Arg Asp Lys Thr Ile Ser Phe Ala Gly Cys	
85 90 95	
Ile Thr Gln Cys Tyr Phe Tyr Phe Phe Leu Gly Thr Val Glu Phe Leu	
100 105 110	
Leu Leu Thr Val Met Ser Tyr Asp Arg Tyr Ala Thr Ile Cys Cys Pro	
115 120 125	
Leu Arg Tyr Thr Thr Ile Met Arg Pro Ser Val Cys Ile Gly Thr Val	
130 135 140	
Val Phe Ser Trp Val Gly Gly Phe Leu Ser Val Leu Phe Pro Thr Ile	
145 150 155 160	
Leu Ile Ser Gln Leu Pro Phe Cys Gly Ser Asn Ile Ile Asn His Phe	
165 170 175	

Phe Cys Asp Ser Gly Pro Leu Leu Ala Leu Ala Cys Ala Asp Thr Thr
 180 185 190
 Ala Ile Glu Leu Met Asp Phe Met Leu Ser Ser Met Val Ile Leu Cys
 195 200 205
 Cys Ile Val Leu Val Ala Tyr Ser Tyr Thr Tyr Ile Ile Leu Thr Ile
 210 215 220
 Val Arg Ile Pro Ser Ala Ser Gly Arg Lys Lys Ala Phe Asn Thr Cys
 225 230 235 240
 Ala Ser His Leu Thr Ile Val Ile Ile Pro Ser Gly Ile Thr Val Phe
 245 250 255
 Ile Tyr Val Thr Pro Ser Gln Lys Glu Tyr Leu Glu Ile Asn Lys Ile
 260 265 270
 Pro Leu Val Leu Ser Ser Val Val Thr Pro Phe Leu Asn Pro Phe Ile
 275 280 285
 Tyr Thr Val Arg Asn Asp Thr Val Gln Gly Val Leu Arg Asp Val Trp
 290 295 300
 Val Arg Val Arg Gly Val Phe Glu Lys Arg Met Arg Ala Val Leu
 305 310 315

<210> 1159

<211> 313

<212> PRT

<213> Unknown (H38g76 protein)

<220>

<223> Synthetic construct

<400> 1159

Met Glu Thr Ala Asn Tyr Thr Lys Val Thr Glu Phe Val Leu Thr Gly
 1 5 10 15
 Leu Ser Gln Thr Arg Glu Val Gln Leu Val Leu Phe Val Ile Phe Leu
 20 25 30
 Ser Phe Tyr Leu Phe Ile Leu Pro Gly Asn Ile Leu Ile Ile Cys Thr
 35 40 45
 Ile Arg Leu Asp Pro His Leu Thr Ser Pro Met Tyr Phe Leu Leu Ala
 50 55 60
 Asn Leu Ala Leu Leu Asp Ile Trp Tyr Ser Ser Ile Thr Ala Pro Lys
 65 70 75 80
 Met Leu Ile Asp Phe Phe Val Glu Arg Lys Ile Ile Ser Phe Gly Gly
 85 90 95
 Cys Ile Ala Gln Leu Phe Phe Leu His Phe Val Gly Ala Ser Glu Met
 100 105 110
 Phe Leu Leu Ile Val Met Ala Tyr Asp Arg Tyr Ala Ala Ile Cys Arg
 115 120 125
 Pro Leu His Tyr Ala Thr Ile Met Asn Arg Arg Leu Cys Cys Ile Leu
 130 135 140
 Val Ala Leu Ser Trp Met Gly Gly Phe Ile His Ser Ile Ile Gln Val
 145 150 155 160
 Ala Leu Ile Val Arg Leu Pro Phe Cys Gly Pro Asn Glu Leu Asp Ser
 165 170 175
 Tyr Phe Cys Asp Ile Thr Gln Val Val Arg Ile Ala Cys Ala Asn Thr
 180 185 190
 Phe Pro Glu Glu Leu Val Met Ile Cys Ser Ser Gly Leu Ile Ser Val
 195 200 205
 Val Trp Phe Ile Ala Leu Leu Met Ser Tyr Ala Phe Leu Leu Ala Leu
 210 215 220
 Leu Lys Lys His Ser Gly Ser Asp Glu Asn Thr Asn Arg Ala Met Ser
 225 230 235 240
 Thr Cys Tyr Ser His Ile Thr Ile Val Val Leu Met Phe Gly Pro Ser
 245 250 255
 Ile Tyr Ile Tyr Ala Arg Pro Phe Asp Ser Phe Ser Leu Asp Lys Val

	260		265		270
Val Ser Val Phe His Thr Val Ile Phe Pro Leu Leu Asn Pro Ile Ile					
	275		280		285
Tyr Thr Leu Arg Asn Lys Glu Val Lys Ala Ala Met Arg Lys Val Val					
	290		295		300
Thr Lys Tyr Ile Leu Cys Glu Glu Lys					
305		310			

<210> 1160

<211> 313

<212> PRT

<213> Unknown (H38g77 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(313)

<223> Xaa = Any Amino Acid

<400> 1160

Met Glu Ser Gln Arg Asn Ile Xaa Lys Phe Ile Leu Met Ser Leu Ser					
1	5		10		15
Ser Ile Gln Asn Ile Gln Ile Phe Val Phe Val Phe Leu Phe Cys Asn					
	20		25		30
Val Ala Ile Leu Val Gly Asn Phe Leu Ile Leu Ile Ser Ile Xaa Cys					
	35		40		45
Ser Pro Leu Phe Asn Gln Pro Met His Tyr Phe Leu Gly Tyr Met Asn					
	50		55		60
Ile Tyr Tyr Thr Ser Cys Val Thr Pro Lys Ile Ile Gly Asp Leu Val					
65	70		75		80
Val Gly Arg Ile Asn Ile Ser Tyr Asp Arg Ile Phe Pro Met His Phe					
	85		90		95
Phe Gly Ile Ile Glu Ile Phe Ile Leu Thr Val Met Ala Phe Asp His					
	100		105		110
Tyr Val Ala Ile Cys Lys Pro Pro Arg Tyr Leu Ile Ile Met Asn Arg					
	115		120		125
Thr Lys Tyr Asn Thr Leu Ile Ser Val Ala Trp Leu Gly Leu Ile					
	130		135		140
His Ser Leu Phe Gln Phe Ser Met Lys Ile Trp Leu Pro Phe Cys Gly					
145	150		155		160
Ser Asn Lys Val Asp Asp Xaa Tyr Xaa Asp Ile Phe Pro Leu Leu Lys					
	165		170		175
Val Ala Cys Thr Asp Thr Cys Ile Thr Gly Val Leu Val Val Ala Asn					
	180		185		190
Ser Gly Met Phe Ala Leu Val Thr Phe Val Leu Ser Phe Gly Ser Tyr					
	195		200		205
Val Ile Ile Leu Phe Pro Leu Lys Asn His Ser Val Glu Gly Arg Cys					
	210		215		220
Lys Ala Leu Ser Thr Cys Gly Ser His Ile Thr Met Val Ile Phe Phe					
225	230		235		240
Phe Glu Pro Ser Ile Phe Ala Tyr Leu Arg Pro Ser Thr Phe Pro Glu					
	245		250		255
Asp Lys Ile Ser Ala Leu Phe Tyr Thr Ile Ile Ala Pro Met Phe Asn					
	260		265		270
His Leu Ile Tyr Asn Leu Arg Asn Thr Glu Met Lys Lys Ala Met Arg					
	275		280		285
Lys Val Trp Tyr Gln Ile Ser Phe Ser Glu Glu Lys Gln Leu Ile Cys					
	290		295		300
Pro Thr Xaa Cys Thr Lys Glu Leu Tyr					
305		310			

<210> 1161
 <211> 304
 <212> PRT
 <213> Unknown (H38g78 protein)

<220>
 <223> Synthetic construct

<400> 1161
 Met Arg Asn Gly Thr Val Ile Thr Glu Phe Ile Leu Leu Gly Phe Pro
 1 5 10 15
 Val Ile Gln Gly Leu Gln Thr Pro Leu Phe Ile Ala Ile Phe Leu Thr
 20 25 30
 Tyr Ile Leu Thr Leu Ala Gly Asn Gly Leu Ile Ile Ala Thr Val Trp
 35 40 45
 Ala Glu Pro Arg Leu Gln Ile Pro Met Tyr Phe Phe Leu Cys Asn Leu
 50 55 60
 Ser Phe Leu Glu Ile Trp Tyr Thr Thr Thr Val Ile Pro Lys Leu Leu
 65 70 75 80
 Gly Thr Phe Val Val Ala Arg Thr Val Ile Cys Met Ser Cys Cys Leu
 85 90 95
 Leu Gln Ala Phe Phe His Phe Phe Val Gly Thr Thr Glu Phe Leu Ile
 100 105 110
 Leu Thr Ile Met Ser Phe Asp Arg Tyr Leu Thr Ile Cys Asn Pro Leu
 115 120 125
 His His Pro Thr Ile Met Thr Ser Lys Leu Cys Leu Gln Leu Ala Leu
 130 135 140
 Ser Ser Trp Val Val Gly Phe Thr Ile Val Phe Cys Gln Thr Met Leu
 145 150 155 160
 Leu Ile Gln Leu Pro Phe Cys Gly Asn Asn Val Ile Ser His Phe Tyr
 165 170 175
 Cys Asp Val Gly Pro Ser Leu Lys Ala Ala Cys Ile Asp Thr Ser Ile
 180 185 190
 Leu Glu Leu Leu Gly Val Ile Ala Thr Ile Leu Val Ile Pro Gly Ser
 195 200 205
 Leu Leu Phe Asn Met Ile Ser Tyr Ile Tyr Ile Leu Ser Ala Ile Leu
 210 215 220
 Arg Ile Pro Ser Ala Thr Gly His Gln Lys Thr Phe Ser Thr Cys Ala
 225 230 235 240
 Ser His Leu Thr Val Val Ser Leu Leu Tyr Gly Ala Val Leu Phe Met
 245 250 255
 Tyr Leu Arg Pro Thr Ala His Ser Ser Phe Lys Ile Asn Lys Val Val
 260 265 270
 Ser Val Leu Asn Thr Ile Leu Thr Pro Leu Leu Asn Pro Phe Ile Tyr
 275 280 285
 Thr Ile Arg Asn Lys Glu Val Lys Gly Ala Leu Arg Lys Ala Met Thr
 290 295 300

<210> 1162
 <211> 321
 <212> PRT
 <213> Unknown (H38g79 protein)

<220>
 <223> Synthetic construct

<400> 1162
 Met Thr Ile Leu Leu Asn Ser Ser Leu Gln Arg Ala Thr Phe Phe Leu
 1 5 10 15
 Thr Gly Phe Gln Gly Leu Glu Gly Leu His Gly Trp Ile Ser Ile Pro

```
<210> 1163
<211> 323
<212> PRT
<213> Unknown (H38g80 protein)
```

```
<220>
<223> Synthetic construct
<221> VARIANT
<222> (1)...(323)
<223> Xaa = Any Amino Acid
```

<400> 1163															
Met	Gly	Asn	His	Thr	Thr	Val	Thr	Glu	Phe	Val	Leu	Leu	Gly	Leu	Ser
1				5					10					15	
Glu	Thr	Cys	Glu	Leu	Gln	Met	Leu	Ile	Phe	Leu	Gly	Leu	Leu	Leu	Thr
			20					25					30		
Tyr	Leu	Leu	Thr	Leu	Leu	Gly	Asn	Leu	Val	Ile	Val	Val	Ile	Thr	Leu
		35					40					45			
Met	Asp	Arg	Arg	Leu	His	Thr	Met	Tyr	Tyr	Phe	Leu	Arg	Asn	Phe	
	50					55				60					

Ala Val Pro Glu Ile Trp Phe Thr Ser Val Ile Phe Pro Lys Val Leu
 65 70 75 80
 Ala Asn Ile Leu Thr Gly Tyr Lys Thr Ile Ser Leu Pro Gly Cys Phe
 85 90 95
 Leu Gln Ser Leu Leu Tyr Phe Phe Leu Gly Thr Thr Glu Phe Phe Leu
 100 105 110
 Leu Ala Val Met Ser Phe Asp Arg Tyr Val Ala Val Cys Asn Pro Leu
 115 120 125
 His Tyr Ala Thr Ile Met Ser Lys Arg Val Cys Val Gln Leu Val Leu
 130 135 140
 Cys Xaa Trp Met Thr Gly Phe Leu Leu Ile Ile Ile Pro Ser Phe Leu
 145 150 155 160
 Val Leu Gln Gln Pro Phe Cys Gly Pro Asn Ile Ile Asn His Phe Phe
 165 170 175
 Cys Asp Asn Phe Pro Leu Leu Lys Leu Ile Cys Ala Asp Met Thr Leu
 180 185 190
 Ile Glu Leu Leu Gly Phe Val Ile Ala Asn Val Ser Leu Leu Gly Thr
 195 200 205
 Leu Ser Met Thr Ala Thr Cys Tyr Gly His Ile Leu His Ala Ile Leu
 210 215 220
 His Ile Pro Ser Ala Lys Glu Lys Gln Lys Ala Phe Ser Ala Cys Ser
 225 230 235 240
 Ser His Ile Ile Val Val Ser Leu Phe Tyr Gly Ser Cys Ile Phe Met
 245 250 255
 Tyr Ile Gln Ser Gly Lys Ser Asp Gln Lys Glu Asp Arg Asn Lys Val
 260 265 270
 Ala Ala Leu Leu Asn Thr Val Val Thr Leu Met Leu Asn Pro Phe Ile
 275 280 285
 Tyr Thr Leu Arg Asn Lys Gln Val Lys Gln Val Phe Arg Gln Gln Val
 290 295 300
 Ser Lys Leu Leu Ile Xaa Ser Cys Val Lys Lys Lys Leu Lys Leu Ser
 305 310 315 320
 Ile Pro Arg

<210> 1164

<211> 317

<212> PRT

<213> Unknown (H38g81 protein)

<220>

<223> Synthetic construct

<400> 1164

Glu Ile Lys Ile Ala Asn Asn Thr Val Val Thr Glu Phe Ile Leu Leu
 1 5 10 15
 Gly Leu Thr Gln Ser Gln Asp Ile Gln Leu Leu Val Phe Val Leu Ile
 20 25 30
 Leu Ile Phe Tyr Leu Ile Ile Leu Pro Gly Asn Phe Leu Ile Ile Phe
 35 40 45
 Thr Ile Lys Ser Asp Pro Gly Leu Thr Ala Pro Leu Tyr Phe Phe Leu
 50 55 60
 Gly Asn Leu Ala Phe Leu Asp Ala Ser Tyr Ser Phe Ile Val Ala Pro
 65 70 75 80
 Arg Met Leu Val Asp Phe Leu Ser Ala Lys Asn Val Ile Ser Tyr Arg
 85 90 95
 Gly Cys Ile Thr Gln Leu Phe Phe Leu His Phe Leu Gly Gly Gly Glu
 100 105 110
 Gly Leu Leu Leu Val Ile Val Ala Phe Asp Arg Tyr Ile Ala Ile Cys
 115 120 125
 Arg Pro Leu His Tyr Ser Thr Leu Met Asn Pro Arg Ala Cys Tyr Ala

```

      130              135              140
Met Met Leu Ala Leu Trp Leu Gly Gly Phe Val His Ser Ile Ile Gln
145              150              155              160
Val Val Leu Ile Leu Arg Leu Pro Phe Cys Gly Pro Asn Gln Leu Asp
      165              170              175
Asn Phe Phe Cys Asp Val Pro Gln Val Ile Lys Leu Ala Cys Thr Asp
      180              185              190
Thr Phe Val Val Glu Leu Leu Met Val Phe Asn Ser Gly Leu Met Thr
      195              200              205
Leu Leu Cys Phe Leu Gly Leu Leu Ala Ser Tyr Ala Val Ile Leu Cys
      210              215              220
His Val Arg Lys Ala Ala Ser Glu Leu Lys Asn Lys Ala Met Ser Thr
225              230              235              240
Cys Thr Thr His Val Ile Ile Ile Leu Leu Met Phe Gly Pro Ala Ile
      245              250              255
Phe Ile Tyr Met His Pro Phe Arg Ala Leu Pro Ala Asp Lys Val Val
      260              265              270
Ser Phe Phe His Thr Val Ile Phe Pro Leu Met Asn Pro Met Ile Tyr
      275              280              285
Thr Leu Arg Asn Gln Glu Val Lys Thr Ser Met Lys Arg Leu Leu Ser
      290              295              300
Arg His Val Val Cys Gln Val Asp Phe Ile Ile Arg Asn
305              310              315

```

<210> 1165

<211> 287

<212> PRT

<213> Unknown (H38g82 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(287)

<223> Xaa = Any Amino Acid

<400> 1165

```

Val Ile Arg Asn Gln Thr Met Val Thr Glu Phe Thr Leu Val Ser Leu
1      5      10      15
Pro Ala Val Gln Glu Leu Gln Ile Trp Leu Cys Val Leu Leu Trp Leu
      20      25      30
Val His Met Leu Thr Ile Thr Gly Asn Leu Phe Val Ile Phe Leu Thr
      35      40      45
Trp Thr Asp Asn Cys Leu Gln Thr Pro Met Asp Leu Phe Leu Glu Lys
      50      55      60
Lys Val Ile Ser Phe Ser Gly Cys Ile Thr Gln Ile Tyr Phe Tyr Phe
65      70      75      80
Phe Leu Gly Thr Val Ala Phe Ile Pro Leu Ala Val Thr Ser Phe Lys
      85      90      95
His Cys Met Ala Thr Cys Asp Pro Leu Cys Ser Thr Ile Ile Ala Lys
      100      105      110
Ser Arg Ala Cys Leu Leu Leu Ala Leu Gly Cys Trp Met Gly Thr Phe
      115      120      125
Leu Ala Val Leu Arg Leu Thr Ile Val Val Ser Arg Leu Pro Asp Cys
      130      135      140
Thr Glu Lys Ile Ser Pro Phe Phe Cys Asp Ile Ala Ser Leu Leu Gln
145      150      155      160
Val Ala Cys Ile Asp Ile His Phe Ile Glu Met Ile Ser Phe Leu Xaa
      165      170      175
Ser Ser Leu Met Val Leu Thr Ser Leu Val Leu Asn Ala Thr Ser Tyr
      180      185      190

```

Ala Tyr Ile Ile Ser Thr Leu Leu Cys Ile Pro Ser Ala Gln Gly Cys
 195 200 205
 Gln Glu Ala Phe Ser Thr Cys Ala Ser His Ile Thr Ile Ile Phe Ile
 210 215 220
 Ala Cys Arg Asn Ser Ile Ser Thr Cys Val Arg Pro Asn Pro Arg Tyr
 225 230 235 240
 Xaa Leu Asp Phe Asp Lys Val Thr Ala Ile Leu Thr Ile Val Val Thr
 245 250 255
 Ser Phe Leu Asn Pro Arg Ile Tyr Ser Leu Arg Xaa Arg Lys Tyr Glu
 260 265 270
 Gly Ser Thr Ile Cys Thr Ile Leu Ser Pro His Ser Lys Gly Thr
 275 280 285

<210> 1166

<211> 307

<212> PRT

<213> Unknown (H38g83 protein)

<220>

<223> Synthetic construct

<400> 1166

Met Glu Ser Glu Asn Arg Thr Val Ile Arg Glu Phe Ile Leu Leu Gly
 1 5 10 15
 Leu Thr Gln Ser Gln Asp Ile Gln Leu Val Phe Val Leu Val Leu
 20 25 30
 Ile Phe Tyr Phe Ile Ile Leu Pro Gly Asn Phe Leu Ile Ile Phe Thr
 35 40 45
 Ile Lys Ser Asp Pro Gly Leu Thr Ala Pro Leu Tyr Phe Phe Leu Gly
 50 55 60
 Asn Leu Ala Phe Leu Asp Ala Ser Tyr Ser Phe Thr Val Ala Pro Arg
 65 70 75 80
 Met Leu Val Asp Phe Leu Ser Ala Lys Lys Ile Ile Ser Tyr Arg Gly
 85 90 95
 Cys Ile Thr Gln Leu Phe Phe Leu His Phe Leu Gly Gly Gly Glu Gly
 100 105 110
 Leu Leu Leu Val Val Met Ala Phe Asp Arg Tyr Ile Ala Ile Cys Arg
 115 120 125
 Pro Leu His Tyr Pro Thr Val Met Asn Pro Arg Thr Cys Tyr Ala Met
 130 135 140
 Met Leu Ala Leu Trp Leu Gly Gly Phe Val His Ser Ile Ile Gln Val
 145 150 155 160
 Val Leu Ile Leu Arg Leu Pro Phe Cys Gly Pro Asn Gln Leu Asp Asn
 165 170 175
 Phe Phe Cys Asp Val Pro Gln Val Ile Lys Leu Ala Cys Thr Asp Thr
 180 185 190
 Phe Val Val Glu Leu Leu Met Val Phe Asn Ser Gly Leu Met Thr Leu
 195 200 205
 Leu Cys Phe Leu Gly Leu Leu Ala Ser Tyr Ala Val Ile Leu Cys Arg
 210 215 220
 Ile Arg Gly Ser Ser Ser Glu Ala Lys Asn Lys Ala Met Ser Thr Cys
 225 230 235 240
 Ile Thr His Ile Ile Val Ile Phe Phe Met Phe Gly Pro Gly Ile Phe
 245 250 255
 Ile Tyr Thr Arg Pro Phe Arg Ala Phe Pro Ala Asp Lys Val Val Ser
 260 265 270
 Leu Phe His Thr Val Ile Phe Pro Leu Leu Asn Pro Val Ile Tyr Thr
 275 280 285
 Leu Arg Asn Gln Glu Val Lys Ala Ser Met Lys Lys Val Phe Asn Lys
 290 295 300
 His Ile Ala

```

Ile Trp Lys Asp Pro His Leu His Ile Pro Met Tyr Leu Phe Leu Gly
 50          55          60
Ser Leu Ala Phe Val Asp Ala Ser Leu Ser Ser Thr Val Thr Pro Lys
65          70          75          80
Met Leu Ile Asn Phe Leu Ala Lys Ser Lys Met Ile Ser Leu Ser Glu
          85          90          95
Cys Met Val Gln Phe Phe Ser Leu Val Thr Thr Val Thr Thr Glu Cys
          100          105          110
Phe Leu Leu Ala Thr Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys
          115          120          125
Ala Leu Leu Tyr Pro Val Ile Met Thr Asn Glu Leu Cys Ile Gln Leu
          130          135          140
Leu Val Leu Ser Phe Ile Gly Gly Leu Leu His Ala Leu Ile His Glu
145          150          155          160
Ala Phe Ser Phe Arg Leu Thr Phe Cys Asn Ser Asn Ile Ile Gln His
          165          170          175
Phe Tyr Cys Asp Ile Ile Pro Leu Leu Lys Ile Ser Cys Thr Asp Ser
          180          185          190
Ser Ile Asn Phe Leu Met Val Phe Ile Phe Ala Gly Ser Val Gln Val
          195          200          205
Phe Thr Ile Gly Thr Ile Leu Ile Ser Tyr Thr Ile Ile Leu Phe Thr
          210          215          220
Ile Leu Glu Lys Lys Ser Ile Lys Gly Ile Arg Lys Ala Val Ser Thr
225          230          235          240
Cys Gly Ala His Leu Ser Val Ser Leu Tyr Tyr Gly Pro Leu Thr
          245          250          255
Phe Lys Tyr Leu Gly Ser Ala Ser Pro Gln Ala Asp Asp Gln Asp Met
          260          265          270
Met Glu Ser Leu Phe Tyr Thr Val Ile Val Pro Leu Leu Asn Pro Met
          275          280          285
Ile Tyr Ser Leu Arg Asn Lys Gln Val Ile Ala Ser Phe Thr Lys Met
          290          295          300
Phe Lys Ser Asn Val
305

```

<210> 1207

<211> 308

<212> PRT

<213> Unknown (H38g124 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(308)

<223> Xaa = Any Amino Acid

<400> 1207

```

Met Ala Asn Arg Asn Asn Val Thr Glu Phe Ile Leu Leu Gly Leu Thr
 1          5          10          15
Glu Asn Pro Lys Met Gln Lys Ile Ile Phe Val Val Phe Val Ile Tyr
          20          25          30
Ile Thr Thr Met Ile Gly Asn Val Leu Ile Val Val Thr Ile Thr Ala
          35          40          45
Ser Pro Ser Leu Arg Ser Pro Met Xaa Phe Phe Leu Ala Tyr Leu Ser
          50          55          60
Phe Ile Asp Ala Cys Tyr Ser Ser Val Asn Val Ser Lys Leu Ile Thr
65          70          75          80
Asp Ser Leu Tyr Glu Asn Lys Thr Ile Leu Leu Asn Gly Cys Met Thr
          85          90          95
Gln Val Phe Gly Glu His Phe Phe Arg Gly Val Glu Val Ile Leu Leu

```

305

<210> 1167

<211> 309

<212> PRT

<213> Unknown (H38g84 protein)

<220>

<223> Synthetic construct

<400> 1167

```

Met Glu Asn Gln Asn Asn Val Thr Glu Phe Ile Leu Leu Gly Leu Thr
 1           5           10           15
Glu Asn Leu Glu Leu Trp Lys Ile Phe Ser Ala Val Phe Leu Val Met
 20           25           30
Tyr Val Ala Thr Val Leu Glu Asn Leu Leu Ile Val Val Thr Ile Ile
 35           40           45
Thr Ser Gln Ser Leu Arg Ser Pro Met Tyr Phe Phe Leu Thr Phe Leu
 50           55           60
Ser Leu Leu Asp Val Met Phe Ser Ser Val Val Ala Pro Lys Val Ile
 65           70           75           80
Val Asp Thr Leu Ser Lys Ser Thr Thr Ile Ser Leu Lys Gly Cys Leu
 85           90           95
Thr Gln Leu Phe Val Glu His Phe Phe Gly Gly Val Gly Ile Ile Leu
 100          105          110
Leu Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu
 115          120          125
His Tyr Thr Ile Ile Met Ser Pro Arg Val Cys Cys Leu Met Val Gly
 130          135          140
Gly Ala Trp Val Gly Gly Phe Met His Ala Met Ile Gln Leu Leu Phe
 145          150          155          160
Met Tyr Gln Ile Pro Phe Cys Gly Pro Asn Ile Ile Asp His Phe Ile
 165          170          175
Cys Asp Leu Phe Gln Leu Leu Thr Leu Ala Cys Thr Asp Thr His Ile
 180          185          190
Leu Gly Leu Leu Val Thr Leu Asn Ser Gly Met Met Cys Val Ala Ile
 195          200          205
Phe Leu Ile Leu Ile Ala Ser Tyr Thr Val Ile Leu Cys Ser Leu Lys
 210          215          220
Ser Tyr Ser Ser Lys Gly Arg His Lys Ala Leu Ser Thr Cys Ser Ser
 225          230          235          240
His Leu Thr Val Val Val Leu Phe Phe Val Pro Cys Ile Phe Leu Tyr
 245          250          255
Met Arg Pro Val Val Thr His Pro Ile Asp Lys Ala Met Ala Val Ser
 260          265          270
Asp Ser Ile Ile Thr Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg
 275          280          285
Asn Ala Glu Val Lys Ser Ala Met Lys Lys Leu Trp Met Lys Trp Glu
 290          295          300
Ala Leu Ala Gly Lys
305

```

<210> 1168

<211> 311

<212> PRT

<213> Unknown (H38g85 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(311)

<223> Xaa = Any Amino Acid

<400> 1168

```

Val Glu Asp Met Val Pro Phe Ser Met Arg Ile Ser Gly Ile Phe Gln
 1          5          10          15
Ile Phe Phe Tyr Gly Tyr His His Leu Ile Tyr Xaa Tyr Ser Val Leu
          20          25          30
Thr Cys Val Pro Phe Gln Phe Thr Tyr Ser His Ile Val Lys Cys Xaa
          35          40          45
Leu Gln Gly Asn Leu Pro Gln Thr Gln Thr Ile Asn Val Thr Ser Glu
          50          55          60
Thr Ile Trp Ile Lys Ile Ile His Asp Phe Leu His Glu Pro Lys Thr
65          70          75          80
Ile Ser Phe Glu Gly Cys Met Ala Gln Ile Phe Leu Phe His Val Phe
          85          90          95
Ala Gly Gly Glu Met Val Leu Leu Val Ala Met Ala Tyr Asp Ile Tyr
          100          105          110
Val Ala Ile Cys Lys Pro Leu His Tyr Ala Thr Ile Met Asn Leu Cys
          115          120          125
Thr Cys Thr Gly Leu Val Val Gly Ser Trp Val Thr Gly Val Met His
          130          135          140
Ser Leu Ser Gln Leu Ala Phe Thr Val Ser Leu Pro Phe Cys Gly Pro
145          150          155          160
Asn Ile Val Asp Ser Tyr Tyr Cys Asp Leu Thr Leu Val Ile Lys Leu
          165          170          175
Ala Cys Thr Asp Thr Tyr Ile Pro Glu Ala Leu Met Leu Leu Asp Ser
          180          185          190
Gly Leu Met Gly Val Thr Ser Phe Leu Leu Leu Ile Ser Tyr Thr
          195          200          205
Val Ile Leu Ile Thr Val Gln Arg Pro Ser Ser Ala Gly Met Ala Lys
          210          215          220
Ala Arg Ser Thr Leu Thr Ala His Val Thr Val Val Thr Leu Phe Phe
225          230          235          240
Gly Pro Cys Ile Phe Ile Tyr Ala Trp Pro Phe Ser Asn Leu Pro Val
          245          250          255
Asp Asn Ile Leu Ser Val Phe Ser Thr Val Phe Thr Pro Ile Leu Asn
          260          265          270
Pro Leu Ile Tyr Thr Leu Arg Asn Lys Glu Val Lys Ser Ala Ile His
          275          280          285
Asn Leu Lys Thr Gln Tyr Val Thr Ser Arg Leu Ser Ser Gln Leu Ser
          290          295          300
Leu Ile Gly Leu Asp Leu Leu
305          310

```

<210> 1169

<211> 210

<212> PRT

<213> Unknown (H38g86 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(210)

<223> Xaa = Any Amino Acid

<400> 1169

```

Leu Gly Asn Val Ser Thr Glu Thr Thr Phe Ile Phe Val Cys Phe Thr
 1          5          10          15
Asn Gly Gln Gln Phe Gln Pro Val Cys Phe Ser Ser Phe Xaa Val Leu

```

```

      20      25      30
Gly His Ser Val Leu Gly Leu Ser Leu Leu Asn Ile His Gly Glu
      35      40      45
Leu Val Phe Ser Leu Phe Ser Phe Val Phe Val Phe Gln Met Ser Tyr
      50      55      60
Ser Phe Val Ile Leu Ile Lys Met Ile Met Asn Ser Ile Ser Glu Arg
      65      70      75      80
Tyr Ile Thr Thr Asn Leu Lys Cys Lys Thr Ser Ala Leu Val Phe Ile
      85      90      95
Cys Phe Ala Ile Ser Glu Thr Leu Ile Leu Leu Ala Trp Gly His Cys
      100      105      110
Gly Ile Cys Val Pro Gln Val Cys Ser Leu Thr Met Leu Gly Leu His
      115      120      125
Gly Val Gly Ile Asp Gly Val Met Ala His Pro Glu Ala Met Val Ser
      130      135      140
Leu Ser Phe Cys Asp Arg Ser Ile Ile Asn His Cys Val Trp His Thr
      145      150      155      160
Ser Phe His Gln Thr Leu Leu Arg Ala Pro Ala Ser Gln Ala Gly Asp
      165      170      175
Phe Val Val Ile Ala Xaa Xaa Leu Ile Ile Phe Ile Ser Asp Ile Leu
      180      185      190
Ile Leu Ser Thr Ile Leu His Phe Leu Phe Pro Glu Ala Asn Ser Lys
      195      200      205
Ala Phe
      210

```

<210> 1170

<211> 274

<212> PRT

<213> Unknown (H38g87 protein)

<220>

<223> Synthetic construct

<400> 1170

```

Met Gly Asn Leu Gly Met Ile Met Val Ile Arg Ile Asn Pro Lys Leu
1      5      10      15
His Thr Pro Met Tyr Phe Phe Leu Ser His Leu Ser Phe Val Asp Phe
      20      25      30
Cys Tyr Ser Thr Thr Ile Thr Pro Lys Leu Leu Glu Asn Leu Val Val
      35      40      45
Glu Asp Arg Ile Ile Ser Phe Thr Gly Cys Ile Met Gln Phe Phe Phe
      50      55      60
Ala Cys Ile Phe Val Val Thr Glu Thr Phe Met Leu Ala Ala Met Ala
      65      70      75      80
Tyr Asp Arg Phe Val Ala Val Cys Asn Pro Leu Leu Tyr Thr Val Ala
      85      90      95
Met Ser Gln Arg Leu Cys Ser Leu Leu Val Ala Ala Ser Tyr Ser Trp
      100      105      110
Ser Leu Val Cys Ser Leu Thr Tyr Thr Tyr Phe Leu Leu Thr Leu Ser
      115      120      125
Phe Cys Arg Thr Asn Phe Ile Asn Asn Phe Val Cys Glu His Ala Ala
      130      135      140
Ile Val Ala Val Ser Cys Ser Asp Pro Tyr Met Ser Gln Lys Val Ile
      145      150      155      160
Leu Val Ser Ala Thr Phe Asn Glu Ile Ser Ser Leu Val Ile Ile Leu
      165      170      175
Thr Ser Tyr Ala Phe Ile Phe Ile Thr Val Met Lys Met Pro Ser Thr
      180      185      190
Gly Gly Arg Lys Lys Ala Phe Ser Thr Cys Ala Ser His Leu Thr Ala
      195      200      205

```

Ile Thr Ile Phe His Gly Thr Ile Leu Phe Leu Tyr Cys Val Pro Asn
 210 215 220
 Ser Lys Ser Ser Trp Leu Met Val Lys Val Ala Ser Val Phe Tyr Thr
 225 230 235 240
 Val Val Ile Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys
 245 250 255
 Asp Val Lys Glu Thr Val Arg Lys Leu Val Ile Thr Lys Leu Leu Cys
 260 265 270
 His Lys

<210> 1171

<211> 348

<212> PRT

<213> Unknown (H38g88 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(348)

<223> Xaa = Any Amino Acid

<400> 1171

Met Thr Asn Ser Ser Val Lys Gly Asp Phe Ile Leu Val Gly Phe Ser
 1 5 10 15
 His Gln Pro His Leu Glu Lys Ile Leu Phe Val Ala Val Leu Ile Ser
 20 25 30
 Tyr Leu Leu Thr Leu Val Gly Asn Thr Val Ile Ile Leu Ile Cys Ser
 35 40 45
 Val Asp Pro Lys Leu Lys Thr Pro Met Tyr Phe Phe Leu Ser His Leu
 50 55 60
 Ser Leu Val Asp Ile Cys Phe Thr Thr Ser Ile Val Pro Gln Leu Leu
 65 70 75 80
 Trp Asn Leu Lys Gly Pro Asp Lys Thr Ile Thr Phe Leu Gly Cys Val
 85 90 95
 Ile Gln Leu Tyr Ile Ser Leu Ala Leu Gly Ser Thr Glu Cys Val Leu
 100 105 110
 Leu Ala Val Met Ala Phe Asp Arg Tyr Ala Ala Val Cys Lys Pro Leu
 115 120 125
 His Tyr Thr Ala Val Met Asn Pro Gln Leu Cys Gln Val Leu Ala Gly
 130 135 140
 Val Ala Trp Leu Ser Gly Val Gly Asn Thr Leu Ile Gln Gly Thr Val
 145 150 155 160
 Thr Leu Trp Leu Pro Arg Cys Gly His Arg Leu Leu Gln His Phe Phe
 165 170 175
 Cys Glu Val Pro Ser Met Ile Lys Leu Ala Cys Val Asp Ile His Asp
 180 185 190
 Asn Glu Val Gln Leu Phe Val Ala Ser Leu Val Leu Leu Leu Leu Pro
 195 200 205
 Leu Val Leu Ile Leu Leu Ser Tyr Gly His Ile Ala Lys Val Val Ile
 210 215 220
 Arg Ile Lys Ser Val Gln Ala Trp Cys Lys Gly Leu Gly Thr Cys Gly
 225 230 235 240
 Ser His Leu Ile Val Val Ser Leu Phe Cys Gly Thr Ile Thr Ala Val
 245 250 255
 Tyr Ile Gln Ser Asn Ser Ser Tyr Ala His Ala His Gly Lys Phe Ile
 260 265 270
 Ser Leu Phe Tyr Thr Val Val Thr Pro Thr Leu Asn Pro Leu Ile Tyr
 275 280 285
 Thr Leu Arg Asn Asn Asp Val Lys Gly Ala Leu Arg Leu Phe Asn Arg

290 295 300
 Asp Leu Gly Thr Xaa Lys Met Lys Gln Ser Thr Gln Arg Ser Thr Phe
 305 310 315 320
 Phe Thr Lys Gln Leu Xaa Arg Ser Tyr Leu Tyr Asn Phe Ser Leu Lys
 325 330 335
 Asn Phe Ala Ser Leu Xaa Arg Lys Arg Cys Asn Leu
 340 345

<210> 1172
 <211> 319
 <212> PRT
 <213> Unknown (H38g89 protein)

<220>
 <223> Synthetic construct

<400> 1172
 Met Asp Lys Ser Asn Ser Ser Val Val Ser Glu Phe Val Leu Leu Gly
 1 5 10 15
 Leu Cys Ser Ser Gln Lys Leu Gln Leu Phe Tyr Phe Cys Phe Phe Ser
 20 25 30
 Val Leu Tyr Thr Val Ile Val Leu Gly Asn Leu Leu Ile Ile Leu Thr
 35 40 45
 Val Thr Ser Asp Thr Ser Leu His Ser Pro Met Tyr Phe Leu Leu Gly
 50 55 60
 Asn Leu Ser Phe Val Asp Ile Cys Gln Ala Ser Phe Ala Thr Pro Lys
 65 70 75 80
 Met Ile Ala Asp Phe Leu Ser Ala His Glu Thr Ile Ser Phe Ser Gly
 85 90 95
 Cys Ile Ala Gln Ile Phe Phe Ile His Leu Phe Thr Gly Gly Glu Met
 100 105 110
 Val Leu Leu Val Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys
 115 120 125
 Pro Leu Tyr Tyr Val Val Ile Met Ser Arg Arg Thr Cys Thr Val Leu
 130 135 140
 Val Met Ile Ser Trp Ala Val Ser Leu Val His Thr Leu Ser Gln Leu
 145 150 155 160
 Ser Phe Thr Val Asn Leu Pro Phe Cys Gly Pro Asn Val Val Asp Ser
 165 170 175
 Phe Phe Cys Asp Leu Pro Arg Val Thr Lys Leu Ala Cys Leu Asp Ser
 180 185 190
 Tyr Ile Ile Glu Ile Leu Ile Val Val Asn Ser Gly Ile Leu Ser Leu
 195 200 205
 Ser Thr Phe Ser Leu Leu Val Ser Ser Tyr Ile Ile Ile Leu Val Thr
 210 215 220
 Val Trp Leu Lys Ser Ser Ala Ala Met Ala Lys Ala Phe Ser Thr Leu
 225 230 235 240
 Ala Ser His Ile Ala Val Val Ile Leu Phe Phe Gly Pro Cys Ile Phe
 245 250 255
 Ile Tyr Val Trp Pro Phe Thr Ile Ser Pro Leu Asp Lys Phe Leu Ala
 260 265 270
 Ile Phe Tyr Thr Val Phe Thr Pro Val Leu Asn Pro Ile Ile Tyr Thr
 275 280 285
 Leu Arg Asn Arg Asp Met Lys Ala Ala Val Arg Lys Ile Val Asn His
 290 295 300
 Tyr Leu Arg Pro Arg Arg Ile Ser Glu Met Ser Leu Val Val Arg
 305 310 315

<210> 1173
 <211> 312
 <212> PRT

<213> Unknown (H38g90 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(312)

<223> Xaa = Any Amino Acid

<400> 1173

```

Met Pro Ala Lys Asn Ser Ser Ser Val Thr Ala Phe Ile Leu Ser Gly
 1           5           10           15
Leu Thr Asp Gln Pro Gly Leu Gln Ile Pro Ala Phe Phe Leu Phe Leu
          20           25           30
Gly Phe Tyr Ala Val Thr Val Val Gly Asn Leu Gly Leu Ile Ile Leu
          35           40           45
Ile Gly Leu Asn Ser Arg Leu His Ile Pro Met Tyr Phe Phe Pro Phe
          50           55           60
Asn Leu Ser Phe Ile Asp Phe Ser Tyr Ser Thr Thr Leu Ala Pro Lys
65          70          75          80
Met Leu Met Ser Phe Val Ser Glu Asn Ile Ile Ser Tyr Ala Gly Cys
          85          90          95
Met Thr Gln Leu Phe Phe Phe Cys Phe Phe Val Phe Ser Glu Ser Tyr
          100         105         110
Ile Leu Ser Ala Met Ala Tyr Asp Arg Tyr Val Gly Ile Cys Asn Pro
          115         120         125
Leu Leu Tyr Thr Val Thr Met Ser Pro Gln Met Cys Leu Leu Leu Leu
          130         135         140
Leu Gly Val Tyr Gly Met Gly Tyr Phe Gly Ala Val Ala His Met Gly
145         150         155         160
Asn Ile Met Phe Met Ser Phe Cys Gly Asp Asn Leu Val Asn His Tyr
          165         170         175
Met Cys Asp Ile Leu Pro Leu Leu Glu Leu Ser Cys Asn Ser Ser Tyr
          180         185         190
Ile Asn Leu Leu Val Val Phe Ile Ile Val Thr Val Gly Ile Gly Val
          195         200         205
Pro Ile Val Thr Ile Phe Leu Ser Tyr Gly Phe Ile Leu Ser Ser Ile
          210         215         220
Leu His Ile Ser Ser Thr Glu Gly Arg Ser Lys Ala Phe Ser Thr Cys
225         230         235         240
Ser Ser His Ile Ile Val Val Ser Leu Phe Phe Gly Ser Gly Ala Phe
          245         250         255
Met Tyr Leu Lys Pro Pro Ser Ile Leu Pro Leu Asp Gln Gly Lys Val
          260         265         270
Ser Ser Ile Phe Cys Thr Ala Val Val Pro Met Phe Asn Pro Leu Ile
          275         280         285
Tyr Ser Leu Arg Asn Lys Asp Val Lys Val Ala Leu Arg Arg Thr Phe
290         295         300
Cys Arg Lys Leu Val Ser Xaa Lys
305         310

```

<210> 1174

<211> 357

<212> PRT

<213> Unknown (H38g91 protein)

<220>

<223> Synthetic construct

<400> 1174

Met Asn Trp Val Asn Lys Ser Val Pro Gln Glu Phe Ile Leu Leu Val

```

1           5           10           15
Phe Ser Asp Gln Pro Trp Leu Glu Ile Pro Pro Phe Val Met Phe Leu
20           25           30
Phe Ser Tyr Ile Leu Thr Ile Phe Gly Asn Leu Thr Ile Ile Leu Val
35           40           45
Ser His Val Asp Phe Lys Leu His Thr Pro Met Tyr Phe Phe Leu Ser
50           55           60
Asn Leu Ser Leu Leu Asp Leu Cys Tyr Thr Thr Ser Thr Val Pro Gln
65           70           75           80
Met Leu Val Asn Ile Cys Asn Thr Arg Lys Val Ile Ser Tyr Gly Gly
85           90           95
Cys Val Ala Gln Leu Phe Ile Phe Leu Ala Leu Gly Ser Thr Glu Cys
100           105           110
Leu Leu Leu Ala Val Met Cys Phe Asp Arg Phe Val Ala Ile Cys Arg
115           120           125
Pro Leu His Tyr Ser Ile Ile Met His Gln Arg Leu Cys Phe Gln Leu
130           135           140
Ala Ala Ala Ser Trp Ile Ser Gly Phe Ser Asn Ser Val Leu Gln Ser
145           150           155           160
Thr Trp Thr Leu Lys Met Pro Leu Cys Gly His Lys Glu Val Asp His
165           170           175
Phe Phe Cys Glu Val Pro Ala Leu Leu Lys Leu Ser Cys Val Asp Thr
180           185           190
Thr Ala Asn Glu Ala Glu Leu Phe Phe Ile Ser Val Leu Phe Leu Leu
195           200           205
Ile Pro Val Thr Leu Ile Leu Ile Ser Tyr Ala Phe Ile Val Gln Ala
210           215           220
Val Leu Arg Ile Gln Ser Ala Glu Gly Gln Arg Lys Ala Phe Gly Thr
225           230           235           240
Cys Gly Ser His Leu Ile Val Val Ser Leu Phe Tyr Gly Thr Ala Ile
245           250           255
Ser Met Tyr Leu Gln Pro Pro Ser Pro Ser Ser Lys Asp Arg Gly Lys
260           265           270
Met Val Ser Leu Phe Cys Gly Ile Ile Ala Pro Met Leu Asn Pro Leu
275           280           285
Ile Tyr Thr Leu Arg Asn Lys Glu Val Lys Glu Ala Phe Lys Arg Leu
290           295           300
Val Ala Lys Ser Leu Leu Asn Gln Glu Ile Arg Asn Met Gln Met Ile
305           310           315           320
Ser Phe Ala Lys Asp Thr Val Leu Thr Tyr Leu Thr Asn Phe Ser Ala
325           330           335
Ser Cys Pro Ile Phe Val Ile Thr Ile Glu Asn Tyr Cys Asn Leu Pro
340           345           350
Gln Arg Lys Phe Pro
355

```

<210> 1175

<211> 320

<212> PRT

<213> Unknown (H38g92 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(320)

<223> Xaa = Any Amino Acid

<400> 1175

```

His Thr Glu Pro Arg Asn Leu Thr Gly Ala Xaa Glu Leu Leu Leu Leu
1           5           10           15

```

Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Ile Leu Ala Gly Leu Ser
 20 25 30
 Leu Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ile Ser Leu
 35 40 45
 Ala Val Ser Ser Asp Ser His Leu His Thr Pro Met Cys Phe Phe Leu
 50 55 60
 Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Thr Val Pro
 65 70 75 80
 Lys Met Ile Val Asp Met Arg Ser His Ser Gly Val Ile Ser Tyr Ala
 85 90 95
 Asp Cys Leu Thr Arg Met Ser Phe Leu Val Leu Phe Ala Cys Val Glu
 100 105 110
 Asp Met Leu Leu Thr Val Met Ala Tyr Asp Cys Phe Val Ala Ile Cys
 115 120 125
 Arg Pro Leu His Tyr Pro Val Ile Val Asn Pro His Leu Cys Val Phe
 130 135 140
 Leu Val Ser Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu Arg
 145 150 155 160
 Ser Trp Ile Val Leu Gln Phe Thr Phe Phe Lys Asn Val Glu Ile Ser
 165 170 175
 Asn Phe Val Cys Asp Pro Ser Gln Pro Leu Lys Leu Ala Cys Ser Asp
 180 185 190
 Ser Ile Ile Asp Ser Met Phe Ile Tyr Phe Asp Ser Thr Met Phe Gly
 195 200 205
 Phe Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys Ile Val Pro
 210 215 220
 Ser Ile Leu Arg Ile Ser Ser Ser Asp Gly Xaa Tyr Lys Ala Phe Ser
 225 230 235 240
 Ala Cys Gly Ser His Leu Pro Val Val Cys Leu Phe Tyr Gly Thr Gly
 245 250 255
 Ile Gly Val Tyr Leu Thr Ser Ala Val Ala Pro Pro Leu Arg Asn Gly
 260 265 270
 Val Val Ala Ser Val Thr Tyr Ala Val Val Thr Pro Met Leu Asn Pro
 275 280 285
 Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu Trp Arg
 290 295 300
 Leu Arg Ser Arg Thr Val Lys Ser His Asp Leu Phe His Pro Phe Ser
 305 310 315 320

<210> 1176

<211> 313

<212> PRT

<213> Unknown (H38g93 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(313)

<223> Xaa = Any Amino Acid

<400> 1176

Met Glu Gly Phe Asn Cys Ser Arg Val Ser Glu Phe Met Leu Leu Gly
 1 5 10 15
 Leu Thr Asp Ser Pro Glu Leu Gln Arg Phe Phe Phe Val Val Phe Ser
 20 25 30
 Val Phe Tyr Leu Met Thr Met Leu Gly Asn Cys Leu Ile Leu Leu Thr
 35 40 45
 Val Leu Ser Thr Ser His Leu His Ser Pro Met Tyr Phe Leu Leu Ser
 50 55 60
 Asn Leu Ser Leu Ile Asp Met Cys Leu Ser Ser Phe Ala Thr Pro Lys

```

65      70      75      80
Met Ile Met Asp Phe Phe Ala Leu Arg Lys Thr Ile Ser Phe Glu Gly
      85      90      95
Cys Ile Ser Gln Ile Phe Phe Leu His Leu Phe Thr Gly Thr Glu Ile
      100     105     110
Val Leu Leu Ile Ser Met Ser Phe Asp Arg Tyr Ile Ala Ile Cys Lys
      115     120     125
Pro Leu His Tyr Ser Thr Ile Met Ser Gln Arg Val Cys Val Glu Leu
      130     135     140
Val Ala Val Ser Trp Thr Val Gly Phe Leu His Thr Met Ser Gln Leu
145      150     155     160
Ala Phe Thr Leu Tyr Leu Pro Phe Cys Gly Pro Asn Val Glu Ser Phe
      165     170     175
Phe Cys Asp Leu Pro Leu Val Ile Gln Leu Ala Cys Met Asp Ile Tyr
      180     185     190
Val Leu Gly Ile Phe Met Ile Ser Thr Ser Gly Val Ile Ala Leu Ile
      195     200     205
Ser Phe Leu Leu Leu Leu Thr Ser Tyr Ile Ile Val Leu Ile Thr Val
      210     215     220
Arg Asp Tyr Ser Ser Thr Gly Ser Ser Lys Ala Leu Ser Thr Cys Thr
225      230     235     240
Ala His Phe Ile Val Val Leu Met Phe Phe Gly Pro Cys Ile Phe Ile
      245     250     255
Tyr Val Trp Pro Ser Thr Asn Phe Leu Val Asp Lys Ile Leu Ser Val
      260     265     270
Phe Tyr Thr Ile Phe Thr Pro Phe Leu Asn Pro Leu Ile Tyr Thr Leu
      275     280     285
Arg Asn Gln Glu Val Lys Thr Ala Met Lys Lys Xaa Leu Asn Ile Gln
290      295     300
Tyr Phe Ser Leu Gly Lys Thr Ala Pro
305      310

```

<210> 1177

<211> 338

<212> PRT

<213> Unknown (H38g94 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(338)

<223> Xaa = Any Amino Acid

<400> 1177

```

Met Ile Leu Pro Ala Ser Phe Ser Xaa Gly Thr Met Glu Thr Ser Ser
1      5      10      15
Val Ser Ser Gly Thr Asp Phe Ile Leu Leu Gly Phe Ser Asp Arg Pro
      20      25      30
Gln Leu Glu His Ile Ile Ser Val Val Val Phe Ile Ile Tyr Ile Val
      35      40      45
Thr Leu Val Gly Asn Thr Thr Ile Ile Leu Val Ser Tyr Leu Asp Thr
50      55      60
Gln Leu His Thr Phe Met Tyr Phe Phe Leu Ser Asn Leu Ser Phe Leu
65      70      75      80
Asp Leu Cys Tyr Thr Thr Ser Ile Ile Pro Gln Met Leu Ala Asn Gln
      85      90      95
Trp Gly Pro Lys Lys Ser Ile Thr Tyr Gly Gly Cys Val Leu Gln Phe
      100     105     110
Phe Phe Val Leu Asp Leu Gly Ala Thr Glu Cys Leu Leu Leu Ala Val
115      120     125

```

```

Met Ala Tyr Asp Arg Tyr Ala Ala Val Cys Gln Pro Leu His Tyr Thr
 130          135          140
Leu Lys Cys Thr Leu Ser Phe Ala Thr Ala Trp Leu Ser Gly Leu Ala
145          150          155          160
Ser Ala Leu Ile Val Cys Ser Leu Thr Leu Lys Leu Pro Arg Cys Gly
          165          170          175
His Arg Glu Val Asp Asn Phe Phe Cys Glu Met Pro Ala Leu Ile Lys
          180          185          190
Met Ala Cys Val Tyr Ser Lys Val Ile Glu Ile Val Val Phe Ala Phe
 195          200          205
Gly Val Val Phe Leu Phe Val Pro Leu Ser Leu Ile Leu Ile Ser Tyr
 210          215          220
Gly Val Ile Thr Gln Ala Val Met Arg Ile Lys Ser Ala Thr Arg Leu
225          230          235          240
Gln Lys Ile Leu Asn Thr Cys Gly Ser His Leu Thr Val Val Ile Leu
          245          250          255
Phe Tyr Gly Thr Ile Ile Tyr Ile Tyr Met Lys Pro Gln Asn Thr Ile
 260          265          270
Ser Gln Asp Glu Gly Lys Phe Ser Leu Phe Tyr Thr Ile Ile Thr Pro
 275          280          285
Ser Leu Asn Leu Pro Ile Tyr Thr Leu Arg Asn Lys Asp Val Lys Ser
 290          295          300
Ala Leu Lys Arg Ile Leu Trp Met Lys Lys Ser Ser Ala Glu Xaa Met
305          310          315          320
Asn Xaa Met Glu Lys Ser Arg Met Xaa Ser Thr Lys Glu Ile Leu Ala
          325          330          335
Phe Ile

```

<210> 1178

<211> 314

<212> PRT

<213> Unknown (H38g95 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(314)

<223> Xaa = Any Amino Acid

<400> 1178

```

Met His Gln Gly Asn Xaa Thr Thr Val Ser Lys Phe Phe Leu Leu Gly
 1          5          10          15
Ile Thr Thr Lys Pro Lys Glu Gln Gln Phe Ile Phe Met Leu Phe Leu
          20          25          30
Cys Thr Tyr Leu Val Thr Met Val Arg Asn Leu Leu Ile Ile Leu Ala
 35          40          45
Val Val Ser Asp Ala His Leu His Gly Pro Ile Tyr Phe Phe Leu Ala
 50          55          60
Asn Leu Ser Phe Thr Asn Val Cys Ile Thr Thr Thr Thr Val Pro Lys
 65          70          75          80
Ile Leu Ala Asp Ile Gln Ser Gln Asn Ser Thr Ile Ser Phe Glu Gly
          85          90          95
Cys Pro Ala Gln Met Xaa Phe Xaa Ile Phe Leu Val Asp Leu Asp Asn
100          105          110
Phe Leu Leu Val Asp Met Ala Tyr Asn Xaa Tyr Ile Ala Ile Cys His
115          120          125
Pro Leu His Tyr Thr Val Val Leu Ser Pro Lys Asn Cys Ala Leu
130          135          140
Leu Val Val Thr Pro Trp Val Ile Ser Asn Leu Val Ser Ile Leu His

```

```

145          150          155          160
Leu Ser Leu Leu Ser His Leu Thr Phe Cys Ile Ser His Ile Phe Tyr
          165          170          175
Asp Leu Glu Pro Ile Leu Gly Leu Ala Cys Ser Asp Thr Gln Ile Asn
          180          185          190
Asn Leu Ile Ile Thr Ala Ile Gly Glu Val Val Ile Phe Ile Pro Phe
          195          200          205
Thr Cys His Ile Leu Val Ser Tyr Gly Leu Ile Gly Ser Thr Met Leu
          210          215          220
Gly Val Pro Ser Ala Lys Gly Lys Xaa Lys Thr Phe Ser Thr Cys Gly
225          230          235          240
Ser His Leu Ser Val Val Pro Gln Val Phe Tyr Gly Phe Ile Ile Gly
          245          250          255
Val Tyr Phe Leu Ser Phe Phe Ala Tyr Ser Ala Glu Arg Asp Glu Val
          260          265          270
Ala Ala Ile Met Tyr Thr Thr Val Thr His Leu Ile Lys Ser Phe Ile
          275          280          285
Cys Ser Leu Arg Asn Glu Asp Met Lys Gly Ala Leu Arg Arg Pro Leu
          290          295          300
Ser Arg Gln Gly Phe Ser Gly Val Val Ser
305          310

```

<210> 1179

<211> 314

<212> PRT

<213> Unknown (H38g96 protein)

<220>

<223> Synthetic construct

<400> 1179

```

Met Met Lys Lys Asn Gln Thr Met Ile Ser Glu Phe Leu Leu Leu Gly
1          5          10          15
Leu Pro Ile Gln Pro Glu Gln Arg Asn Leu Phe Tyr Ala Leu Phe Leu
          20          25          30
Ala Val Tyr Leu Thr Thr Leu Leu Gly Asn Leu Leu Val Ile Val Leu
          35          40          45
Ile Arg Leu Asp Ser His Leu His Met Pro Met Tyr Leu Cys Leu Ser
          50          55          60
Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys
65          70          75          80
Leu Leu Gln Asn Met Gln Ser Gln Asn Pro Ser Ile Pro Phe Ala Asp
          85          90          95
Cys Leu Ala Gln Met Tyr Phe His Leu Phe Tyr Gly Val Leu Glu Ser
          100          105          110
Phe Leu Leu Val Val Met Ala Tyr His Cys Tyr Val Ala Ile Cys Phe
          115          120          125
Pro Leu His Tyr Thr Thr Ile Met Ser Pro Lys Cys Cys Leu Gly Leu
          130          135          140
Leu Thr Leu Ser Trp Leu Leu Thr Thr Ala His Ala Thr Leu His Thr
145          150          155          160
Leu Leu Met Ala Arg Leu Ser Phe Cys Ala Glu Asn Val Ile Pro His
          165          170          175
Phe Phe Cys Asp Thr Ser Thr Leu Leu Lys Leu Ala Cys Ser Asn Thr
          180          185          190
Gln Val Asn Gly Trp Val Met Phe Phe Met Gly Gly Leu Ile Leu Val
          195          200          205
Ile Pro Phe Leu Leu Leu Ile Met Ser Cys Ala Arg Ile Val Ser Thr
          210          215          220
Ile Leu Arg Val Pro Ser Thr Gly Gly Ile Gln Lys Ala Phe Ser Thr
225          230          235          240

```

Cys Gly Pro His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile
 245 250 255
 Gly Leu Tyr Leu Cys Pro Leu Thr Asn His Asn Thr Val Lys Asp Thr
 260 265 270
 Val Met Ala Val Met Tyr Thr Gly Val Thr His Met Leu Asn Pro Phe
 275 280 285
 Ile Tyr Ser Leu Arg Asn Arg Asp Met Arg Gly Asn Pro Gly Gln Ser
 290 295 300
 Leu Gln His Lys Glu Asn Phe Phe Val Phe
 305 310

<210> 1180

<211> 331

<212> PRT

<213> Unknown (H38g97 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(331)

<223> Xaa = Any Amino Acid

<400> 1180

Met Ala Ala Glu Asn Ser Ser Ser Val Thr Glu Phe Ile Leu Ala Gly
 1 5 10 15
 Leu Ile His Gln Pro Gly Leu Gln Val Pro Val Phe Phe Leu Phe Leu
 20 25 30
 Gly Phe Tyr Ala Val Thr Val Val Gly Asn Leu Gly Leu Ile Ile Leu
 35 40 45
 Ile Gly Leu Asn Ser Arg Leu His Ile Pro Met Tyr Phe Phe Pro Phe
 50 55 60
 Asn Leu Ser Leu Val Asp Phe Ser Phe Ser Thr Thr Ile Ile Pro Lys
 65 70 75 80
 Met Leu Met Ser Phe Val Ser Arg Lys Asn Ile Ile Ser Phe Thr Gly
 85 90 95
 Cys Met Ser Gln Phe Phe Phe Phe Cys Phe Phe Val Phe Ser Glu Ser
 100 105 110
 Phe Ile Leu Ser Ala Met Val Xaa Asp Arg Tyr Val Gly Ile Cys Asn
 115 120 125
 Pro Leu Leu Tyr Thr Ile Thr Met Ser Pro Gln Val Cys Leu Leu Leu
 130 135 140
 Leu Leu Gly Val Tyr Gly Met Gly Val Phe Gly Ala Val Ala His Thr
 145 150 155 160
 Gly Asn Ile Val Phe Leu Thr Phe Cys Ala Asp Asn Leu Val Asn His
 165 170 175
 Tyr Met Cys Asp Ile Leu Pro Leu Leu Glu Leu Ser Cys Asn Gly Ser
 180 185 190
 Tyr Ile Asn Val Leu Val Ile Phe Ile Val Val Thr Val Gly Ile Gly
 195 200 205
 Val Pro Ile Val Ala Val Phe Ile Ser Tyr Gly Phe Ile Leu Ser Ser
 210 215 220
 Ile Leu Arg Val Ser Ser Ala Glu Gly Arg Ser Lys Ala Phe Ser Ser
 225 230 235 240
 Cys Ser Ser Tyr Ile Ile Ala Val Ser Leu Phe Phe Gly Ser Gly Ala
 245 250 255
 Phe Thr Tyr Leu Lys Pro Pro Ser Ile Leu Pro Leu Asp Gln Gly Lys
 260 265 270
 Val Ser Ser Leu Phe Tyr Thr Thr Val Val Pro Met Phe Asn Pro Leu
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Leu Ala Leu Lys Arg Thr

290 295 300
 Phe Ser Arg Ile Ser Phe Ser Glu Lys Asn Phe Arg Asn Arg Lys Glu
 305 310 315 320
 Ile Leu Gly Phe Phe Xaa Asn Gln Ile Ala Phe
 325 330

<210> 1181
 <211> 314
 <212> PRT
 <213> Unknown (H38g98 protein)

<220>
 <223> Synthetic construct

<400> 1181
 Met Ser Asn Glu Asp Met Glu Gln Asp Asn Thr Thr Leu Leu Thr Glu
 1 5 10 15
 Phe Val Leu Thr Gly Leu Thr Tyr Gln Pro Glu Trp Lys Met Pro Leu
 20 25 30
 Phe Leu Val Phe Leu Val Ile Tyr Leu Ile Thr Ile Val Trp Asn Leu
 35 40 45
 Gly Leu Ile Ala Leu Ile Trp Asn Asp Pro Gln Leu His Ile Pro Met
 50 55 60
 Tyr Phe Phe Leu Gly Ser Leu Ala Phe Val Asp Ala Trp Ile Ser Ser
 65 70 75 80
 Thr Val Thr Pro Lys Met Leu Val Asn Phe Leu Ala Lys Asn Arg Met
 85 90 95
 Ile Ser Leu Ser Glu Cys Met Ile Gln Phe Phe Ser Phe Ala Phe Gly
 100 105 110
 Gly Thr Thr Glu Cys Phe Leu Leu Ala Thr Met Ala Tyr Asp Arg Tyr
 115 120 125
 Val Ala Ile Cys Lys Pro Leu Leu Tyr Pro Val Ile Met Asn Asn Ser
 130 135 140
 Leu Cys Ile Arg Leu Leu Ala Phe Ser Phe Leu Gly Gly Phe Leu His
 145 150 155 160
 Ala Leu Ile His Glu Val Leu Ile Phe Arg Leu Thr Phe Cys Asn Ser
 165 170 175
 Asn Ile Ile His His Phe Tyr Cys Asp Ile Ile Pro Leu Phe Met Ile
 180 185 190
 Ser Cys Thr Asp Pro Ser Ile Asn Phe Leu Met Val Phe Ile Leu Ser
 195 200 205
 Gly Ser Ile Gln Val Phe Thr Ile Val Thr Val Leu Asn Ser Tyr Thr
 210 215 220
 Phe Ala Leu Phe Thr Ile Leu Lys Lys Lys Ser Val Arg Gly Val Arg
 225 230 235 240
 Lys Ala Phe Ser Thr Cys Gly Ala His Leu Leu Ser Val Ser Leu Tyr
 245 250 255
 Tyr Gly Pro Leu Ile Phe Met Tyr Leu Arg Pro Ala Ser Pro Gln Ala
 260 265 270
 Asp Asp Gln Asp Met Ile Asp Ser Val Phe Tyr Thr Ile Ile Ile Pro
 275 280 285
 Leu Leu Asn Pro Ile Ile Tyr Ser Leu Arg Asn Lys Gln Val Ile Asp
 290 295 300
 Ser Phe Thr Lys Met Val Lys Arg Asn Val
 305 310

<210> 1182
 <211> 313
 <212> PRT
 <213> Unknown (H38g99 protein)

<220>

<223> Synthetic construct.

<400> 1182

```

Met Glu Gly Lys Asn Leu Thr Ser Ile Ser Glu Cys Phe Leu Leu Gly
 1           5           10           15
Phe Ser Glu Gln Leu Glu Glu Gln Lys Pro Leu Phe Gly Ser Phe Leu
 20           25           30
Phe Met Tyr Leu Val Thr Val Ala Gly Asn Leu Leu Ile Ile Leu Val
 35           40           45
Ile Ile Thr Asp Thr Gln Leu His Thr Pro Met Tyr Phe Phe Leu Ala
 50           55           60
Asn Leu Ser Leu Ala Asp Ala Cys Phe Val Ser Thr Thr Val Pro Lys
 65           70           75           80
Met Leu Ala Asn Ile Gln Ile Gln Ser Gln Ala Ile Ser Tyr Ser Gly
 85           90           95
Cys Leu Leu Gln Leu Tyr Phe Phe Met Leu Phe Val Met Leu Glu Ala
 100          105          110
Phe Leu Leu Ala Val Met Ala Tyr Asp Cys Tyr Val Ala Ile Cys His
 115          120          125
Pro Leu His Tyr Ile Leu Ile Met Ser Pro Gly Leu Cys Ile Phe Leu
 130          135          140
Val Ser Ala Ser Trp Ile Met Asn Ala Leu His Ser Leu Leu His Thr
 145          150          155          160
Leu Leu Met Asn Ser Leu Ser Phe Cys Ala Asn His Glu Ile Pro His
 165          170          175
Phe Phe Cys Asp Ile Asn Pro Leu Leu Ser Leu Ser Cys Thr Asp Pro
 180          185          190
Phe Thr Asn Glu Leu Val Ile Phe Ile Thr Gly Gly Leu Thr Gly Leu
 195          200          205
Ile Cys Val Leu Cys Leu Ile Ile Ser Tyr Thr Asn Val Phe Ser Thr
 210          215          220
Ile Leu Lys Ile Pro Ser Ala Gln Gly Lys Arg Lys Ala Phe Ser Thr
 225          230          235          240
Cys Ser Ser His Leu Ser Val Val Ser Leu Phe Phe Gly Thr Ser Phe
 245          250          255
Cys Val Asp Phe Ser Ser Pro Ser Thr His Ser Ala Gln Lys Asp Thr
 260          265          270
Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe
 275          280          285
Ile Tyr Ser Leu Arg Asn Gln Glu Ile Lys Ser Ser Leu Arg Lys Leu
 290          295          300
Ile Trp Val Arg Lys Ile His Ser Pro
305          310

```

<210> 1183

<211> 310

<212> PRT

<213> Unknown (H38g100 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(310)

<223> Xaa = Any Amino Acid

<400> 1183

```

Met Glu Glu Glu Asn Ala Thr Leu Leu Thr Glu Phe Val Leu Thr Gly
 1           5           10           15
Leu Leu Tyr Gln Pro Gln Trp Lys Ile Pro Leu Phe Leu Thr Phe Leu

```

```

      20      25      30
Val Ile Tyr Leu Ile Thr Ile Met Gly Asn Leu Gly Leu Ile Ala Val
      35      40      45
Ile Trp Lys Asp Pro His Leu Gln Ile Pro Met Tyr Leu Leu Leu Gly
      50      55      60
Asn Leu Ala Phe Val Asp Ala Trp Ile Ser Ser Thr Val Thr Pro Lys
      65      70      75      80
Met Leu Asn Asn Phe Leu Ala Lys Ser Lys Met Val Ser Leu Pro Glu
      85      90      95
Ser Lys Ile Gln Phe Phe Ser Phe Ala Ile Ser Val Thr Thr Glu Cys
      100      105      110
Phe Leu Leu Ala Thr Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys
      115      120      125
Pro Leu Leu Tyr Pro Ala Ile Met Thr Asn Gly Leu Cys Ile Arg Leu
      130      135      140
Leu Gly Gly Leu Leu His Ala Leu Ile His Glu Gly Phe Leu Phe Arg
      145      150      155      160
Leu Thr Phe Cys Asn Ser Asn Val Val His His Ile Tyr Cys Asp Ile
      165      170      175
Ile Pro Leu Ser Lys Ile Ser Cys Thr Asp Ser Ser Ile Asn Phe Leu
      180      185      190
Met Val Phe Ile Phe Ser Gly Ser Ile Gln Val Phe Thr Ile Gly Thr
      195      200      205
Gly Leu Ile Ser Tyr Thr Phe Val Leu Phe Thr Ile Leu Lys Lys Lys
      210      215      220
Ser Val Lys Gly Ile Arg Lys Ala Phe Ser Thr Cys Gly Ala His Leu
      225      230      235      240
Leu Ser Val Ser Leu Tyr His Gly Pro Leu Asp Phe Met Tyr Met Gly
      245      250      255
Ser Ala Ser Pro Gln Ala Asp Asp Glu Asp Met Met Glu Ser Leu Phe
      260      265      270
Tyr Thr Val Ile Val Pro Leu Leu Asn Pro Met Thr Tyr Ser Leu Arg
      275      280      285
Asn Lys Gln Val Ile Ala Ser Phe Thr Lys Met Phe Lys Arg Asn Asn
      290      295      300
Ile Xaa Ile Ser Tyr Ser
      305      310

```

<210> 1184

<211> 231

<212> PRT

<213> Unknown (H38g101 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(231)

<223> Xaa = Any Amino Acid

<400> 1184

```

Phe Cys Leu Phe Pro Ala Thr Val Ser Lys Ala Val Val Lys Phe Leu
1      5      10      15
Ala Glu Thr Ile Ser Phe Ser Tyr Tyr Val Ile Gln Met Leu Val Phe
      20      25      30
Leu Phe Phe Val Thr Thr Glu Cys Asn Leu Leu Ala Ser Leu Gly Lys
      35      40      45
Asp Ile Tyr Met Pro Ile Arg Gln Pro Met Leu Tyr Pro Val Thr Met
      50      55      60
Ser Gln Val Cys Cys Ile Gln Leu Val Ala Ser Cys Tyr Gly His Gly
      65      70      75      80

```

Val Ile His Thr Met Phe Leu Gly Gly Ser Ile Ser Ile Phe Ala Phe
 85 90 95
 Cys Lys Ser Gln Thr Ile Ile Ser Phe Phe Gly Asp Ser Phe Pro Leu
 100 105 110
 Leu Val Leu Ser Cys Ser Asp Thr Tyr Ile Met Asn Ser Leu Phe Phe
 115 120 125
 Phe Thr Gly Cys Phe Ile Trp Met Ser Ser Xaa Pro Val Ile Leu Val
 130 135 140
 Ser His Met Phe Ile Ile Val Thr Phe Leu Arg Ile Phe Ser Val Val
 145 150 155 160
 Val Glu Ser Lys Gly Phe Leu Ala Phe Ser Ser His Leu Thr Ala Ile
 165 170 175
 Ile Leu Phe Tyr Gly Asp Ile Met Ser Leu Tyr Met Xaa His Ser Ser
 180 185 190
 Asn Tyr Phe Leu Asn Gln Asp Gln Thr Val Ser Ile Phe Tyr Met Val
 195 200 205
 Arg Ile Leu Leu Leu Ser Pro Ile Ile Tyr Cys Leu Ile Lys Met Gln
 210 215 220
 Val Ile Cys Phe Leu Glu Asn
 225 230

<210> 1185

<211> 216

<212> PRT

<213> Unknown (H38g102 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(216)

<223> Xaa = Any Amino Acid

<400> 1185

Leu Phe Phe Phe Val Xaa His Ser Ile Leu Thr Xaa Xaa Glu Gly Val
 1 5 10 15
 Lys Glu Ile Trp Tyr Phe Gln Glu Phe Leu Thr Tyr Pro Arg His Arg
 20 25 30
 Xaa Leu Leu Phe Val Ser Ser Cys Met Tyr Tyr Ser Ser Arg Ile Phe
 35 40 45
 Leu Arg Arg Thr Val Asn Ile Leu Phe Leu Leu Lys Val Ile Ser Leu
 50 55 60
 Leu Cys Tyr Gly Ser Lys Leu Ser Leu Phe Ile Phe Val Val Thr Ala
 65 70 75 80
 Glu Phe Xaa Leu Leu Ala Ser Arg Ile Cys His Cys Tyr Ile Ile Ile
 85 90 95
 Cys Asn Pro Phe Ser Thr Gln Phe Ser His Xaa Lys Leu Leu Ile Ser
 100 105 110
 Ile Leu Thr Ala His Tyr Asn Lys Arg Val Cys Ile Ser Ile Thr Thr
 115 120 125
 Ser Asn Thr Met Ser Xaa Leu Phe Phe Gly Arg Ser Asn Val Val Asn
 130 135 140
 Asn Phe Ser Asp Leu Leu Leu Leu Asp Leu Ser Cys Thr Phe Val
 145 150 155 160
 Ser Phe Xaa Ser Pro Ser Gln Leu Pro Asp His Ser Pro Gly Pro His
 165 170 175
 Asn Phe Ile Ile Val Val Asn Ile Lys Ile Xaa Leu Ala Glu Gly Lys
 180 185 190
 His Lys Asp Phe Ser Ile Cys Pro Leu Xaa Phe Ala Thr Val Ser Asn
 195 200 205
 Phe Leu Met Ala His Ile His Ile

210

215

<210> 1186
 <211> 312
 <212> PRT
 <213> Unknown (H38g103 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(312)
 <223> Xaa = Any Amino Acid

<400> 1186
 Phe Met Glu Asn Arg Asn Ile Val Thr Val Phe Ile Leu Leu Gly Leu
 1 5 10 15
 Ser Gln Asn Lys Asn Ile Glu Val Phe Trp Phe Val Leu Phe Val Phe
 20 25 30
 Cys Tyr Ile Ala Ile Trp Met Glu Asn Phe Ile Ile Met Ile Ser Ile
 35 40 45
 Met Tyr Ile Xaa Leu Ile Asp Gln Pro Met Tyr Phe Phe Leu Asn Tyr
 50 55 60
 Leu Ala Leu Ser Asp Leu Cys Tyr Ile Ser Thr Val Ala Pro Lys Leu
 65 70 75 80
 Met Ile Asp Leu Leu Thr Glu Arg Lys Ile Val Ser Tyr Asn Asn Cys
 85 90 95
 Met Ile Gln Leu Phe Ile Thr His Phe Leu Gly Asp Ile Glu Ile Phe
 100 105 110
 Ile Leu Lys Ala Met Ala Tyr Asp His Tyr Ile Ala Ile Cys Lys His
 115 120 125
 Leu His Tyr Thr Ile Ile Thr Lys Gln Ser Cys Asn Thr Ile Ile
 130 135 140
 Ile Ala Cys Trp Thr Gly Gly Phe Ile His Ser Ala Ser Gln Phe Leu
 145 150 155 160
 Leu Thr Ile Phe Leu Pro Phe Cys Gly Leu Asn Glu Ile Asp Gln Tyr
 165 170 175
 Phe Cys Tyr Val Tyr Pro Leu Leu Lys Leu Ala Arg Ile Asp Ile Tyr
 180 185 190
 Arg Ile Gly Phe Leu Val Ile Val Asn Ser Gly Leu Ile Ser Leu Leu
 195 200 205
 Ala Phe Val Ile Leu Met Val Ser Tyr Tyr Leu Ile Leu Ser Thr Ile
 210 215 220
 Arg Val Tyr Ser Ala Glu Ser His Thr Lys Ala Leu Ser Thr Cys Ser
 225 230 235 240
 Ser His Ile Ile Val Val Val Leu Phe Phe Val Pro Ala Leu Phe Ile
 245 250 255
 Tyr Ile Arg Pro Ala Ile Thr Phe Pro Glu Asp Lys Val Phe Val Leu
 260 265 270
 Phe Cys Ala Ile Ile Ala Pro Met Phe Ser Leu Leu Ile Tyr Met Leu
 275 280 285
 Arg Lys Val Glu Met Lys Asn Ala Val Arg Lys Met Trp Cys His Gln
 290 295 300
 Leu Leu Leu Ala Arg Lys Xaa Leu
 305 310

<210> 1187
 <211> 308
 <212> PRT
 <213> Unknown (H38g104 protein)

<220>

<223> Synthetic construct

<400> 1187

```

Met Ala Met Asp Asn Val Thr Ala Val Phe Gln Phe Leu Leu Ile Gly
 1           5           10           15
Ile Ser Asn Tyr Pro Gln Trp Arg Asp Thr Phe Phe Thr Leu Val Leu
          20           25           30
Ile Ile Tyr Leu Ser Thr Leu Leu Gly Asn Gly Phe Met Ile Phe Leu
          35           40           45
Ile His Phe Asp Pro Asn Leu His Thr Pro Ile Tyr Phe Phe Leu Ser
          50           55           60
Asn Leu Ser Phe Leu Asp Leu Cys Tyr Gly Thr Ala Ser Met Pro Gln
65           70           75           80
Ala Leu Val His Cys Phe Ser Thr His Pro Tyr Leu Ser Tyr Pro Arg
          85           90           95
Cys Leu Ala Gln Thr Ser Val Ser Leu Ala Leu Ala Thr Ala Glu Cys
          100          105          110
Leu Leu Leu Ala Ala Met Ala Tyr Asp Arg Val Val Ala Ile Ser Asn
          115          120          125
Pro Leu Arg Tyr Ser Val Val Met Asn Gly Pro Val Cys Val Cys Leu
          130          135          140
Val Ala Thr Ser Trp Gly Thr Ser Leu Val Leu Thr Ala Met Leu Ile
145          150          155          160
Leu Ser Leu Arg Leu His Phe Cys Gly Ala Asn Val Ile Asn His Phe
          165          170          175
Ala Cys Glu Ile Leu Ser Leu Ile Lys Leu Thr Cys Ser Asp Thr Ser
          180          185          190
Leu Asn Glu Phe Met Ile Leu Ile Thr Ser Ile Phe Thr Leu Leu Leu
          195          200          205
Pro Phe Gly Phe Val Leu Leu Ser Tyr Ile Arg Ile Ala Met Ala Ile
          210          215          220
Ile Arg Ile Arg Ser Leu Gln Gly Arg Leu Lys Ala Phe Thr Thr Cys
225          230          235          240
Gly Ser His Leu Thr Val Val Thr Ile Phe Tyr Gly Ser Ala Ile Ser
          245          250          255
Met Tyr Met Lys Thr Gln Ser Lys Ser Tyr Pro Asp Gln Asp Lys Phe
          260          265          270
Ile Ser Val Phe Tyr Gly Ala Leu Thr Pro Met Leu Asn Pro Leu Ile
          275          280          285
Tyr Ser Leu Arg Lys Lys Asp Val Lys Arg Ala Ile Arg Lys Val Met
          290          295          300
Leu Lys Arg Thr
305

```

<210> 1188

<211> 324

<212> PRT

<213> Unknown (H38g105 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(324)

<223> Xaa = Any Amino Acid

<400> 1188

```

Met Glu Ala Glu Asn Leu Thr Glu Leu Ser Glu Phe Leu Leu Leu Gly
 1           5           10           15
Leu Ser Met Ile Leu Asn Cys Ser Pro Phe Leu Phe Gly Leu Phe Leu

```

```

      20      25      30
Ser Met Tyr Leu Val Met Val Leu Gly Asn Leu Leu Ile Ile Leu Ala
      35      40      45
Val Ser Ser Asp Ser His Leu His Ser Pro Met Xaa Phe Phe Leu Ser
      50      55      60
Asn Leu Ser Phe Val Asp Thr Cys Phe Ile Cys Thr Thr Val Pro Lys
      65      70      75      80
Met Leu Val Asn Ile Gln Ala Arg Ser Lys Asp Ile Ser Tyr Met Gly
      85      90      95
Cys Leu Thr Gln Val Tyr Phe Xaa Met Met Phe Ala Gly Met Asp Thr
      100      105      110
Phe Leu Leu Ala Val Ile Ala Tyr Asp Arg Phe Val Ala Ile Cys His
      115      120      125
Pro Leu Gln Tyr Met Val Ile Ile Asn Pro His Leu Cys Gly Leu Leu
      130      135      140
Val Leu Ala Ser Trp Phe Ile Ile Phe Trp Phe Ser Leu Val His Ile
      145      150      155      160
Leu Leu Met Lys Arg Leu Thr Phe Ser Thr Gly Thr Glu Ile Pro His
      165      170      175
Phe Phe Cys Glu Leu Ala Gln Val Leu Lys Val Ala Arg Ser Asp Ala
      180      185      190
Leu Leu Ile Asn Ile Val Leu Tyr Val Ala Thr Ala Leu Leu Gly Val
      195      200      205
Phe Pro Val Ala Gly Ile Leu Phe Ser Tyr Ser Gln Ile Val Ser Ser
      210      215      220
Leu Met Arg Met Ser Ser Thr Glu Gly Lys Tyr Lys Ala Phe Ser Thr
      225      230      235      240
Cys Gly Ser His Leu Cys Val Val Ser Leu Phe Tyr Gly Thr Gly Leu
      245      250      255
Gly Val Tyr Leu Ser Ser Ala Val Thr His Ser Ser Gln Ser Ser Ser
      260      265      270
Met Ala Ser Val Met Tyr Ala Met Val Thr Pro Met Leu Asn Pro Phe
      275      280      285
Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Gly Ala Leu Gly Arg Leu
      290      295      300
Leu Ser Arg Ala Ala Ser Cys Pro Leu Thr Val His Asn Leu Arg Thr
      305      310      315      320
Lys Arg Met Leu

```

<210> 1189

<211> 291

<212> PRT

<213> Unknown (H38g106 protein)

<220>

<223> Synthetic construct

<400> 1189

```

Met Glu Gly Phe Asn Tyr Ser Arg Val Ser Glu Phe Met Leu Leu Gly
1      5      10      15
Leu Thr Asp Ser Pro Glu Leu Gln Ile Phe Phe Ser Val Val Phe Ser
      20      25      30
Val Phe Tyr Leu Met Thr Met Leu Gly Asn Cys Leu Ile Leu Leu Thr
      35      40      45
Val Leu Ser Thr Ser His Leu His Ser Arg Met Tyr Phe Leu Leu Ser
      50      55      60
Asn Met Ser Ile Asp Met Cys Leu Ser Ser Phe Ala Thr Pro Lys Met
      65      70      75      80
Ile Met Asp Phe Phe Ala Leu Arg Asn Thr Ile Ser Phe Glu Gly Cys
      85      90      95

```

```

Ile Ser Gln Ile Phe Phe Leu His Leu Phe Asn Gly Thr Glu Ile Val
      100      105      110
Leu Leu Ile Ser Met Ser Phe Asp Arg Tyr Ile Ala Ile Cys Lys Pro
      115      120      125
Leu His Tyr Ser Thr Ile Met Ser Gln Arg Val Cys Val Glu Leu Val
      130      135      140
Ala Val Ser Cys Trp Thr Val Gly Phe Leu His Thr Met Ser Gln Leu
      145      150      155      160
Val Phe Ala Leu Tyr Leu Pro Phe Cys Val Pro Asn Val Val Asp Ser
      165      170      175
Phe Phe Cys Asp Leu Pro Leu Val Ile Gln Leu Ala Cys Ile Asp Ile
      180      185      190
Tyr Val Leu Gly Thr Ser Met Ile Ser Thr Ser Gly Val Ile Ala Leu
      195      200      205
Ile Ser Phe Leu Leu Leu Leu Thr Ser Tyr Ile Ile Val Leu Asn Ile
      210      215      220
Val Arg Asp Tyr Ser Ser Thr Gly Ser Ser Lys Ala Leu Ser Thr Cys
      225      230      235      240
Thr Ala His Phe Ile Val Val Leu Met Phe Phe Gly Pro Cys Ile Phe
      245      250      255
Ile Tyr Val Trp Pro Ser Thr Asn Phe Leu Val Asp Lys Ile Leu Ser
      260      265      270
Val Phe Tyr Thr Ile Phe Thr Pro Phe Leu Asn Pro Leu Ile Tyr Thr
      275      280      285
Leu Arg Asn
      290

```

<210> 1190

<211> 328

<212> PRT

<213> Unknown (H38g107 protein)

<220>

<223> Synthetic construct

<400> 1190

```

Tyr Thr Glu Pro Gln Asn Leu Thr Gly Val Ser Glu Phe Leu Leu Leu
  1      5      10      15
Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Gly Leu Phe
      20      25      30
Leu Ser Met Tyr Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu
      35      40      45
Ala Val Ser Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu
      50      55      60
Ser Asn Leu Ser Leu Ala Asp Ile Gly Phe Thr Ser Thr Thr Val Pro
      65      70      75      80
Lys Met Ile Val Asp Met Gln Thr His Ser Arg Val Ile Ser Tyr Glu
      85      90      95
Gly Cys Leu Thr Gln Met Ser Phe Phe Val Leu Phe Ala Cys Met Asp
      100      105      110
Asp Met Leu Leu Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys
      115      120      125
His Pro Leu His Tyr Arg Ile Ile Met Asn Pro Arg Leu Cys Gly Phe
      130      135      140
Leu Ile Leu Leu Ser Phe Phe Ile Ser Leu Leu Asp Ser Gln Leu His
      145      150      155      160
Asn Leu Ile Met Leu Gln Leu Thr Cys Phe Lys Asp Val Asp Ile Ser
      165      170      175
Asn Phe Phe Cys Asp Pro Ser Gln Leu Leu His Leu Arg Cys Ser Asp
      180      185      190
Thr Phe Ile Asn Glu Met Val Ile Tyr Phe Met Gly Ala Ile Phe Gly

```

```

      195              200              205
Cys Leu Pro Ile Ser Gly Ile Leu Phe Ser Tyr Tyr Lys Ile Val Ser
  210              215              220
Pro Ile Leu Arg Val Pro Thr Ser Asp Gly Lys Tyr Lys Ala Phe Ser
  225              230              235              240
Thr Cys Gly Ser His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Gly
      245              250              255
Leu Val Gly Tyr Leu Ser Ser Ala Val Leu Pro Ser Pro Arg Lys Ser
      260              265              270
Met Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro
      275              280              285
Phe Ile Tyr Ser Leu Arg Asn Lys Asp Ile Gln Ser Ala Leu Cys Arg
      290              295              300
Leu His Gly Arg Ile Ile Lys Ser His His Leu His Pro Phe Val Ile
  305              310              315              320
Trp Asp Arg Asn Gly Ser Lys Ile
      325

```

<210> 1191

<211> 325

<212> PRT

<213> Unknown (H38g108 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(325)

<223> Xaa = Any Amino Acid

<400> 1191

```

Leu Thr Met Pro His Leu Ser Asn Thr Thr Ser Glu Phe Pro Ile Phe
  1              5              10              15
Leu Leu Thr Gly Phe Pro Gly Leu Glu Ala Phe His Ile Trp Ile Ser
      20              25              30
Ile Pro Phe Phe Leu Leu Ser Thr Val Ala Leu Leu Gly Asn Ser Met
      35              40              45
Ile Leu Leu Val Val Ile Leu Glu Pro Asn Leu His Glu Pro Met Tyr
      50              55              60
Cys Phe Leu Phe Met Leu Ser Ala Ala Asp Leu Gly Leu Thr Leu Ser
  65              70              75              80
Thr Met Pro Thr Thr Leu Ser Val Leu Trp Phe Ser Ala Arg Glu Ile
      85              90              95
Ile Leu Asn Ala Cys Ile Ile Gln Leu Phe Phe Leu His Ser Ser Gly
      100              105              110
Phe Met Glu Ser Ser Val Leu Met Ala Met Ala Phe Asp Arg Phe Val
      115              120              125
Ala Ile Cys Arg Pro Leu Arg Tyr Ala Thr Ile Leu Thr Asp Ser Arg
      130              135              140
Ile Leu Lys Ile Gly Val Ala Ile Val Leu Arg Thr Leu Ile Ser Leu
  145              150              155              160
Ser Pro Ser Leu Phe Leu Ile Lys Arg Leu Ser Phe Cys Lys Val Asn
      165              170              175
Val Leu Ser His Ser Tyr Cys Phe His Pro Asp Ala Leu Lys Val Ala
      180              185              190
Cys Ser Asp Ser Arg Met Asn Ser Tyr Gly Gly Leu Ala Val Leu Ile
      195              200              205
Leu Val Thr Gly Val Gly Thr Pro Cys Val Ala Leu Ser Tyr Ile Leu
      210              215              220
Ile Ile His Ser Val Leu Asn Ile Ile Ser Ser Glu Gly Arg Arg Lys
  225              230              235              240

```

Ala Phe Asp Thr Cys Gly Ser His Ile Gly Ala Val Ala Val Phe Tyr
 245 250 255
 Ile Pro Trp Val Val Leu Ser Val Val His Arg Phe Phe His Lys Ala
 260 265 270
 Ser Pro Tyr Val His Pro Leu Leu Ser Asn Ile Tyr Phe Leu Gly Pro
 275 280 285
 Ser Arg Leu Asn Pro Ile Ile Tyr Ser Val Lys Thr Lys Gln Ile Arg
 290 295 300
 Arg Ala Ile Leu Lys Leu Phe Gln Thr Lys Ser Lys Glu Met Xaa Trp
 305 310 315 320
 Gly Leu Phe Phe Leu
 325

<210> 1192

<211> 295

<212> PRT

<213> Unknown (H38g109 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(295)

<223> Xaa = Any Amino Acid

<400> 1192

Ile Gln Cys Lys Gly Xaa Xaa Lys Xaa Ile Lys Thr Phe Ser Val Thr
 1 5 10 15
 Pro Ile Leu Asn Gly Asn Arg Glu Ile Ala Arg Phe Leu Ser Asn Leu
 20 25 30
 Ser Leu Ala Gly Ile Gly Phe Pro Ser Thr Ile Val Ser Lys Met Ile
 35 40 45
 Val Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala Gly Cys Leu
 50 55 60
 Thr Gln Val Ser Leu Phe Ala Val Phe Gly Cys Met Glu Asp Met Leu
 65 70 75 80
 Leu Ser Val Met Ala Tyr Asp Arg Phe Val Asp Ile Cys His Pro Leu
 85 90 95
 Asp Tyr Pro Val Ile Met Asn Pro Cys Phe Cys Gly Phe Leu Val Leu
 100 105 110
 Leu Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His Asn Trp Ile
 115 120 125
 Ala Leu Gln Ile Thr Cys Phe Lys Asp Val Glu Ile Pro Asn Phe Phe
 130 135 140
 Cys Asp Pro Ser Gln His Pro Thr Leu Ala Cys Cys Asp Thr Phe Thr
 145 150 155 160
 Asn Asp Ile Val Met Tyr Phe Leu Ala Ala Ile Phe Gly Phe Leu Pro
 165 170 175
 Ile Ser Gly Thr Phe Ser Ser Tyr Tyr Lys Ile Val Ser Ser Ile Leu
 180 185 190
 Arg Val Ser Ser Ser Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly
 195 200 205
 Ser His Leu Ser Val Val Cys Leu Phe Tyr Gly Thr Gly Phe Gly Gly
 210 215 220
 Asp Leu Ser Ser Asp Met Ser Ser Tyr Pro Arg Lys Gly Ala Val Ala
 225 230 235 240
 Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe Ile Tyr
 245 250 255
 Ser Arg Asn Arg Glu Ile Lys Ser Ala Leu Arg Gln Leu His Cys Arg
 260 265 270
 Ile Val Xaa Ser His Phe Leu Ile Ile Cys Ser Ile Pro Ser Val Val

275 280 285
 Xaa Val Arg Lys Gly Ser Lys
 290 295

<210> 1193
 <211> 320
 <212> PRT
 <213> Unknown (H38g110 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(320)
 <223> Xaa = Any Amino Acid

<400> 1193
 Tyr Thr Asp Ser Gln Asn Leu Thr Gly Val Leu Glu Phe Leu Phe Leu
 1 5 10 15
 Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Val Gly Leu Phe
 20 25 30
 Leu Ser Met Tyr Leu Ile Thr Val Leu Gly Asn Leu Leu Ile Ile Leu
 35 40 45
 Ala Val Ser Cys Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu
 50 55 60
 Ser Asn Leu Ser Leu Ala Asp Ile Gly Leu Thr Ser Ala Thr Ile Pro
 65 70 75 80
 Lys Met Ile Val Asp Met Gln Ser His Ser Arg Ile Ile Ser Tyr Glu
 85 90 95
 Gly Cys Leu Met Gln Met Tyr Phe Ile Tyr Phe Val Cys Met Asn Asp
 100 105 110
 Met Val Leu Thr Val Met Ala Tyr Asp Gln Phe Val Ala Ile Cys His
 115 120 125
 Pro Leu Arg Tyr Pro Val Ile Met Asn Pro His Leu Cys Val Phe Leu
 130 135 140
 Val Leu Val Ser Phe Ile Leu Ser Leu Leu Asn Ser Gln Leu His Asn
 145 150 155 160
 Gln Ile Val Leu Gln Phe Thr Cys Phe Lys Asn Val Glu Ile Phe Asn
 165 170 175
 Phe Phe Cys Glu Pro Ser Gln Leu Leu Asn Leu Ala Cys Ser Asp Ser
 180 185 190
 Val Ile Asn Asn Ile Phe Met Tyr Leu Asp Ser Val Ile Phe Gly Phe
 195 200 205
 Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys Ile Val Ser Ser
 210 215 220
 Ile Leu Arg Ile Pro Ser Ser Asp Gly Lys Tyr Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Gly Ser His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Gly Leu
 245 250 255
 Gly Ala Tyr Leu Ser Ser Ala Ala Ser Ser Phe Pro Arg Lys Gly Ala
 260 265 270
 Val Thr Ser Val Met Tyr Thr Val Ile Pro Met Leu Asn Pro Phe
 275 280 285
 Ile Tyr Ser Leu Arg Asn Arg Asp Ile Lys Ser Ala Leu Trp Arg Leu
 290 295 300
 His Ser Arg Thr Val Xaa Ser His Tyr Leu Phe His Pro Phe Cys Ser
 305 310 315 320

<210> 1194
 <211> 318
 <212> PRT

<213> Unknown (H38g111 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(318)

<223> Xaa = Any Amino Acid

<400> 1194

His	Thr	Glu	Pro	Gln	Asn	Leu	Thr	Gly	Val	Ser	Glu	Phe	Leu	Leu	Leu
1				5					10					15	
Gly	Leu	Ser	Glu	Asp	Pro	Glu	Leu	Gln	Pro	Leu	Leu	Ala	Gly	Leu	Phe
			20					25					30		
Leu	Ser	Met	Cys	Leu	Val	Thr	Met	Leu	Gly	Asn	Leu	Leu	Ile	Ile	Leu
		35					40					45			
Ala	Val	Ser	Pro	Asp	Ser	His	Leu	His	Ile	Pro	Met	Tyr	Phe	Phe	Leu
	50					55					60				
Ser	Asn	Leu	Ser	Leu	Pro	Asp	Ile	Gly	Phe	Thr	Leu	Ala	Thr	Val	Pro
65					70				75					80	
Lys	Met	Ile	Val	Asp	Met	Gln	Ser	His	Ser	Arg	Val	Ile	Ser	His	Ala
				85					90					95	
Gly	Cys	Leu	Thr	Gln	Ile	Pro	Phe	Phe	Val	Leu	Phe	Val	Cys	Ile	Asp
			100					105					110		
Asp	Met	Leu	Leu	Thr	Val	Met	Ala	Tyr	Asp	Xaa	Phe	Val	Ala	Ile	Cys
		115					120					125			
His	Pro	Leu	His	Tyr	Pro	Val	Ile	Met	Asn	Pro	His	Leu	Cys	Val	Phe
	130					135					140				
Leu	Val	Leu	Met	Ser	Phe	Ile	Leu	Ser	Leu	Leu	Asp	Ser	Xaa	Leu	His
145					150				155					160	
Asn	Trp	Ile	Val	Gln	Phe	Thr	Cys	Phe	Lys	Asn	Val	Glu	Ile	Ser	Asn
				165					170					175	
Phe	Phe	Cys	Asp	Xaa	Ser	Gln	Leu	Leu	Asn	Leu	Ala	Cys	Ser	Asp	Val
		180					185					190			
Ile	Ser	Asn	Ile	Phe	Ile	His	Leu	Asp	Ser	Thr	Ile	Phe	Gly	Phe	Leu
		195					200					205			
Pro	Ile	Ser	Gly	Ile	Leu	Leu	Ser	Tyr	Tyr	Lys	Ile	Val	Pro	Ser	Ile
	210					215					220				
Leu	Arg	Ile	Pro	Leu	Ser	Asp	Gly	Lys	Tyr	Lys	Ala	Phe	Ser	Thr	Cys
225					230				235					240	
Gly	Ser	His	Leu	Ala	Ile	Val	Cys	Leu	Phe	Tyr	Gly	Thr	Gly	Ile	Gly
				245					250					255	
Met	Tyr	Leu	Thr	Ser	Ala	Val	Ser	Pro	Ala	Pro	Arg	Asn	Gly	Val	Val
		260						265					270		
Ala	Ser	Val	Leu	Tyr	Ala	Met	Val	Thr	Pro	Met	Leu	Asn	Pro	Phe	Ile
		275					280					285			
Cys	Ser	Leu	Arg	Asn	Arg	Gly	Ile	Gln	Ser	Ala	Leu	Trp	Arg	Leu	Cys
	290					295					300				
Arg	Arg	Lys	Val	Xaa	Ser	His	Asp	Leu	Phe	His	Pro	Phe	Ser		
305					310					315					

<210> 1195

<211> 350

<212> PRT

<213> Unknown (H38g112 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(350)

<223> Xaa = Any Amino Acid

<400> 1195

```

Met Ser Gln Leu Gly Arg Asp Asn Ile Thr Trp Val Ser Glu Phe Ile
 1           5           10           15
Leu Met Gly Leu Ser Ser Asp Arg Gln Thr Gln Ala Gly Leu Phe Ile
           20           25           30
Leu Phe Gly Ala Ala Tyr Leu Leu Thr Leu Leu Gly Asn Gly Leu Ile
           35           40           45
Leu Leu Leu Ile Trp Leu Asp Val Arg Leu His Leu Pro Met Tyr Phe
           50           55           60
Phe Leu Cys Asn Leu Ser Leu Val Asn Ile Cys Tyr Thr Ser Ser Arg
65           70           75           80
Val Pro Gln Met Leu Val His Leu His Gln Gln Arg Lys Thr Ile Ser
           85           90           95
Phe Ala Arg Cys Gly Thr Gln Leu Phe Phe Ser Leu Ala Leu Gly Gly
           100          105          110
Thr Glu Phe Leu Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val Ala
           115          120          125
Val Cys Asp Pro Leu Cys Tyr Ile Ala Val Met Ser Pro Arg Leu Cys
           130          135          140
Met Ala Leu Ala Ala Val Ser Trp Leu Val Gly Leu Ala Asn Ser Ala
145          150          155          160
Met Glu Thr Ala Leu Thr Met His Leu Pro Thr Cys Gly His Asn Val
           165          170          175
Leu Asn His Val Ala Cys Glu Thr Leu Ala Leu Val Arg Ser Ala Cys
           180          185          190
Val Asp Ile Thr Phe Asn Gln Val Val Ile Val Ala Ser Ser Val Val
           195          200          205
Val Leu Leu Val Pro Cys Cys Leu Val Ser Leu Ser Tyr Thr Leu Ile
           210          215          220
Val Val Ala Val Leu Gln Ile His Ser Thr Gln Gly His Arg Lys Ala
225          230          235          240
Phe Gly Thr Cys Ala Ser His Leu Thr Val Val Ser Ile Ser Tyr Gly
           245          250          255
Met Ala Leu Phe Thr Tyr Met Gln Pro Arg Ser Met Ala Ser Ala Glu
           260          265          270
Gln Glu Lys Val Met Val Leu Ser Tyr Ala Val Val Thr Pro Met Leu
           275          280          285
Asn Pro Phe Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Ala Ala Leu
           290          295          300
Ser Arg Ala Leu Met Arg Ser Ser Glu Leu Lys His Xaa Arg Val Val
305          310          315          320
Xaa Val Thr Arg Arg Pro His Ser Glu Asn Ser Gly His Trp Thr Val
           325          330          335
Leu Ser Ser Ile Thr Cys Val Arg Met Cys Val Tyr Val Cys
           340          345          350

```

<210> 1196

<211> 320

<212> PRT

<213> Unknown (H38g113 protein)

<220>

<223> Synthetic construct

<400> 1196

```

Met Asp Ser Pro Ser Asn Ala Thr Val Pro Cys Gly Phe Leu Leu Gln
 1           5           10           15
Gly Phe Ser Glu Phe Pro His Leu Arg Pro Val Leu Phe Leu Leu
           20           25           30

```

Leu Gly Val His Leu Ala Thr Leu Gly Gly Asn Leu Leu Ile Leu Val
 35 40 45
 Ala Val Ala Ser Met Pro Ser Arg Gln Pro Met Leu Leu Phe Leu Cys
 50 55 60
 Gln Leu Ser Ala Ile Glu Leu Cys Tyr Thr Leu Val Val Val Pro Arg
 65 70 75 80
 Ser Leu Val Asp Leu Ser Ser Arg Gly His Arg Arg Gly Ser Pro Ile
 85 90 95
 Ser Phe Leu Ser Cys Ala Phe Gln Met Gln Met Phe Val Ala Leu Gly
 100 105 110
 Gly Ala Glu Cys Phe Leu Leu Ala Ala Met Ala Asn Asp Arg Tyr Val
 115 120 125
 Ala Ile Cys His Pro Leu Arg Tyr Arg Ala Val Val Thr Pro Gly Leu
 130 135 140
 Cys Ala Arg Leu Val Ser Gly Cys Cys Leu Arg Gly Leu Ala Val Ser
 145 150 155 160
 Leu Gly Leu Thr Val Leu Ile Phe His Leu Pro Phe Cys Gly Ser Arg
 165 170 175
 Leu Leu Leu His Phe Phe Cys Asp Ile Thr Ala Leu Leu His Leu Ala
 180 185 190
 Cys Thr Arg Thr Thr Pro His Glu Leu Pro Leu Leu Gly Ala Cys Leu
 195 200 205
 Val Leu Leu Leu Leu Pro Ser Val Leu Ile Leu Ala Ser Tyr Gly Ala
 210 215 220
 Ile Ala Ala Ala Leu Val Arg Leu Arg Cys Pro Lys Gly Arg Gly Lys
 225 230 235 240
 Ala Ala Ser Thr Cys Ala Leu His Leu Ala Val Thr Phe Leu His Tyr
 245 250 255
 Gly Cys Ala Thr Phe Met Tyr Val Arg Pro Arg Ala Ser Tyr Ser Pro
 260 265 270
 Arg Leu Asp Arg Thr Leu Ala Leu Val Tyr Thr Asn Val Thr Pro Leu
 275 280 285
 Leu Cys Pro Leu Ile Tyr Ser Leu Arg Asn Arg Glu Ile Thr Ala Ala
 290 295 300
 Leu Ser Arg Val Leu Gly Arg Arg Arg Pro Gly Gln Ala Pro Gly Gly
 305 310 315 320

<210> 1197

<211> 315

<212> PRT

<213> Unknown (H38g114 protein)

<220>

<223> Synthetic construct

<400> 1197

Met Gly Asp Trp Asn Asn Ser Asp Ala Val Glu Pro Ile Phe Ile Leu
 1 5 10 15
 Arg Gly Phe Pro Gly Leu Glu Tyr Val His Ser Trp Leu Ser Ile Leu
 20 25 30
 Phe Cys Leu Ala Tyr Leu Val Ala Phe Met Gly Asn Val Thr Ile Leu
 35 40 45
 Ser Val Ile Trp Ile Glu Ser Ser Leu His Gln Pro Met Tyr Tyr Phe
 50 55 60
 Ile Ser Ile Leu Ala Val Asn Asp Leu Gly Met Ser Leu Ser Thr Leu
 65 70 75 80
 Pro Thr Met Leu Ala Val Leu Trp Leu Asp Ala Pro Glu Ile Gln Ala
 85 90 95
 Ser Ala Cys Tyr Ala Gln Leu Phe Phe Ile His Thr Phe Thr Phe Leu
 100 105 110
 Glu Ser Ser Val Leu Leu Ala Met Ala Phe Asp Arg Phe Val Ala Ile

115	120	125
Cys His Pro Leu His Tyr Pro Thr Ile Leu Thr Asn Ser Val Ile Gly		
130	135	140
Lys Ile Gly Leu Ala Cys Leu Leu Arg Ser Leu Gly Val Val Leu Pro		
145	150	155
Thr Pro Leu Leu Leu Arg His Tyr His Tyr Cys His Gly Asn Ala Leu		
	165	170
Ser His Ala Phe Cys Leu His Gln Asp Val Leu Arg Leu Ser Cys Thr		
	180	185
Asp Ala Arg Thr Asn Ser Ile Tyr Gly Leu Cys Val Val Ile Ala Thr		
	195	200
Leu Gly Val Asp Ser Ile Phe Ile Leu Leu Ser Tyr Val Leu Ile Leu		
	210	215
Asn Thr Val Leu Asp Ile Ala Ser Arg Glu Glu Gln Leu Lys Ala Leu		
225	230	235
Asn Thr Cys Val Ser His Ile Cys Val Val Leu Ile Phe Phe Val Pro		
	245	250
Val Ile Gly Val Ser Met Val His Arg Phe Gly Lys His Leu Ser Pro		
	260	265
Ile Val His Ile Leu Met Ala Asp Ile Tyr Leu Leu Leu Pro Pro Val		
	275	280
Leu Asn Pro Ile Val Tyr Ser Val Arg Thr Lys Gln Ile Arg Leu Gly		
	290	295
Ile Leu His Lys Phe Val Leu Arg Arg Arg Phe		
305	310	315

<210> 1198

<211> 289

<212> PRT

<213> Unknown (H38g115 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(289)

<223> Xaa = Any Amino Acid

<400> 1198

Phe His Gly Trp Ile Ser Met Pro Phe Cys Cys Ile Tyr Leu Met Pro		
1	5	10
Leu Leu Ser Asn Ala Thr Ile Leu Leu Thr Ile Trp Ser Asp Arg Thr		
	20	25
Leu Arg Asp Pro Met Phe Tyr Phe Leu Ala Ile Leu Ser Ala Ile Asp		
	35	40
Leu Ala Leu Ser Thr Ser Ser Val Pro Arg Met Leu Gly Ile Phe Trp		
	50	55
Phe Asp Ala His Lys Ile Gly Phe Gly Ala Trp Val Ala Gln Met Phe		
65	70	75
Leu Ile His Thr Phe Thr Gly Met Glu Ser Thr Val Leu Leu Ala Met		
	85	90
Ala Phe Asp Arg Tyr Val Ala Ile Cys Thr Ser Leu His Tyr Thr Ser		
	100	105
Thr Leu Thr Pro Arg Val Leu Ala Gly Ile Gly Val Ser Ile Ile Met		
	115	120
Arg Pro Val Leu Leu Met Leu Pro Ile Leu Tyr Leu Thr His Arg Leu		
	130	135
Pro Phe Cys Glu Ala Arg Ile Ile Ala His Ser Tyr Cys Glu His Met		
145	150	155
Gly Ile Ala Lys Leu Ala Cys Ala Ser Ile His Ile Asn Ala Ile Tyr		
	165	170
		175

Gly Leu Phe Val Ala Ser Phe Leu Asp Val Ala Leu Val Gly Ile Ser
 180 185 190
 Tyr Thr Tyr Ile Leu Arg Ala Val Phe His Leu Pro Ser Gln Asp Ala
 195 200 205
 Arg His Lys Ala Leu Arg Thr Cys Gly Ser His Val Gly Val Met Cys
 210 215 220
 Val Phe Tyr Thr Pro Ser Leu Phe Ser Phe Leu Thr Tyr Arg Phe Ala
 225 230 235 240
 Lys Lys Ile Pro Arg Tyr Val His Ile Leu Val Ala Asn Leu Tyr Val
 245 250 255
 Val Ile Pro Pro Ala Leu Asn Pro Ile Ile Tyr Gly Val Arg Thr Lys
 260 265 270
 Gln Ile His Glu His Val Val His Thr Phe Thr Ser Lys Xaa Gly Leu
 275 280 285
 Leu

<210> 1199
 <211> 174
 <212> PRT
 <213> Unknown (H38g116 protein)

<220>
 <223> Synthetic construct
 <221> VARIANT
 <222> (1)...(174)
 <223> Xaa = Any Amino Acid

<400> 1199
 Thr Cys Trp Val Leu Met Val Asn Val Val Asn Ala Tyr Thr Xaa Gly
 1 5 10 15
 Leu Ser Gly Ala Thr Phe Asn Thr Ile Cys Thr Phe Ala Arg Phe Phe
 20 25 30
 Cys Asp Asp Asn Xaa Ile Lys Phe Cys His Ile Leu Pro Leu Leu Lys
 35 40 45
 Leu Ile Xaa Asn Thr Ser Gly Asn Ser Lys Ile Ile Ile Val Ile Phe
 50 55 60
 Asp Ser Phe Leu Ile Ile Ala Gly Thr Arg Val Ile Leu Ile Ser Tyr
 65 70 75 80
 Leu Leu Ile Ile Arg Ala Leu Arg Met Lys Ser Ser Ser Gly Lys Ala
 85 90 95
 Lys Xaa Phe Tyr Pro Ser Thr Cys Ala Ser His Leu Thr Ala Met Thr
 100 105 110
 Phe Leu Trp Asp Pro His Leu Gln Tyr Met Xaa Ser Thr Ser Asp Lys
 115 120 125
 Ser Leu Thr Glu Asp Lys Leu Ala Ser Val Thr Cys Thr Ile Phe Ile
 130 135 140
 Pro Met Leu Glu Leu Leu Ile Gln Ser Leu Lys Lys Asp Ile Gln Val
 145 150 155 160
 Ala Phe Lys Lys Ala Ile Gly Asn Phe Trp Val Phe Glu Arg
 165 170

<210> 1200
 <211> 318
 <212> PRT
 <213> Unknown (H38g117 protein)

<220>
 <223> Synthetic construct

<221> VARIANT

<222> (1)...(318)

<223> Xaa = Any Amino Acid

<400> 1200

```

Ile Ser Thr Met Ser Val Phe Lys Ser Ser Ala Xaa Asn Pro Arg Phe
 1           5           10           15
Leu Gln Thr Gly Leu Ser Gly Leu Glu Ser Arg Tyr Asp Leu Ile Ser
          20           25           30
Leu Pro Ile Phe Leu Val Tyr Ala Thr Ser Ile Ala Gly Asn Ile Ser
          35           40           45
Ile Leu Phe Ile Ile Arg Thr Glu Ser Ser Leu His Gln Pro Met Tyr
          50           55           60
Tyr Phe Leu Ser Met Leu Ala Phe Thr Asp Leu Gly Leu Ser Asn Thr
          65           70           75           80
Thr Leu Pro Thr Met Phe Ser Val Phe Trp Phe His Ala Arg Glu Ile
          85           90           95
Ser Phe Asn Ala Cys Leu Val Gln Met Tyr Phe Ile His Val Phe Ser
          100          105          110
Ile Ile Glu Ser Ala Val Leu Leu Ala Met Ala Phe Asp Cys Phe Ile
          115          120          125
Ala Ile Xaa Glu Pro Leu Arg Tyr Ala Ala Ile Leu Thr Asn Asp Val
          130          135          140
Ile Ile Gly Ile Gly Leu Ala Ile Ala Gly Arg Ala Leu Ala Leu Val
          145          150          155          160
Phe Pro Ala Ser Phe Leu Leu Lys Arg Leu Gln Tyr His Asp Val Asn
          165          170          175
Ile Leu Ser Tyr Leu Phe Cys Leu His Gln Asp Leu Ile Lys Thr Thr
          180          185          190
Val Ser Asn Cys Arg Val Ser Ser Ile Tyr Gly Leu Met Val Val Ile
          195          200          205
Cys Ser Met Gly Leu Asp Ser Val Leu Leu Leu Leu Ser Tyr Val Leu
          210          215          220
Ile Leu Gly Thr Ala Leu Ser Ile Ala Ser Lys Ala Glu Arg Val Arg
          225          230          235          240
Ala Leu Asn Thr Cys Ile Ser His Ile Cys Ala Val Leu Thr Phe Tyr
          245          250          255
Thr Pro Met Ile Gly Leu Ser Met Ile His Arg Tyr Gly Gln Asn Ala
          260          265          270
Pro His Ile Val His Val Leu Met Ala Asn Val Tyr Leu Met Gly Pro
          275          280          285
Pro Leu Met Asn Pro Val Phe Tyr Ser Val Lys Thr Arg Gln Ile Arg
          290          295          300
Asp Arg Ile Phe Gln Ile Lys Phe Arg Asn Met Lys Cys Arg
          305          310          315

```

<210> 1201

<211> 315

<212> PRT

<213> Unknown (H38g118 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(315)

<223> Xaa = Any Amino Acid

<400> 1201

```

Met Glu Glu Glu Asn Ala Thr Leu Leu Thr Glu Phe Val Leu Thr Gly
 1           5           10           15

```

Phe Leu Cys Gln Gln Gly Phe Leu Trp Glu Ile Pro Leu Phe Leu Ala
 20 25 30
 Phe Leu Val Ile Asp Leu Ile Thr Ile Met Gly Asn Leu Gly Leu Ile
 35 40 45
 Phe Leu Ile Trp Lys Asp Pro His Leu His Ile Ser Met Tyr Leu Phe
 50 55 60
 Leu Gly Ser Leu Ala Phe Val Asp Thr Trp Leu Ser Ser Thr Val Thr
 65 70 75 80
 Pro Lys Met Leu Ile Asn Phe Leu Ala Lys Ser Lys Met Ile Ser Leu
 85 90 95
 Ser Glu Cys Met Val Gln Phe Phe Ser Leu Ala Ile Ser Val Thr Thr
 100 105 110
 Glu Cys Phe Ile Ser Ala Ser Met Ala Tyr Asp Arg Tyr Ala Asp Ile
 115 120 125
 Cys Lys Pro Leu Leu Tyr Pro Val Ile Met Thr Asn Glu Leu Cys Ile
 130 135 140
 Trp Leu Phe Val Leu Ser Phe Leu Gly Gly Leu Phe His Ala Leu Ile
 145 150 155 160
 His Glu Gly Phe Leu Phe Arg Leu Thr Phe Cys Asn Ser Asn Met Ile
 165 170 175
 Gln His Phe Tyr Cys Asp Ile Ile Pro Leu Leu Lys Ile Ser Cys Thr
 180 185 190
 Asp Ser Cys Ile Asn Phe Leu Met Phe Phe Ile Phe Ser Gly Ser Ile
 195 200 205
 Gln Val Leu Thr Ile Gly Ile Val Phe Val Ser Tyr Met Phe Val Leu
 210 215 220
 Phe Thr Ile Leu Lys Lys Lys Ser Asn Lys Gly Ile Arg Glu Ala Phe
 225 230 235 240
 Ser Thr Cys Gly Ala His Tyr Ile Pro Leu Ser Leu Cys Tyr Gly Leu
 245 250 255
 Leu Leu Phe Met Tyr Val Gly Pro Ala Ala Pro Gln Ala Asp Asn Gln
 260 265 270
 Asp Met Met Glu Tyr Leu Phe Tyr Pro Ile Ile Val Arg Leu Leu Asn
 275 280 285
 Pro Tyr Tyr Tyr Ser Leu Arg Asn Lys Gln Val Ile Gly Ser Leu Thr
 290 295 300
 Lys Met Leu Lys Xaa Asn Ile Cys Ile Ala Tyr
 305 310 315

<210> 1202

<211> 313

<212> PRT

<213> Unknown (H38g119 protein)

<220>

<223> Synthetic construct

<400> 1202

Met Ser Ile Ile Asn Thr Ser Tyr Val Glu Ile Thr Thr Phe Phe Leu
 1 5 10 15
 Val Gly Met Pro Gly Leu Glu Tyr Ala His Ile Trp Ile Ser Ile Pro
 20 25 30
 Ile Cys Ser Met Tyr Leu Ile Ala Ile Leu Gly Asn Gly Thr Ile Leu
 35 40 45
 Phe Ile Ile Lys Thr Glu Pro Ser Leu His Gly Pro Met Tyr Tyr Phe
 50 55 60
 Leu Ser Met Leu Ala Met Ser Asp Leu Gly Leu Ser Leu Ser Ser Leu
 65 70 75 80
 Pro Thr Val Leu Ser Ile Phe Leu Phe Asn Ala Pro Glu Thr Ser Ser
 85 90 95
 Ser Ala Cys Phe Ala Gln Glu Phe Phe Ile His Gly Phe Ser Val Leu

```

      100      105      110
Glu Ser Ser Val Leu Leu Ile Met Ser Phe Asp Arg Phe Leu Ala Ile
      115      120      125
His Asn Pro Leu Arg Tyr Thr Ser Ile Leu Thr Thr Val Arg Val Ala
      130      135      140
Gln Ile Gly Ile Val Phe Ser Phe Lys Ser Met Leu Leu Val Leu Pro
      145      150      155      160
Phe Pro Phe Thr Leu Arg Ser Leu Arg Tyr Cys Lys Lys Asn Gln Leu
      165      170      175
Ser His Ser Tyr Cys Leu His Gln Asp Val Met Lys Leu Ala Cys Ser
      180      185      190
Asp Asn Arg Ile Asp Val Ile Tyr Gly Phe Phe Gly Ala Leu Cys Leu
      195      200      205
Met Val Asp Phe Ile Leu Ile Ala Val Ser Tyr Thr Leu Ile Leu Lys
      210      215      220
Thr Val Pro Gly Ile Ala Ser Lys Lys Glu Glu Leu Lys Ala Leu Asn
      225      230      235      240
Thr Cys Val Ser His Ile Cys Ala Val Ile Ile Phe Tyr Leu Pro Ile
      245      250      255
Ile Asn Leu Ala Val Val His Arg Phe Ala Gly His Val Ser Pro Leu
      260      265      270
Ile Asn Val Leu Met Ala Asn Val Leu Leu Leu Val Pro Pro Leu Met
      275      280      285
Lys Pro Ile Val Tyr Cys Val Lys Thr Lys Gln Ile Arg Val Arg Val
      290      295      300
Val Ala Lys Leu Cys Gln Trp Lys Ile
      305      310

```

<210> 1203

<211> 314

<212> PRT

<213> Unknown (H38g120 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(314)

<223> Xaa = Any Amino Acid

<400> 1203

```

Met Glu Glu Lys Asn Ala Thr Leu Leu Thr Glu Phe Val Leu Thr Leu
  1      5      10      15
Phe Leu Tyr Gln Pro His Trp Lys Ile Pro Leu Phe Leu Ala Phe Leu
  20      25      30
Val Ile Tyr Leu Ile Thr Ile Phe Gly Asn Leu Gly Leu Ile Ala Val
  35      40      45
Val Trp Lys Asp Pro His Leu His Ile Pro Ile Tyr Leu Phe Leu Glu
  50      55      60
Asn Leu Ala Phe Val Asp Asp Leu Leu Ser Ser Thr Val Thr Leu Lys
  65      70      75      80
Met Leu Ile Asn Phe Phe Thr Lys Ser Lys Leu Ile Ser Leu Glu Cys
  85      90      95
Trp Ile His Phe Phe Ser Phe Ala Ile Gly Val Thr Thr Glu Cys Phe
  100      105      110
Ile Leu Ala Thr Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro
  115      120      125
Leu Leu Tyr Pro Val Ile Met Thr Asn Gly Leu Cys Ile Trp Leu Leu
  130      135      140
Ile Leu Ser Phe Leu Gly Gly Leu Leu His Ala Leu Ile His Glu Ala
  145      150      155      160

```

Phe Ser Tyr Arg Leu Thr Phe Cys Asn Ser Asn Thr Ile His His Phe
 165 170 175
 Xaa Cys Asp Ile Ile Pro Leu Leu Lys Ile Phe Cys Thr Asp Ser Ser
 180 185 190
 Ile Asn Phe Pro Met Val Phe Ile Phe Ser Cys Ser Ile Gln Val Phe
 195 200 205
 Thr Ile Gly Thr Val Leu Val Ser Tyr Thr Phe Val Leu Ser Thr Ile
 210 215 220
 Leu Lys Lys Lys Ser Val Lys Gly Ile Arg Lys Asp Phe Ser Thr Cys
 225 230 235 240
 Gly Ala His Ile Leu Pro Val Ser Leu Tyr Tyr Gly Pro Leu Ala Phe
 245 250 255
 Met Tyr Val Gly Ser Ala Ser Gln Arg Ala Asp Asp Gln Asp Met Met
 260 265 270
 Glu Ser Leu Phe Tyr Thr Val Ile Val Pro Leu Leu Asn Pro Met Ile
 275 280 285
 Tyr Ser Leu Arg Asn Lys Gln Val Ile Asp Ser Phe Thr Lys Met Phe
 290 295 300
 Lys Gly Asn Asn Val Xaa Ile Ser Tyr Ser
 305 310

<210> 1204

<211> 171

<212> PRT

<213> Unknown (H38g121 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(171)

<223> Xaa = Any Amino Acid

<400> 1204

Cys Xaa Val Gln Val Ser Xaa Val Ala Glu Lys Tyr Xaa Xaa Ile Leu
 1 5 10 15
 Phe Val Ala Leu Phe Asn Lys Thr Lys Ser Ile Cys Gln Pro Gln Asn
 20 25 30
 Ile Ala Thr Pro Arg Pro Trp Ala Phe Pro Gln His Ser Phe Thr Ser
 35 40 45
 Thr Ser Cys Phe Gly Gly Thr Ser Thr Gly Leu Ser Xaa Ala Val Lys
 50 55 60
 Ser Pro Ile Ser Ser Val Cys Pro Leu Leu Gln Leu Leu Leu Gln Tyr
 65 70 75 80
 Pro Cys Asn Asn Ile Thr Cys Leu Xaa Asn Ala Ala Asp Arg Glu Phe
 85 90 95
 Leu Ser Phe Xaa Asp Pro Leu Leu Ala Val Gly Ser Phe Thr Ile Ser
 100 105 110
 Ser Cys Leu Leu Met Leu Lys Leu Ile Ser Phe Ser Ser Ser Arg Ile
 115 120 125
 Ile Ala Ser Leu Leu Ser Arg Cys Pro Thr Glu Ser His Arg Ser Pro
 130 135 140
 Phe Xaa Tyr Ser Phe Cys His Leu Phe Cys Leu Phe Phe Phe Met Thr
 145 150 155 160
 Glu Asn Pro Trp Xaa Tyr Leu Xaa Phe Pro Ser
 165 170

<210> 1205

<211> 308

<212> PRT

<213> Unknown (H38g122 protein)

<220>

<223> Synthetic construct

<400> 1205

```

Met Asn Thr Thr Leu Phe His Pro Tyr Ser Phe Leu Leu Leu Gly Ile
 1           5           10           15
Pro Gly Leu Glu Ser Met His Leu Trp Val Gly Phe Pro Phe Phe Ala
          20           25           30
Val Phe Leu Thr Ala Val Leu Gly Asn Ile Thr Ile Leu Phe Val Ile
          35           40           45
Gln Thr Asp Ser Ser Leu His His Pro Met Phe Tyr Phe Leu Ala Ile
          50           55           60
Leu Ser Ser Ile Asp Pro Gly Leu Ser Thr Ser Thr Ile Pro Lys Met
          65           70           75           80
Leu Gly Thr Phe Trp Phe Thr Leu Arg Glu Ile Ser Phe Glu Gly Cys
          85           90           95
Leu Thr Gln Met Phe Phe Ile His Leu Cys Thr Gly Met Glu Ser Ala
          100          105          110
Val Leu Val Ala Met Ala Tyr Asp Cys Tyr Val Ala Ile Cys Asp Pro
          115          120          125
Leu Cys Tyr Thr Leu Val Leu Thr Asn Lys Val Val Ser Val Met Ala
          130          135          140
Leu Ala Ile Phe Leu Arg Pro Leu Val Phe Val Ile Pro Phe Val Leu
          145          150          155          160
Phe Ile Leu Arg Leu Pro Phe Cys Gly His Gln Ile Ile Pro His Thr
          165          170          175
Tyr Gly Glu His Met Gly Ile Ala Arg Leu Ser Cys Ala Ser Ile Arg
          180          185          190
Val Asn Ile Ile Tyr Gly Leu Cys Ala Ile Ser Ile Leu Val Phe Asp
          195          200          205
Ile Ile Ala Ile Val Ile Ser Tyr Val Gln Ile Leu Cys Ala Val Phe
          210          215          220
Leu Leu Ser Ser His Asp Ala Arg Leu Lys Ala Phe Ser Thr Cys Gly
          225          230          235          240
Ser His Val Cys Val Met Leu Thr Phe Tyr Met Pro Ala Phe Phe Ser
          245          250          255
Phe Met Thr His Arg Phe Gly Arg Asn Ile Pro His Phe Ile His Ile
          260          265          270
Leu Leu Ala Asn Phe Tyr Val Val Ile Pro Pro Ala Leu Asn Ser Val
          275          280          285
Ile Tyr Gly Val Arg Thr Lys Gln Ile Arg Ala Gln Val Leu Lys Met
          290          295          300
Phe Phe Asn Lys
          305

```

<210> 1206

<211> 309

<212> PRT

<213> Unknown (H38g123 protein)

<220>

<223> Synthetic construct

<400> 1206

```

Met Glu Glu Glu Asn Ala Thr Leu Leu Thr Glu Phe Val Leu Thr Gly
 1           5           10           15
Phe Leu His Gln Pro Asp Cys Lys Ile Pro Leu Phe Leu Ala Phe Leu
          20           25           30
Val Ile Tyr Leu Ile Thr Ile Met Gly Asn Leu Gly Leu Ile Val Leu
          35           40           45

```

```

      100      105      110
Thr Val Met Ala Tyr Asp Cys Tyr Val Val Ile Cys Lys Pro Leu Arg
      115      120      125
Tyr Thr Thr Ile Met Lys Gln His Val Cys Ser Leu Leu Val Gly Val
      130      135      140
Ser Arg Val Gly Gly Phe Leu His Ala Thr Ile Gln Ile Leu Phe Ile
      145      150      155      160
Phe Gln Leu Pro Phe Cys Ser Ser Asn Val Ile Asp His Phe Ile Cys
      165      170      175
Asp Leu Asn Pro Leu Leu Asn Leu Ala Cys Thr Asn Thr His Thr Leu
      180      185      190
Gly Leu Phe Val Ala Ala Asn Ser Gly Phe Ile Cys Leu Leu Asn Phe
      195      200      205
Leu Leu Leu Leu Val Ser Tyr Val Val Ile Leu Tyr Ser Leu Arg Thr
      210      215      220
His Ser Leu Glu Ala Arg His Lys Gly Leu Ser Thr Cys Val Ser His
      225      230      235      240
Asn Thr Val Val Ile Leu Phe Phe Ile Pro Cys Ile Phe Val Tyr Met
      245      250      255
Arg Pro Pro Ala Thr Leu Pro Ile Asp Lys Ala Val Ala Val Phe Tyr
      260      265      270
Thr Met Ile Thr Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn
      275      280      285
Ala Gln Met Lys Asn Ala Ile Arg Lys Leu Cys Ser Arg Lys Ala Ile
      290      295      300
Ser Ser Val Lys
305

```

<210> 1208

<211> 321

<212> PRT

<213> Unknown (H38g125 protein)

<220>

<223> Synthetic construct

<400> 1208

```

Met Phe Leu Pro Asn Asp Thr Gln Phe His Pro Ser Ser Phe Leu Leu
  1      5      10
Leu Gly Ile Pro Gly Leu Glu Thr Leu His Ile Trp Ile Gly Phe Pro
      20      25      30
Phe Cys Ala Val Tyr Met Ile Ala Leu Ile Gly Asn Phe Thr Ile Leu
      35      40      45
Leu Val Ile Lys Thr Asp Ser Ser Leu His Gln Pro Met Phe Tyr Phe
      50      55      60
Leu Ala Met Leu Ala Thr Thr Asp Val Gly Leu Ser Thr Ala Thr Ile
      65      70      75      80
Pro Lys Met Leu Gly Ile Phe Trp Ile Asn Leu Arg Gly Ile Ile Phe
      85      90      95
Glu Ala Cys Leu Thr Gln Met Phe Phe Ile His Asn Phe Thr Leu Met
      100      105      110
Glu Ser Ala Val Leu Val Ala Met Ala Tyr Asp Ser Tyr Val Ala Ile
      115      120      125
Cys Asn Pro Leu Gln Tyr Ser Ala Ile Leu Thr Asn Lys Val Val Ser
      130      135      140
Val Ile Gly Leu Gly Val Phe Val Arg Ala Leu Ile Phe Val Ile Pro
      145      150      155      160
Ser Ile Leu Leu Ile Leu Arg Leu Pro Phe Cys Gly Asn His Val Ile
      165      170      175
Pro His Thr Tyr Cys Glu His Met Gly Leu Ala His Leu Ser Cys Ala
      180      185      190

```

Ser Ile Lys Ile Asn Ile Ile Tyr Gly Leu Cys Ala Ile Cys Asn Leu
 195 200 205
 Val Phe Asp Ile Thr Val Ile Ala Leu Ser Tyr Val His Ile Leu Cys
 210 215 220
 Ala Val Phe Arg Leu Pro Thr His Glu Pro Arg Leu Lys Ser Leu Ser
 225 230 235 240
 Thr Cys Gly Ser His Val Cys Val Ile Leu Ala Phe Tyr Thr Pro Ala
 245 250 255
 Leu Phe Ser Phe Met Thr His Cys Phe Gly Arg Asn Val Pro Arg Tyr
 260 265 270
 Ile His Ile Leu Leu Ala Asn Leu Tyr Val Val Val Pro Pro Met Leu
 275 280 285
 Asn Pro Val Ile Tyr Gly Val Arg Thr Lys Gln Ile Tyr Lys Cys Val
 290 295 300
 Lys Lys Ile Leu Leu Gln Glu Gln Gly Met Glu Lys Glu Glu Tyr Leu
 305 310 315 320
 Ile

<210> 1209

<211> 298

<212> PRT

<213> Unknown (H38g126 protein)

<220>

<223> Synthetic construct

<400> 1209

Met Arg Asn His Thr Met Val Thr Glu Phe Ile Leu Leu Gly Ile Pro
 1 5 10 15
 Glu Thr Glu Gly Leu Glu Thr Ala Leu Phe Leu Phe Ser Ser Phe
 20 25 30
 Tyr Leu Cys Thr Leu Leu Gly Asn Val Leu Ile Leu Thr Ala Ile Ile
 35 40 45
 Ser Ser Thr Arg Leu His Thr Pro Met Tyr Phe Phe Leu Gly Asn Leu
 50 55 60
 Ser Ile Phe Asp Leu Gly Phe Ser Ser Thr Thr Val Pro Lys Met Leu
 65 70 75 80
 Phe Tyr Leu Ser Gly Asn Ser His Ala Ile Ser Tyr Ala Gly Cys Val
 85 90 95
 Ser Gln Leu Phe Phe Tyr His Phe Leu Gly Cys Thr Glu Cys Phe Leu
 100 105 110
 Tyr Thr Val Met Ala Cys Asp Arg Phe Val Ala Ile Cys Phe Pro Leu
 115 120 125
 Arg Tyr Thr Val Ile Met Asn His Arg Val Cys Phe Met Leu Ala Thr
 130 135 140
 Gly Thr Trp Met Ile Gly Cys Val His Ala Met Ile Leu Thr Pro Leu
 145 150 155 160
 Thr Phe Gln Leu Pro Tyr Cys Gly Pro Asn Lys Val Gly Tyr Tyr Phe
 165 170 175
 Cys Asp Ile Pro Ala Val Leu Pro Leu Ala Cys Lys Asp Thr Ser Leu
 180 185 190
 Ala Gln Arg Val Gly Phe Thr Asn Val Gly Leu Leu Ser Leu Ile Cys
 195 200 205
 Phe Phe Leu Ile Leu Val Ser Tyr Thr Cys Ile Gly Ile Ser Ile Ser
 210 215 220
 Lys Ile Arg Ser Ala Glu Gly Arg Gln Arg Ala Phe Ser Thr Cys Ser
 225 230 235 240
 Ala His Leu Thr Ala Ile Leu Cys Ala Tyr Gly Pro Val Ile Val Ile
 245 250 255
 Tyr Leu Gln Pro Asn Pro Ser Ala Leu Leu Gly Ser Ile Ile Gln Ile

260 265 270
 Leu Asn Asn Leu Val Thr Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu
 275 280 285
 Arg Asn Lys Asp Val Lys Ser Asp Gln Pro
 290 295

<210> 1210
 <211> 324
 <212> PRT
 <213> Unknown (H38g127 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(324)
 <223> Xaa = Any Amino Acid

<400> 1210
 Met Glu Glu Glu Asn Thr Thr Leu Leu Thr Glu Phe Val Leu Thr Gly
 1 5 10 15
 Phe Leu Tyr Gln Pro Gln Trp Lys Ile Pro Leu Phe Leu Ala Phe Leu
 20 25 30
 Val Ile Xaa Leu Ile Thr Ile Met Gly Asn Leu Gly Leu Ile Val Leu
 35 40 45
 Ile Trp Lys Asp Pro His Leu His Ile Pro Met Tyr Leu Phe Arg Gly
 50 55 60
 Ser Leu Ala Phe Val Asp Ala Trp Leu Ser Ser Thr Val Thr Pro Lys
 65 70 75 80
 Met Leu Ile Asn Phe Leu Ala Lys Ser Lys Met Ile Ser Leu Ser Glu
 85 90 95
 Cys Met Val Gln Phe Phe Ser Phe Val Ile Ser Val Thr Thr Glu Cys
 100 105 110
 Phe Ile Ser Ala Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys
 115 120 125
 Ala Leu Leu Tyr Pro Val Ile Met Thr Asn Gly Leu Cys Ile Gln Leu
 130 135 140
 Leu Val Leu Ser Phe Ile Gly Gly Leu Leu His Ala Leu Ile His Glu
 145 150 155 160
 Ile Phe Leu Phe Arg Leu Thr Phe Cys Asn Ser Asn Ile Ile Gln His
 165 170 175
 Phe Tyr Cys Asp Ile Ile Pro Leu Leu Lys Ile Ser Cys Thr Asp Ser
 180 185 190
 Phe Ile Asn Phe Leu Met Val Phe Ile Phe Ala Asp Ser Ile Gln Val
 195 200 205
 Phe Thr Ile Gly Thr Ile Leu Ile Ser Tyr Thr Leu Val Leu Ile
 210 215 220
 Ile Leu Lys Asn Lys Ser Val Lys Gly Ile Gln Lys Ala Val Ser Thr
 225 230 235 240
 Cys Gly Ala His Leu Leu Ser Val Ser Leu Tyr Tyr Gly Pro Leu Val
 245 250 255
 Phe Met Tyr Val Gly Ser Ala Ser Pro Gln Ala Asp Asp Gln Asp Met
 260 265 270
 Met Glu Ser Leu Phe Tyr Thr Val Ile Val Pro Leu Leu Asn Ser Met
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Gln Val Ile Ala Ser Phe Thr Lys Met
 290 295 300
 Phe Lys Arg Asn Val Xaa Ile Ser Tyr Asn Leu Cys Ser Leu Phe Thr
 305 310 315 320
 Lys Ile Phe Pro

<210> 1211
 <211> 308
 <212> PRT
 <213> Unknown (H38g128 protein)

<220>
 <223> Synthetic construct

<400> 1211
 Met Met Ser Asn Gln Thr Leu Val Thr Glu Phe Ile Leu Gln Gly Phe
 1 5 10 15
 Ser Glu His Pro Glu Tyr Arg Val Phe Leu Phe Ser Cys Phe Leu Phe
 20 25 30
 Leu Tyr Ser Gly Ala Leu Thr Gly Asn Val Leu Ile Thr Leu Ala Ile
 35 40 45
 Thr Phe Asn Pro Gly Leu His Ala Pro Met Tyr Phe Phe Leu Leu Asn
 50 55 60
 Leu Ala Thr Met Asp Ile Ile Cys Thr Ser Ser Ile Met Pro Lys Ala
 65 70 75 80
 Leu Ala Ser Leu Val Ser Glu Glu Ser Ser Ile Ser Tyr Gly Gly Cys
 85 90 95
 Met Ala Gln Leu Tyr Phe Leu Thr Trp Ala Ala Ser Ser Glu Leu Leu
 100 105 110
 Leu Leu Thr Val Met Ala Tyr Asp Arg Tyr Ala Ala Ile Cys His Pro
 115 120 125
 Leu His Tyr Ser Ser Met Met Ser Lys Val Phe Cys Ser Gly Leu Ala
 130 135 140
 Thr Ala Val Trp Leu Leu Cys Ala Val Asn Thr Ala Ile His Thr Gly
 145 150 155 160
 Leu Met Leu Arg Leu Asp Phe Cys Gly Pro Asn Val Ile Ile His Phe
 165 170 175
 Phe Cys Glu Val Pro Pro Leu Leu Leu Leu Ser Cys Ser Ser Thr Tyr
 180 185 190
 Val Asn Gly Val Met Ile Val Leu Ala Asp Ala Phe Tyr Gly Ile Val
 195 200 205
 Asn Phe Leu Met Thr Ile Ala Ser Tyr Gly Phe Ile Val Ser Ser Ile
 210 215 220
 Leu Lys Val Lys Thr Ala Trp Gly Arg Gln Lys Ala Phe Ser Thr Cys
 225 230 235 240
 Ser Ser His Leu Thr Val Val Cys Met Tyr Tyr Thr Ala Val Phe Tyr
 245 250 255
 Ala Tyr Ile Ser Pro Val Ser Gly Tyr Ser Ala Gly Lys Ser Lys Leu
 260 265 270
 Ala Gly Leu Leu Tyr Thr Val Leu Ser Pro Thr Leu Asn Pro Leu Ile
 275 280 285
 Tyr Thr Leu Arg Asn Lys Glu Val Lys Ala Ala Leu Arg Lys Leu Phe
 290 295 300
 Pro Phe Phe Arg
 305

<210> 1212
 <211> 319
 <212> PRT
 <213> Unknown (H38g129 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(319)

<223> Xaa = Any Amino Acid

<400> 1212

```

Met Asp Asp Glu Asn Ala Thr Leu Leu Thr Glu Phe Val Leu Thr Gly
 1          5          10          15
Leu Thr Tyr Gln Ser Glu Trp Lys Ile Pro Leu Phe Leu Ala Phe Leu
          20          25          30
Val Ile Tyr Leu Ile Thr Ile Met Ala Asn Leu Gly Leu Ile Ala Val
          35          40          45
Ile Trp Lys Asp Ser His Leu His Ile Pro Met Tyr Leu Phe Leu Gly
          50          55          60
Ser Leu Ala Phe Val Asp Ala Trp Leu Ser Ser Ser Val Thr Pro Lys
65          70          75          80
Met Leu Ile Ser Phe Leu Ala Lys Ser Met Ile Ile Ser Val Ser Glu
          85          90          95
Cys Lys Ile Gln Phe Phe Ser Phe Gly Ile Ser Gly Thr Thr Glu Cys
          100          105          110
Phe Leu Leu Ala Thr Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys
          115          120          125
Pro Leu Leu Tyr Pro Val Ile Met Thr Asn Gly Leu Cys Ile Trp Leu
          130          135          140
Leu Val Leu Ser Phe Ile Gly Gly Phe Leu His Ala Leu Ile His Glu
145          150          155          160
Gly Ile Leu Phe Arg Leu Thr Phe Cys Asn Ser Asn Ile Ile His His
          165          170          175
Phe Tyr Cys Asp Ile Ile Pro Leu Leu Lys Ile Ser Cys Thr Asp Pro
          180          185          190
Ser Ile Asn Phe Leu Met Leu Phe Ile Leu Ser Gly Ser Ile Gln Val
          195          200          205
Phe Thr Ile Leu Thr Val Leu Val Ser Tyr Thr Phe Val Leu Phe Thr
          210          215          220
Ile Leu Lys Lys Lys Ser Ala Lys Asp Ile Arg Lys Ala Phe Ser Thr
225          230          235          240
Cys Gly Ala His Leu Leu Ser Val Ser Leu Tyr Tyr Gly Pro Leu Leu
          245          250          255
Phe Met Tyr Val His Pro Ala Ser Pro Gln Ala Asp Asp Gln Asp Met
          260          265          270
Val Glu Ser Leu Phe Tyr Thr Val Ile Ile Pro Phe Leu Asn Pro Ile
          275          280          285
Ile Tyr Ser Leu Arg Asn Lys Gln Val Ile Asp Ser Leu Thr Lys Thr
          290          295          300
Leu Lys Gly Asn Val Xaa Ile Ser Tyr Trp Asn Val Phe Ser Ile
305          310          315

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<210> 1213

<211> 311

<212> PRT

<213> Unknown (H38g130 protein)

<220>

<223> Synthetic construct

<400> 1213

```

Met Val Glu Glu Asn His Thr Met Lys Asn Glu Phe Ile Leu Thr Gly
 1          5          10          15
Phe Thr Asp His Pro Glu Leu Lys Thr Leu Leu Phe Val Val Phe Phe
          20          25          30
Ala Ile Tyr Leu Ile Thr Val Val Gly Asn Ile Ser Leu Val Ala Leu
          35          40          45
Ile Phe Thr His Arg Arg Leu His Thr Pro Met Tyr Ile Phe Leu Gly
50          55          60

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Asn Leu Ala Leu Val Asp Ser Cys Cys Ala Cys Ala Ile Thr Pro Lys
65              70              75              80
Met Leu Glu Asn Phe Phe Ser Glu Gly Lys Arg Ile Ser Leu Tyr Glu
            85              90              95
Cys Ala Val Gln Phe Tyr Phe Leu Cys Thr Val Glu Thr Ala Asp Cys
            100             105             110
Phe Leu Leu Ala Ala Val Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn
            115             120             125
Pro Leu Gln Tyr His Ile Met Met Ser Lys Lys Leu Cys Ile Gln Met
            130             135             140
Thr Thr Gly Ala Phe Ile Ala Gly Asn Leu His Ser Met Ile His Val
145              150              155              160
Gly Leu Val Phe Arg Leu Val Phe Cys Gly Leu Asn His Ile Asn His
            165              170              175
Phe Tyr Cys Asp Thr Leu Pro Leu Tyr Arg Leu Ser Cys Val Asp Pro
            180             185             190
Phe Ile Asn Glu Leu Val Leu Phe Ile Phe Ser Gly Ser Val Gln Val
            195             200             205
Phe Thr Ile Gly Ser Val Leu Ile Ser Tyr Leu Tyr Ile Leu Leu Thr
            210             215             220
Ile Phe Arg Met Lys Ser Lys Glu Gly Arg Ala Lys Ala Phe Ser Thr
225              230              235              240
Cys Ala Ser His Phe Ser Ser Val Ser Leu Phe Tyr Gly Ser Ile Phe
            245             250             255
Phe Leu Tyr Ile Arg Pro Asn Leu Leu Glu Glu Gly Gly Asn Asp Ile
            260             265             270
Pro Ala Ala Ile Leu Phe Thr Ile Val Val Pro Leu Leu Asn Pro Phe
            275             280             285
Ile Tyr Ser Leu Arg Asn Lys Glu Val Ile Ser Val Leu Arg Lys Ile
            290             295             300
Leu Leu Lys Ile Lys Ser Gln
305              310

```

<210> 1214

<211> 328

<212> PRT

<213> Unknown (H38g131 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(328)

<223> Xaa = Any Amino Acid

<400> 1214

```

Tyr Thr Asp Pro Gln Asn Leu Thr Asp Val Phe Ile Phe Leu Leu Leu
1              5              10              15
Glu Leu Ser Glu Asp Pro Ala Leu Gln Leu Val Val Thr Gly Leu Cys
            20              25              30
Leu Met Cys Leu Val Thr Val Leu Trp Asn Leu Leu Ser Ile Leu Ala
            35              40              45
Val Ser Pro Asp Ser His Leu His Thr Pro Met His Phe Phe Leu Cys
            50              55              60
Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro Lys
65              70              75              80
Met Ile Val Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala Gly
            85              90              95
Cys Leu Thr Gln Met Ser Leu Ser Ala Ile Phe Gly Gly Met Glu Glu
            100             105             110
Asn Met Leu Leu Ser Val Met Ala Tyr Asp Gln Phe Val Ala Ile Cys

```

```

      115      120      125
His Pro Leu Tyr His Ser Ala Ile Met Asn Pro Cys Phe Cys Gly Phe
 130      135      140
Leu Val Leu Leu Ser Phe Phe Ser Val Phe Xaa His Ser Gln Leu
 145      150      155      160
Gln Asn Leu Ile Ala Leu Gln Ile Thr Cys Ser Lys Asp Val Glu Ile
      165      170      175
Pro Asn Phe Phe Cys Asp Pro Ser Gln Leu Pro His Leu Ala Cys Cys
      180      185      190
Asp Thr Phe Thr Asn Asn Ile Ile Met Tyr Phe Pro Ala Ala Ile Phe
      195      200      205
Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser Tyr Tyr Lys Ile Val
      210      215      220
Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Ser Tyr Lys Ala Phe
 225      230      235      240
Ala Thr Cys Gly Ser His Leu Ser Val Val Cys Xaa Phe Tyr Gly Thr
      245      250      255
Gly Val Gly Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser Leu Arg Lys
      260      265      270
Arg Ala Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn
      275      280      285
Pro Leu Ile Tyr Ser Leu Arg Asn Arg Asp Ile Lys Gly Val Leu Trp
      290      295      300
Gln Pro Cys Ser Arg Thr Ala Ala Gln Ser Pro Ser Gln Tyr Leu His
 305      310      315      320
Leu Phe His Ser Phe Cys Arg Met
      325

```

<210> 1215

<211> 328

<212> PRT

<213> Unknown (H38g132 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(328)

<223> Xaa = Any Amino Acid

<400> 1215

```

Met Glu Pro Gln Phe Thr Thr Gln Gly Ser Met Phe Val Leu Leu Gly
 1      5      10      15
Xaa Ser Gln Thr Gln Glu Leu Gln Arg Val Met Phe Ile Leu Phe Leu
      20      25      30
Leu Val Tyr Val Thr Thr Ile Val Gly Asn Leu Leu Ile Met Val Thr
      35      40      45
Val Thr Phe Asp Cys Arg Leu His Pro Met Tyr Phe Leu Leu Arg Asn
      50      55      60
Leu Ala Leu Ile Asp Val Cys Tyr Ser Thr Val Thr Ser Pro Lys Met
 65      70      75      80
Leu Val Asp Phe Leu His Glu Thr Lys Thr Ile Ser Tyr Gln Gly Cys
      85      90      95
Met Ala Gln Ile Phe Phe Phe His Leu Gly Gly Gly Thr Val Phe
      100      105      110
Phe Leu Ser Val Met Ala Tyr Asp Arg Tyr Ile Ala Ile Ser Gln Pro
      115      120      125
Leu Arg Tyr Val Thr Ile Met Asn Thr Gln Leu Cys Val Gly Leu Val
      130      135      140
Val Ala Ala Trp Val Gly Phe Val His Ser Ile Val Gln Leu Ala
 145      150      155      160

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```

Val Ile Arg Pro Gln Pro Leu Cys Gly Pro Asn Ile Leu Asp Asn Phe
                165                      170                      175
Tyr Cys Asp Val Pro Gln Val Leu Arg Leu Ala Cys Thr Asp Thr Ser
                180                      185                      190
Leu Leu Glu Phe Leu Met Ile Ser Asn Ser Gly Leu Leu Val Ile Ile
                195                      200                      205
Trp Phe Leu Leu Ser Leu Met Ser Tyr Thr Val Ile Leu Val Met Leu
                210                      215                      220
Arg Ser His Ser Gly Lys Ala Arg Ser Lys Ala Ala Ser Thr Cys Thr
                225                      230                      235                      240
Thr His Ile Ile Val Val Ser Met Ile Phe Ile Pro Cys Ile Tyr Ile
                245                      250                      255
Tyr Thr Trp Pro Phe Thr Pro Phe Ile Met Asp Lys Ala Val Ser Ile
                260                      265                      270
Ser Tyr Thr Val Met Thr Pro Met Leu Asn Pro Met Ile Tyr Thr Leu
                275                      280                      285
Arg Asn Gln Asp Met Lys Ala Ala Met Arg Arg Leu Gly Lys Cys Leu
                290                      295                      300
Val Ile Cys Arg Glu Leu Thr Leu Ser Lys Leu Thr Leu Asn Asp Lys
                305                      310                      315                      320
Leu Leu Trp Ile Cys Tyr Phe Pro
                325

```

<210> 1216

<211> 129

<212> PRT

<213> Unknown (H38g133 protein)

<220>

<223> Synthetic construct

<400> 1216

```

Met Gln Gly Glu Asn Phe Thr Ile Trp Ser Ile Phe Phe Leu Glu Gly
1          5          10          15
Phe Ser Gln Tyr Pro Gly Leu Glu Val Val Leu Phe Val Phe Ser Leu
20          25          30
Val Met Tyr Leu Thr Thr Leu Leu Gly Asn Ser Thr Leu Ile Leu Ile
35          40          45
Thr Ile Leu Asp Ser Arg Leu Lys Thr Pro Met Tyr Leu Phe Leu Gly
50          55          60
Asn Leu Ser Phe Met Asp Ile Cys Tyr Thr Ser Ala Ser Val Pro Thr
65          70          75          80
Leu Leu Val Asn Leu Leu Ser Ser Gln Lys Thr Ile Ile Phe Ser Gly
85          90          95
Cys Ala Val Gln Met Tyr Leu Ser Leu Ala Met Gly Ser Thr Glu Cys
100         105         110
Val Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn
115         120         125
Pro

```

<210> 1217

<211> 335

<212> PRT

<213> Unknown (H38g134 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(335)

<223> Xaa = Any Amino Acid

<400> 1217

```

Ser Thr Asp Pro Gln Asn Leu Thr Asp Val Ser Ile Phe Leu Leu Leu
 1          5          10          15
Gly Thr Ser Glu Asp Pro Glu Arg Gln Leu Val Leu Ala Gly Leu Phe
          20          25          30
Leu Ser Met Cys Leu Val Thr Val Leu Gly Asn Leu Ile Ile Ile Leu
          35          40          45
Asp Val Ser Pro Asp Ser His Leu Pro Thr Pro Met Tyr Phe Phe Leu
          50          55          60
Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro
65          70          75          80
Lys Met Ile Val Asp Ile Gln Ser His Ser Arg Val Ile Phe Tyr Ala
          85          90          95
Gly Cys Leu Thr Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu
          100          105          110
Glu Asn Thr Leu Leu Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile
          115          120          125
Cys His Pro Leu Cys His Ser Ala Ser Met Asn Pro Cys Phe Cys Gly
          130          135          140
Phe Leu Val Leu Leu Ser Phe Phe Phe Leu Ser Leu Leu Asp Thr Gln
145          150          155          160
Leu His Asn Leu Ile Ala Leu Gln Met Thr Cys Phe Lys Asp Val Asp
          165          170          175
Ile Pro Asn Phe Phe Trp Asp Pro Ser Gln Leu Pro His Leu Ala Cys
          180          185          190
Cys Asp Thr Phe Thr Asn Asn Ile Ile Met Tyr Phe Pro Ala Ala Ile
          195          200          205
Phe Gly Phe Leu Gln Ile Ser Gly Thr Leu Phe Ser Tyr Tyr Lys Ile
210          215          220
Val Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Asn Tyr Lys Ala
225          230          235          240
Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Cys Xaa Phe Tyr Gly
          245          250          255
Thr Gly Val Gly Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser Pro Arg
          260          265          270
Lys Gly Ala Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu
          275          280          285
Asn Pro Phe Ile Tyr Ser Leu Arg Asn Gly Asp Ile Lys Ser Val Leu
290          295          300
Arg Arg Pro Gln Gly Ser Lys Val Xaa Tyr Gln Tyr Leu Leu Ile Cys
305          310          315          320
Ser Ile Pro Phe Val Gly Trp Val Lys Lys Gly Ser Lys Val Lys
          325          330          335

```

<210> 1218

<211> 319

<212> PRT

<213> Unknown (H38g135 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(319)

<223> Xaa = Any Amino Acid

<400> 1218

```

Met Lys Asn Lys Arg Asn Val Thr Glu Phe Val Leu Thr Gly Leu Thr
 1          5          10          15

```

Gln Asn Pro Lys Met Glu Lys Val Met Phe Ala Val Phe Leu Val Leu
 20 25 30
 Tyr Met Ile Thr Leu Ser Gly Asn Leu Leu Leu Val Val Thr Ile Thr
 35 40 45
 Thr Ser Gln Ala Leu Ser Ser Pro Met Tyr Phe Phe Leu Ser His Leu
 50 55 60
 Ser Leu Ile Asp Thr Val Tyr Ser Ser Ser Ser Ala Pro Lys Leu Ile
 65 70 75 80
 Val Asp Ser Leu His Glu Lys Lys Ile Ile Ser Phe Asn Gly Cys Met
 85 90 95
 Ala Gln Ala Tyr Glu Glu His Ile Phe Gly Ala Thr Glu Ile Ile Leu
 100 105 110
 Leu Thr Val Met Ala Cys Asp Asn Tyr Val Ala Ile Cys Lys Pro Leu
 115 120 125
 His Tyr Thr Thr Ile Met Ser His Ser Leu Cys Ile Leu Leu Val Val
 130 135 140
 Val Ala Trp Ile Gly Gly Phe Leu His Ala Asn Ile Gln Ile Leu Phe
 145 150 155 160
 Thr Val Trp Leu Pro Phe Cys Gly Pro Asn Val Ile Asp His Phe Met
 165 170 175
 Cys Asp Leu Cys Pro Leu Leu Lys Leu Val Cys Leu Asp Thr His Thr
 180 185 190
 Leu Gly Leu Phe Val Ala Ala Asn Ser Gly Phe Ile Cys Leu Leu Asn
 195 200 205
 Phe Leu Leu Xaa Val Val Ser Tyr Val Ile Ile Leu Arg Cys Leu Lys
 210 215 220
 Asn Tyr Ile Leu Glu Gly Arg Gly Lys Ala Leu Ser Thr Cys Ile Ser
 225 230 235 240
 His Ile Ile Ile Val Val Leu Phe Phe Val Pro Cys Ile Phe Val Tyr
 245 250 255
 Leu His Pro Val Thr Thr Leu Pro Ile Asp Lys Ala Ala Ala Val Phe
 260 265 270
 Tyr Thr Met Val Val Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg
 275 280 285
 Asn Ala Glu Val Lys Ser Ala Ile Arg Lys Leu Trp Arg Lys Lys Val
 290 295 300
 Ile Ser Asp Asn Asp Xaa Ile Arg Pro Leu Ser Thr His His Arg
 305 310 315

<210> 1219

<211> 312

<212> PRT

<213> Unknown (H38g136 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(312)

<223> Xaa = Any Amino Acid

<400> 1219

Met Glu Ile Gly Asn His Thr Thr Val Thr Glu Phe Ile Ile Leu Gly
 1 5 10 15
 Leu Thr Glu Asp Pro Thr Leu Cys Asp Ile Phe Phe Val Ile Phe Leu
 20 25 30
 Gly Ile Tyr Ile Val Thr Leu Ile Gly Asn Ile Ser Ile Ile Lys Lys
 35 40 45
 Arg Ser Gln Leu His Thr Pro Met Tyr Leu Phe Leu Ser His Leu Ala
 50 55 60
 Phe Val Asp Ile Gly Leu Ala Thr Val Val Thr Pro Ile Met Leu Met

```

65          70          75          80
Gly Phe Leu Arg Arg Gly Thr Ala Leu Pro Val Thr Ser Cys Glu Ala
      85          90          95
Gln Leu Cys Ser Val Val Met Phe Gly Thr Ser Glu Cys Phe Leu Leu
      100         105         110
Ala Thr Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Ser Pro Leu Val
      115         120         125
Asn Ser Thr His Leu Ser Pro Ile Ile Cys Ile Leu Leu Val Gly Val
      130         135         140
Cys Tyr Leu Gly Gly Trp Val Asn Ala Ser Thr Phe Thr Ser Cys Leu
145         150         155         160
Leu Ser Leu Ser Phe Cys Gly Pro Asn Gln Ile Asp His Phe Phe Cys
      165         170         175
Asp Phe Ser Pro Leu Leu Lys Leu Ser Cys Ser Asn Ile Ser Ile Pro
      180         185         190
Glu Ile Ile Pro Ser Ile Ser Ser Gly Ser Ile Ile Val Val Thr Val
      195         200         205
Phe Ala Ile Ala Ile Ser Tyr Ile Tyr Ile Leu Ile Thr Ile Leu Lys
      210         215         220
Met Arg Ser Ala Glu Gly Arg His Lys Ala Phe Ser Thr Cys Thr Ser
225         230         235         240
His Leu Ala Ala Val Thr Leu Tyr Tyr Gly Thr Ile Thr Phe Ile Tyr
      245         250         255
Val Met Pro Lys Ser Ser Tyr Ser Thr Ser Gln Asn Arg Leu Ile Ser
      260         265         270
Leu Ser Tyr Thr Val Val Ile Pro Ile Leu Asn Pro Phe Ile Tyr Ser
      275         280         285
Leu Arg Asn Arg Asp Val Lys Glu Ala Leu Arg Lys Ala Thr Val Arg
      290         295         300
Ile Tyr Ser Xaa Asp Gln Phe Val
305          310

```

<210> 1220

<211> 324

<212> PRT

<213> Unknown (H38g137 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(324)

<223> Xaa = Any Amino Acid

<400> 1220

```

His Thr Glu Pro Arg Asn Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu
 1          5          10          15
Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Leu Leu Ser
      20         25         30
Leu Ser Leu Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ser
      35         40         45
Ile Pro Ala Val Ser Ser Asp Ser Pro Leu His Thr Pro Thr Tyr Phe
      50         55         60
Phe Leu Ser Ile Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Thr
65         70         75         80
Val Ser Lys Thr Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser
      85         90         95
His Ala Gly Cys Leu Thr Gln Met Ser Phe Leu Val Leu Phe Ala Cys
      100        105        110
Ile Glu Gly Met Leu Leu Thr Val Met Ala Tyr Asp Cys Phe Val Gly
      115        120        125

```

```

Ile Cys Arg Pro Leu His Tyr Pro Val Ile Val Asn Pro His Leu Cys
 130                      135                      140
Val Phe Phe Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln
145                      150                      155                      160
Leu His Ser Trp Ile Val Leu Gln Phe Thr Ile Ile Lys Asn Val Glu
                      165                      170                      175
Ile Ser Asn Phe Val Cys Asp Pro Ser Gln Leu Leu Lys Leu Ala Cys
                      180                      185                      190
Ser Asp Ser Val Ile Asn Ser Ile Phe Ile Tyr Phe Gly Ser Thr Met
                      195                      200                      205
Phe Gly Phe Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys Ile
210                      215                      220
Val Pro Ser Ile Leu Arg Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala
225                      230                      235                      240
Phe Ser Thr Tyr Gly Ser His Leu Ala Val Phe Cys Xaa Phe Asp Gly
                      245                      250                      255
Thr Gly Ile Gly Val Tyr Leu Thr Ser Ala Val Ala Pro Pro Leu Arg
260                      265                      270
Asn Gly Val Val Val Ser Val Met Xaa Ala Val Val Thr Pro Met Leu
275                      280                      285
Asn Leu Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu
290                      295                      300
Arg Arg Leu Arg Ser Arg Thr Val Glu Ser Pro Xaa Ser Val Pro Ser
305                      310                      315                      320
Phe Phe Trp Cys

```

<210> 1221

<211> 318

<212> PRT

<213> Unknown (H38g138 protein)

<220>

<223> Synthetic construct

<400> 1221

```

Met Ile Gln Pro Met Ala Ser Pro Ser Asn Ser Ser Thr Val Pro Val
 1                      5                      10                      15
Ser Glu Phe Leu Leu Thr Cys Phe Pro Asn Phe Gln Ser Trp Gln His
20                      25                      30
Trp Leu Ser Leu Pro Leu Ser Leu Leu Phe Leu Leu Ala Met Gly Ala
35                      40                      45
Asn Thr Thr Leu Leu Ile Thr Ile Gln Leu Glu Ala Ser Leu His Gln
50                      55                      60
Pro Leu Tyr Tyr Leu Leu Ser Leu Leu Ser Leu Asp Ile Val Leu
65                      70                      75                      80
Cys Leu Thr Val Ile Pro Lys Val Leu Ala Ile Phe Trp Tyr Asp Leu
85                      90                      95
Arg Ser Ile Ser Phe Pro Ala Cys Phe Leu Gln Met Phe Ile Met Asn
100                      105                      110
Ser Phe Leu Pro Met Glu Ser Cys Thr Phe Met Val Met Ala Tyr Asp
115                      120                      125
Arg Tyr Val Ala Ile Cys His Pro Leu Arg Tyr Pro Ser Ile Ile Thr
130                      135                      140
Asn Gln Phe Val Ala Lys Ala Ser Val Phe Ile Val Val Arg Asn Ala
145                      150                      155                      160
Leu Leu Thr Ala Pro Ile Pro Ile Leu Thr Ser Leu Leu His Tyr Cys
165                      170                      175
Gly Glu Asn Val Ile Glu Asn Cys Ile Cys Ala Asn Leu Ser Val Ser
180                      185                      190
Arg Leu Ser Cys Asp Asn Phe Thr Leu Asn Arg Ile Tyr Gln Phe Val

```

```

      195              200              205
Ala Gly Trp Thr Leu Leu Gly Ser Asp Leu Phe Leu Ile Phe Leu Ser
  210              215              220
Tyr Thr Phe Ile Leu Arg Ala Val Leu Arg Phe Lys Ala Glu Gly Ala
  225              230              235              240
Ala Val Lys Ala Leu Ser Thr Cys Gly Ser His Phe Ile Leu Ile Leu
      245              250              255
Phe Phe Ser Thr Ile Leu Leu Val Val Val Leu Thr Asn Val Ala Arg
  260              265              270
Lys Lys Val Pro Met Asp Ile Leu Ile Leu Leu Asn Val Leu His His
  275              280              285
Leu Ile Pro Pro Ala Leu Asn Pro Ile Val Tyr Gly Val Arg Thr Lys
  290              295              300
Glu Ile Lys Gln Gly Ile Gln Lys Leu Leu Gln Arg Gly Arg
  305              310              315

```

<210> 1222

<211> 236

<212> PRT

<213> Unknown (H38g139 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(236)

<223> Xaa = Any Amino Acid

<400> 1222

```

Pro Lys Val Pro Asp Phe Phe Val Phe Gly Leu Arg Ala Ile Ser Phe
  1              5              10              15
Pro Ala Gly Phe Leu Gln Lys Tyr Ile Lys Asn Cys Phe Gln Ala Met
      20              25              30
Glu Phe Trp Pro Phe Lys Val Arg Ala Met Asp Arg Xaa Gly Thr Leu
      35              40              45
Cys His Pro Leu Lys Tyr Pro Ser Ile Ile Thr Asp Pro Phe Gly Val
      50              55              60
Lys Ala Ala Arg Phe Ile Leu Pro Arg Asn Val Leu Met Thr Leu Pro
      65              70              75              80
Ile Pro Ile Leu Ser Ala Gln Leu Arg Tyr Cys Gly Arg Asn Val Ile
      85              90              95
Glu Asn Cys Ile Cys Ala Asn Met Ser Val Ser Arg Leu Ser Cys Asp
      100              105              110
Asp Val Thr Ile Asn His Leu Tyr Gln Phe Ala Gly Gly Trp Thr Leu
      115              120              125
Leu Gly Ser Asp Leu Ile Leu Ile Phe Leu Ser Tyr Thr Phe Ile Leu
      130              135              140
Arg Ala Val Leu Arg Leu Lys Ala Glu Gly Ala Val Ala Lys Ala Leu
      145              150              155              160
Ser Thr Cys Gly Ser His Phe Met Leu Ile Leu Phe Phe Ser Thr Ile
      165              170              175
Leu Leu Val Phe Val Leu Thr His Val Ala Lys Lys Lys Val Ser Pro
      180              185              190
Asp Val Pro Val Leu Leu Asn Val Leu His His Val Ile Pro Ala Ala
      195              200              205
Leu Asn Pro Ile Ile Tyr Gly Val Arg Thr Gln Glu Ile Lys Gln Gly
      210              215              220
Met Gln Arg Leu Leu Lys Gly Cys Xaa Gln Gly
      225              230              235

```

<210> 1223

<211> 308

<212> PRT

<213> Unknown (H38g140 protein)

<220>

<223> Synthetic construct

<400> 1223

```

Met Asn Ser Leu Lys Asp Gly Asn His Thr Ala Leu Thr Gly Phe Ile
 1           5           10           15
Leu Leu Gly Leu Thr Asp Asp Pro Ile Leu Arg Val Ile Leu Phe Met
 20           25           30
Ile Ile Leu Ser Gly Asn Leu Ser Ile Ile Ile Leu Ile Arg Ile Ser
 35           40           45
Ser Gln Leu His His Pro Met Tyr Phe Phe Leu Ser His Leu Ala Phe
 50           55           60
Ala Asp Met Ala Tyr Ser Ser Val Thr Pro Asn Met Leu Val Asn
 65           70           75           80
Phe Leu Val Glu Arg Asn Thr Val Ser Tyr Leu Gly Cys Ala Ile Gln
 85           90           95
Leu Gly Ser Ala Ala Phe Phe Ala Thr Val Glu Cys Val Leu Leu Ala
100           105           110
Ala Met Ala Tyr Asp Arg Phe Val Ala Ile Cys Ser Pro Leu Leu Tyr
115           120           125
Ser Thr Lys Met Ser Thr Gln Val Ser Val Gln Leu Leu Leu Val Val
130           135           140
Tyr Ile Ala Gly Phe Leu Ile Ala Val Ser Tyr Thr Thr Ser Phe Tyr
145           150           155           160
Phe Leu Leu Phe Cys Gly Pro Asn Gln Val Asn His Phe Phe Cys Asp
165           170           175
Phe Ala Pro Leu Leu Glu Leu Ser Cys Ser Asp Ile Ser Val Ser Thr
180           185           190
Val Val Leu Ser Phe Ser Ser Gly Ser Ile Ile Val Val Thr Val Cys
195           200           205
Val Ile Ala Val Cys Tyr Ile Tyr Ile Leu Ile Thr Ile Leu Lys Met
210           215           220
Arg Ser Thr Glu Gly His His Lys Ala Phe Ser Thr Cys Thr Ser His
225           230           235           240
Leu Thr Val Val Thr Leu Phe Tyr Gly Thr Ile Thr Phe Ile Tyr Val
245           250           255
Met Pro Asn Phe Ser Tyr Ser Thr Asp Gln Asn Lys Val Val Ser Val
260           265           270
Leu Tyr Thr Val Val Ile Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu
275           280           285
Arg Asn Lys Glu Ile Lys Gly Ala Leu Lys Arg Glu Leu Val Arg Lys
290           295           300
Ile Leu Ser His
305

```

<210> 1224

<211> 335

<212> PRT

<213> Unknown (H38g141 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(335)

<223> Xaa = Any Amino Acid

<400> 1224

```

Asp Thr Asp Pro Gln Ser Leu Thr Asp Val Ser Ile Phe Leu Leu Leu
1      5      10      15
Glu Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Val Ala Gly Leu Phe
20      25      30
Leu Ser Met Cys Leu Val Met Val Leu Glu Asn Leu Leu Ile Ile Leu
35      40      45
Asp Val Ser Pro Asp Ser His Leu Pro Thr Pro Met Tyr Phe Phe Leu
50      55      60
Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Pro
65      70      75      80
Lys Met Ile Val Asp Ile Gln Ser His Ser Arg Val Ile Tyr Ala Gly
85      90      95
Cys Leu Thr Val Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu Glu
100     105     110
Asn Met Leu Leu Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys
115     120     125
His Pro Leu Tyr Arg Ser Ala Ile Leu Asn Pro Cys Phe Cys Gly Phe
130     135     140
Leu Asp Leu Leu Ser Phe Phe Phe Phe Pro Arg Leu Leu Asp Ser Gln
145     150     155     160
Leu His Asn Leu Ile Ala Leu Gln Met Thr Cys Phe Lys Asp Val Glu
165     170     175
Ile Pro Asn Phe Phe Trp Glu Pro Ser Gln Leu Pro His Leu Ala Cys
180     185     190
Cys Asp Thr Phe Thr Arg Asn Ile Ser Met Tyr Phe Pro Ala Ala Val
195     200     205
Phe Gly Phe Leu Ser Ile Ser Gly Thr Leu Phe Ser Tyr Cys Lys Met
210     215     220
Val Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Lys Tyr Lys Ala
225     230     235     240
Phe Ser Thr Xaa Gly Ser His Leu Ser Val Val Cys Xaa Phe Tyr Gly
245     250     255
Thr Gly Val Gly Glu Tyr Leu Gly Ser Asp Val Ser Ser Ser Pro Arg
260     265     270
Lys Gly Ala Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu
275     280     285
Asn Pro Phe Ile Tyr Ser Leu Arg Asn Gly Asp Ile Lys Ser Val Leu
290     295     300
Arg Arg Pro Gln Gly Ser Thr Val Ser Ser Gln Tyr Leu Leu Ile Cys
305     310     315     320
Ser Ile Pro Phe Val Gly Trp Val Asn Lys Asp Ser Lys Val Lys
325     330     335

```

<210> 1225

<211> 311

<212> PRT

<213> Unknown (H38g142 protein)

<220>

<223> Synthetic construct

<400> 1225

```

Met Gly Thr Gly Asn Asp Thr Thr Val Val Glu Phe Thr Leu Leu Gly
1      5      10      15
Leu Ser Glu Asp Thr Thr Val Cys Ala Ile Leu Phe Leu Val Phe Leu
20      25      30
Gly Ile Tyr Val Val Thr Leu Met Gly Asn Ile Ser Ile Ile Val Leu
35      40      45
Ile Arg Arg Ser His His Leu His Thr Pro Met Tyr Ile Phe Leu Cys
50      55      60

```

```

His Leu Ala Phe Val Asp Ile Gly Tyr Ser Ser Ser Val Thr Pro Val
65              70              75              80
Met Leu Met Ser Phe Leu Arg Lys Glu Thr Ser Leu Pro Val Ala Gly
      85              90              95
Cys Val Ala Gln Leu Cys Ser Val Val Thr Phe Gly Thr Ala Glu Cys
      100             105             110
Phe Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Ser
      115             120             125
Pro Leu Leu Tyr Ser Thr Cys Met Ser Pro Gly Val Cys Ile Ile Leu
      130             135             140
Val Gly Met Ser Tyr Leu Gly Gly Trp Val Asn Ala Trp Thr Phe Ile
145             150             155             160
Gly Cys Leu Leu Arg Leu Ser Phe Cys Gly Pro Asn Lys Val Asn His
      165             170             175
Phe Phe Cys Asp Tyr Ser Pro Leu Leu Lys Leu Ala Cys Ser His Asp
      180             185             190
Phe Thr Phe Glu Ile Ile Pro Ala Ile Ser Ser Gly Ser Ile Ile Val
      195             200             205
Ala Thr Val Cys Val Ile Ala Ile Ser Tyr Ile Tyr Ile Leu Ile Thr
      210             215             220
Ile Leu Lys Met His Ser Thr Lys Gly Arg His Lys Ala Phe Ser Thr
225             230             235             240
Cys Thr Ser His Leu Thr Ala Val Thr Leu Phe Tyr Gly Thr Ile Thr
      245             250             255
Phe Ile Tyr Val Met Pro Lys Ser Ser Tyr Ser Thr Asp Gln Asn Lys
      260             265             270
Val Val Ser Val Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro Leu
      275             280             285
Ile Tyr Ser Leu Arg Asn Lys Glu Ile Lys Gly Ala Leu Lys Arg Glu
      290             295             300
Leu Arg Ile Lys Ile Phe Ser
305             310

```

<210> 1226

<211> 314

<212> PRT

<213> Unknown (H38g143 protein)

<220>

<223> Synthetic construct

<400> 1226

```

Met Leu Leu Ser Asn Ser Ser Trp Arg Leu Ser Gln Pro Ser Phe Leu
1      5      10      15
Leu Val Gly Ile Pro Gly Leu Glu Glu Ser Gln His Trp Ile Ala Leu
      20      25      30
Pro Leu Gly Ile Leu Tyr Leu Leu Ala Leu Val Gly Asn Val Thr Ile
      35      40      45
Leu Phe Ile Ile Trp Met Asp Pro Ser Leu His Gln Ser Met Tyr Leu
      50      55      60
Phe Leu Ser Met Leu Ala Ala Ile Asp Leu Val Leu Ala Ser Ser Thr
65             70             75             80
Ala Pro Lys Ala Leu Ala Val Leu Leu Val His Ala His Glu Ile Gly
      85             90             95
Tyr Ile Val Cys Leu Ile Gln Met Phe Phe Ile His Ala Phe Ser Ser
      100            105            110
Met Glu Ser Gly Val Leu Val Ala Met Ala Leu Asp Arg Tyr Val Ala
      115            120            125
Ile Cys His Pro Leu His His Ser Thr Ile Leu His Pro Gly Val Ile
      130            135            140
Gly Arg Ile Gly Met Val Val Leu Val Arg Gly Leu Leu Leu Ile

```

```

145          150          155          160
Pro Phe Pro Ile Leu Leu Gly Thr Leu Ile Phe Cys Gln Ala Thr Ile
          165          170          175
Ile Gly His Ala Tyr Cys Glu His Met Ala Val Val Lys Leu Ala Cys
          180          185          190
Ser Glu Thr Thr Val Asn Arg Ala Tyr Gly Leu Thr Met Ala Leu Leu
          195          200          205
Val Ile Gly Leu Asp Val Leu Ala Ile Gly Val Ser Tyr Ala His Ile
          210          215          220
Leu Gln Ala Val Leu Lys Val Pro Gly Ser Glu Ala Arg Leu Lys Ala
225          230          235          240
Phe Ser Thr Cys Gly Ser His Ile Cys Val Ile Leu Val Phe Tyr Val
          245          250          255
Pro Gly Ile Phe Ser Phe Leu Thr His Arg Phe Gly His His Val Pro
          260          265          270
His His Val His Val Leu Leu Ala Thr Arg Tyr Leu Leu Met Pro Pro
          275          280          285
Ala Leu Asn Pro Leu Val Tyr Gly Val Lys Thr Gln Gln Ile Arg Gln
          290          295          300
Arg Val Leu Arg Val Phe Thr Gln Lys Asp
305          310

```

<210> 1227

<211> 315

<212> PRT

<213> Unknown (H38gl44 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(315)

<223> Xaa = Any Amino Acid

<400> 1227

```

Met Thr Lys Gly Asn Arg Thr Thr Val Thr Glu Phe Val Leu Met Gly
1          5          10          15
Phe Thr Asp Arg Pro Glu Leu Gln Leu Pro Leu Phe Val Val Phe Leu
          20          25          30
Val Ile Tyr Leu Ile Thr Leu Val Gly Asn Leu Gly Met Ile Leu Leu
          35          40          45
Ile Arg Ala Asp Ser Arg Leu His Thr Pro Met Tyr Tyr Phe Leu Ser
          50          55          60
His Leu Ala Phe Ile Asp Leu Cys Tyr Ser Ser Ile Gly Pro Lys
65          70          75          80
Met Leu Gln Asn Val Leu Val Lys Lys Lys Thr Ile Ser Phe Ser Gly
          85          90          95
Cys Phe Ala Gln Leu Tyr Phe Ser Gly Ala Phe Ala Thr Thr Glu Xaa
          100          105          110
Phe Leu Leu Ala Thr Met Pro Tyr Asp Arg Tyr Val Ala Ile Cys Asn
          115          120          125
Pro Leu Ile Tyr Thr Ala Ile Met Thr Gln Arg Val Cys Arg Glu Leu
          130          135          140
Val Ile Gly Val Tyr Thr Tyr Gly Phe Arg Asn Ser Val Ile Gln Thr
145          150          155          160
Ala Leu Thr Phe Gln Leu Ser Phe Cys Asn Ser Asp Val Ile His His
          165          170          175
Phe Tyr Cys Ala Asp Pro Pro Leu Leu Ala Leu Ser Cys Ser Asp Thr
          180          185          190
His Asn Lys Glu Lys Gln Leu Met Ile Phe Ser Ala Val Asn Leu Thr
          195          200          205

```

Gly Ser Leu Leu Thr Ile Phe Ile Ser Tyr Ile Cys Ile Leu Phe Ser
 210 215 220
 Ile Ile Lys Ile Gln Ser Ser Glu Gly Lys Cys Arg Ala Phe Ser Thr
 225 230 235 240
 Arg Ala Ser His Leu Thr Val Val Thr Ile Phe Tyr Gly Thr Leu Phe
 245 250 255
 Phe Met Tyr Leu Gln Gln Pro Lys Ala Gly Asn Ser Trp Lys Pro Asn
 260 265 270
 Lys Val Val Ser Val Phe Tyr Ser Leu Val Ile Pro Met Leu Asn Pro
 275 280 285
 Leu Ile Tyr Arg Leu Arg Asn Thr Glu Val Lys Asp Ala Leu Lys Lys
 290 295 300
 Met Leu Glu Gly Lys Glu Leu Xaa Xaa Val Ser
 305 310 315

<210> 1228

<211> 202

<212> PRT

<213> Unknown (H38g145 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(202)

<223> Xaa = Any Amino Acid

<400> 1228

Met Thr Thr His Arg Asn Asp Thr Leu Ser Thr Glu Ala Ser Asp Phe
 1 5 10 15
 Leu Leu Asn Cys Phe Val Arg Ser Pro Ser Trp Gln His Trp Leu Ser
 20 25 30
 Leu Pro Leu Ser Leu Leu Phe Leu Leu Ala Val Gly Ala Asn Thr Thr
 35 40 45
 Leu Leu Met Thr Ile Trp Leu Glu Ala Ser Leu His Gln Pro Leu Tyr
 50 55 60
 Tyr Leu Leu Ser Leu Leu Ser Lys Leu Asp Ile Val Leu Cys Leu Thr
 65 70 75 80
 Val Ile Pro Lys Val Leu Thr Ile Phe Trp Phe Asp Leu Arg Pro Ile
 85 90 95
 Ser Phe Pro Ala Cys Phe Leu Gln Met Tyr Ile Met Asn Cys Phe Leu
 100 105 110
 Ala Met Glu Ser Cys Thr Phe Met Val Met Ala Tyr Asp Arg Tyr Val
 115 120 125
 Ala Ile Cys His Pro Leu Arg Tyr Pro Ser Ile Ile Thr Asp His Phe
 130 135 140
 Val Val Lys Ala Ala Met Phe Ile Leu Thr Arg Asn Val Leu Met Thr
 145 150 155 160
 Leu Ala Ile Pro Ile Leu Ser Ala Gln Leu Leu Leu Gly Thr Met Phe
 165 170 175
 Leu Lys Pro Phe Cys Gly Lys Cys Phe Val His Asn Phe Cys Gly Asp
 180 185 190
 Ala Pro Xaa Xaa Pro Tyr Thr Phe Leu Lys
 195 200

<210> 1229

<211> 203

<212> PRT

<213> Unknown (H38g146 protein)

<220>

<223> Synthetic construct

<400> 1229

```

Met Asn Glu Thr Asn His Ser Trp Val Thr Glu Phe Val Leu Leu Gly
 1           5           10           15
Leu Ser Ser Ser Arg Glu Leu Gln Pro Phe Leu Phe Leu Ile Phe Ser
 20           25           30
Leu Leu Tyr Leu Ala Ile Leu Leu Gly Asn Phe Leu Ile Ile Leu Thr
 35           40           45
Val Thr Ser Asp Ser Arg Leu His Thr Pro Met Tyr Phe Leu Leu Ala
 50           55           60
Asn Leu Ser Phe Ile Asp Val Cys Val Ala Ser Ser Ala Thr Pro Lys
 65           70           75           80
Met Ile Ala Asp Phe Leu Val Glu His Lys Thr Ile Ser Phe Asp Ala
 85           90           95
His Leu Ala Gln Ile Phe Phe Val His Leu Phe Thr Gly Ser Glu Met
 100          105          110
Val Leu Leu Val Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys
 115          120          125
Pro Pro His Tyr Met Thr Ile Met Ser Cys Cys Val Cys Val Val Leu
 130          135          140
Val Leu Ile Ser Trp Phe Val Gly Phe Ile His Thr Thr Ser Gln Leu
 145          150          155          160
Ala Phe Thr Val Asn Leu Pro Phe Cys Gly Pro Asn Lys Val Asp Ser
 165          170          175
Phe Phe Cys Asp Leu Pro Leu Ala Ser Lys Leu Ala Cys Ile Asp Thr
 180          185          190
Tyr Val Val Ser Leu Leu Ile Val Ala Asp Ser
 195          200

```

<210> 1230

<211> 304

<212> PRT

<213> Unknown (H38g147 protein)

<220>

<223> Synthetic construct

<400> 1230

```

Met Ala Leu Ser Asn Ser Ser Trp Arg Leu Pro Gln Pro Ser Phe Phe
 1           5           10           15
Leu Val Gly Ile Pro Gly Leu Glu Ser Gln His Trp Ile Ala Leu
 20           25           30
Pro Leu Gly Ile Leu Tyr Leu Leu Ala Leu Val Gly Asn Val Thr Ile
 35           40           45
Leu Phe Ile Ile Trp Met Asp Pro Ser Leu His Gln Ser Met Tyr Leu
 50           55           60
Phe Leu Ser Met Leu Ala Ala Ile Asp Leu Val Val Ala Ser Ser Thr
 65           70           75           80
Ala Pro Lys Ala Leu Ala Val Leu Leu Val Arg Ala Gln Glu Ile Gly
 85           90           95
Tyr Thr Val Cys Leu Ile Gln Met Phe Phe Thr His Ala Phe Ser Ser
 100          105          110
Met Glu Ser Gly Val Leu Val Ala Met Ala Leu Asp Arg Tyr Val Ala
 115          120          125
Ile Cys His Pro Leu His His Ser Thr Ile Leu His Pro Gly Val Ile
 130          135          140
Gly His Ile Gly Met Val Val Leu Val Arg Gly Leu Leu Leu Leu Ile
 145          150          155          160
Pro Phe Leu Ile Leu Leu Arg Lys Leu Ile Phe Cys Gln Ala Thr Ile
 165          170          175

```

```

Ile Gly His Ala Tyr Cys Glu His Met Ala Val Val Lys Leu Ala Cys
      180                      185                      190
Ser Glu Thr Thr Val Asn Arg Ala Tyr Gly Leu Thr Val Ala Leu Leu
      195                      200                      205
Val Val Gly Leu Asp Val Leu Ala Ile Gly Val Ser Tyr Ala His Ile
      210                      215                      220
Leu Gln Ala Val Leu Lys Val Pro Gly Asn Glu Ala Arg Leu Lys Ala
      225                      230                      235                      240
Phe Ser Thr Cys Gly Ser His Val Cys Val Ile Leu Val Phe Tyr Ile
      245                      250                      255
Pro Gly Met Phe Ser Phe Leu Thr His Arg Phe Gly His His Val Pro
      260                      265                      270
His His Val His Val Leu Leu Ala Ile Leu Tyr Arg Leu Val Pro Pro
      275                      280                      285
Ala Leu Asn Pro Leu Val Tyr Arg Val Lys Thr Gln Lys Ile His Gln
      290                      295                      300

```

<210> 1231

<211> 110

<212> PRT

<213> Unknown (H38g148 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(110)

<223> Xaa = Any Amino Acid

<400> 1231

```

Ser His Thr Glu Pro Gln Asn Leu Thr Gly Val Ser Glu Phe Leu Leu
  1      5      10      15
Leu Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Trp Leu
      20      25      30
Ser Leu Ser Ile Tyr Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile
      35      40      45
Leu Ala Val Ser Ser Asp Ser His Leu His Thr Pro Ile Tyr Phe Phe
      50      55      60
Leu Phe Asn Leu Ser Leu Ala Asp Ile Gly Phe Thr Ser Ala Met Val
      65      70      75      80
Pro Lys Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser Tyr
      85      90      95
Ala Gly Cys Leu Thr Xaa Met Ser Phe Phe Val Leu Phe Phe
      100      105      110

```

<210> 1232

<211> 327

<212> PRT

<213> Unknown (H38g149 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(327)

<223> Xaa = Any Amino Acid

<400> 1232

```

Phe Phe Ser Asn Asn Ser Val Leu Phe Pro His Thr Phe Phe Leu Ala
  1      5      10      15
Gly Ile Pro Gly Leu Thr Ala Thr His Ile Trp Ile Leu Leu Pro Phe

```

```
<210> 1233
<211> 241
<212> PRT
<213> Unknown (H38a150 protein)
```

```
<221> VARIANT
<222> (1)...(241)
<223> Xaa = Any Amino Acid
```

562

Ala Val Glu Lys Arg Asp Arg Ser Phe Leu Phe Ile His Phe Leu Leu
 65 70 75 80
 His Xaa Ser Thr Ala Val Ser Asp His Ala Lys Val Glu Pro Gly Val
 85 90 95
 Gly Arg Arg Glu Arg Gly Xaa Gly Lys Ser His Xaa Leu Thr Leu Lys
 100 105 110
 Xaa Asp Gly Phe Thr Phe Ser Gly Pro Gly Gln Cys Leu Leu Phe Leu
 115 120 125
 Thr His Ile Lys Pro Leu Xaa Met His Leu Thr Met Gly Ala Ser Pro
 130 135 140
 Leu Pro Glu Val Arg Pro Pro Asp Phe Phe Gln Phe Pro Val Val Pro
 145 150 155 160
 His Asn Pro His Ser Trp Thr Phe Thr Gln Tyr Val Arg Leu Pro Ser
 165 170 175
 Trp Val Gln Ser Leu Ser Lys Gln Leu Thr His Phe Ser Phe His Gly
 180 185 190
 Gln Ser Phe Lys Ser Ala Tyr Ile Xaa Leu Ala Ile Ser Gly Ala Val
 195 200 205
 Thr Pro Ile Leu Leu Gln Arg Pro Arg Gly Gln Ser Ser Val Ala Val
 210 215 220
 Xaa His Ile Pro Asp Asp Arg Ile His Thr Leu Lys Pro Leu Ser Gly
 225 230 235 240
 Pro

<210> 1234

<211> 313

<212> PRT

<213> Unknown (H38g151 protein)

<220>

<223> Synthetic construct

<400> 1234

Met Ala Ser Pro Asn Asn Asp Ser Thr Ala Pro Val Ser Glu Phe Leu
 1 5 10 15
 Leu Ile Cys Phe Pro Asn Phe Gln Ser Trp Gln His Trp Leu Ser Leu
 20 25 30
 Pro Leu Ser Leu Leu Phe Leu Leu Ala Met Gly Ala Asn Thr Thr Leu
 35 40 45
 Leu Ile Thr Ile Gln Leu Glu Ala Ser Leu His Gln Pro Leu Tyr Tyr
 50 55 60
 Leu Leu Ser Leu Leu Ser Leu Leu Asp Ile Val Leu Cys Leu Thr Val
 65 70 75 80
 Ile Pro Lys Val Leu Ala Ile Phe Trp Phe Asp Leu Arg Ser Ile Ser
 85 90 95
 Phe Pro Ala Cys Phe Leu Gln Met Phe Ile Met Asn Ser Phe Leu Thr
 100 105 110
 Met Glu Ser Cys Thr Phe Met Val Met Ala Tyr Asp Arg Tyr Val Ala
 115 120 125
 Ile Cys His Pro Leu Arg Tyr Pro Ser Ile Ile Thr Asp Gln Phe Val
 130 135 140
 Ala Arg Ala Val Val Phe Val Ile Ala Arg Asn Ala Phe Val Ser Leu
 145 150 155 160
 Pro Val Pro Met Leu Ser Ala Arg Leu Arg Tyr Cys Ala Gly Asn Ile
 165 170 175
 Ile Lys Asn Cys Ile Cys Ser Asn Leu Ser Val Ser Lys Leu Ser Cys
 180 185 190
 Asp Asp Ile Thr Phe Asn Gln Leu Tyr Gln Phe Val Ala Gly Trp Thr
 195 200 205
 Leu Leu Gly Ser Asp Leu Ile Leu Ile Val Ile Ser Tyr Ser Phe Ile

```

      210              215              220
Leu Lys Val Val Leu Arg Ile Lys Ala Glu Gly Ala Val Ala Lys Ala
225              230              235              240
Leu Ser Thr Cys Gly Ser His Phe Ile Leu Ile Leu Phe Phe Ser Thr
      245              250              255
Val Leu Leu Val Leu Val Ile Thr Asn Leu Ala Arg Lys Arg Ile Pro
      260              265              270
Pro Asp Val Pro Ile Leu Leu Asn Ile Leu His His Leu Ile Pro Pro
      275              280              285
Ala Leu Asn Pro Ile Val Tyr Gly Val Arg Thr Lys Glu Ile Lys Gln
      290              295              300
Gly Ile Gln Asn Leu Leu Lys Arg Leu
305              310

```

<210> 1235
 <211> 135
 <212> PRT
 <213> Unknown (H38g152 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(135)
 <223> Xaa = Any Amino Acid

```

<400> 1235
Lys Asp Leu Xaa Arg Arg Ser Asn Ile Asn Phe Arg Ile Glu Arg Leu
 1              5              10              15
Tyr Phe Phe Ile Xaa Gly Trp Glu Met Lys Met Gly Leu Xaa Asn Xaa
      20              25              30
Leu Leu Met Phe Cys Glu Ser Phe Xaa Xaa Xaa Lys Thr Val Leu Arg
      35              40              45
Ile Lys Gly Glu Gly Asp Met Ala Lys Ala Leu Gly Thr Cys Gly Ser
      50              55              60
His Phe Ile Leu Ile Leu Phe Phe Thr Thr Val Leu Leu Val Leu Val
      65              70              75              80
Ile Thr Asn Leu Ala Arg Lys Arg Ile Pro Pro Asp Val Pro Ile Leu
      85              90              95
Leu Asn Ile Leu His His Leu Ile Pro Pro Ala Leu Asn Pro Ile Val
      100              105              110
Tyr Gly Val Arg Thr Lys Glu Ile Lys Gln Gly Ile Gln Asn Leu Leu
      115              120              125
Arg Arg Leu Xaa Lys Ile Lys
      130              135

```

<210> 1236
 <211> 319
 <212> PRT
 <213> Unknown (H38g153 protein)

<220>
 <223> Synthetic construct

```

<400> 1236
Met Ala Pro Thr Asn Leu Thr Ser Ala Pro Val Phe Leu Leu Leu Gly
 1              5              10              15
Leu Val Thr Glu Gln Thr Asp Ala His Pro Leu Leu Phe Leu Leu Cys
      20              25              30
Leu Gly Ile Tyr Leu Leu Asn Ala Leu Ser Asn Leu Ser Met Val Ala
      35              40              45

```

Leu Val Arg Ser Asp Gly Ala Leu Arg Ser Pro Met Tyr Tyr Phe Leu
 50 55 60
 Gly His Leu Ser Leu Val Asp Val Cys Phe Thr Thr Val Thr Val Pro
 65 70 75 80
 Arg Leu Leu Ala Gly Leu Leu His Pro Gly Gln Ala Ile Ser Phe Gln
 85 90 95
 Ala Cys Phe Ala Glu Met Tyr Phe Phe Val Ala Leu Gly Ile Thr Glu
 100 105 110
 Ser Tyr Leu Pro Ala Ala Met Ser Tyr Asp Arg Ala Thr Ala Ala Cys
 115 120 125
 Arg Pro Leu Arg Tyr Gly Ala Leu Val Thr His Gly Arg Cys Ala Ser
 130 135 140
 Leu Val Arg Ala Ser Trp Ala Val Thr His Leu His Ser Leu Leu His
 145 150 155 160
 Thr Leu Leu Leu Ser Ala Leu Ser Tyr Pro Tyr Pro Thr Pro Val Arg
 165 170 175
 Pro Phe Phe Cys Asp Met Thr Val Met Leu Ser Leu Ala Thr Ser Asp
 180 185 190
 Thr Ser Ala Ala Glu Thr Ala Ile Phe Ser Glu Gly Leu Ala Val Val
 195 200 205
 Leu Ala Pro Leu Leu Leu Val Phe Leu Ser Tyr Ala Arg Ile Leu Val
 210 215 220
 Ala Val Leu Gly Leu Pro Arg Pro Arg Arg Ala Phe Ser Thr Cys Gly
 225 230 235 240
 Ala His Leu Val Ala Val Ala Val Ala Val Ala Leu Phe Phe Gly Ser
 245 250 255
 Val Leu Ser Val Tyr Phe Pro Pro Ser Ser Ala Tyr Ser Ala Arg Tyr
 260 265 270
 Asp Arg Leu Ala Ser Val Val Tyr Ala Val Ile Thr Pro Thr Leu Asn
 275 280 285
 Pro Phe Ile Asn Ser Leu Arg Asn Lys Glu Val Lys Gly Ala Leu Lys
 290 295 300
 Arg Gly Leu Arg Trp Arg Ala Ala Pro Gln Glu Ala Trp Arg Ala
 305 310 315

<210> 1237

<211> 325

<212> PRT

<213> Unknown (H38g154 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1) ... (325)

<223> Xaa = Any Amino Acid

<400> 1237

Met Phe Leu Pro Asn Asn Thr Gln Phe His Pro Ser Ser Phe Leu Leu
 1 5 10 15
 Leu Gly Ile Pro Gly Leu Glu Thr Leu His Ile Trp Ile Gly Phe Pro
 20 25 30
 Phe Cys Ala Val Tyr Ile Ile Ala Leu Ile Gly Arg Phe Thr Ile Leu
 35 40 45
 Leu Val Ile Lys Thr Asp Ser Ser Leu Tyr Gln Pro Met Phe Tyr Phe
 50 55 60
 Leu Ala Met Leu Ala Thr Ile Asp Leu Gly Leu Ser Thr Ala Thr Ile
 65 70 75 80
 Pro Lys Met Leu Gly Ile Phe Trp Phe Ser Leu Arg Glu Ile Ile Cys
 85 90 95
 Asp Ala Cys Leu Ile Gln Met Phe Phe Ile His Asn Phe Thr Gly Met

```

      100      105      110
Glu Ser Ala Ala Leu Val Gly Met Ala Tyr Asp His Phe Val Ala Ile
      115      120      125
Cys Asn Pro Leu Arg Tyr Ser Ile Ile Leu Thr Lys Lys Ala Val Ser
      130      135      140
Val Ile Gly Leu Gly Val Leu Val Arg Ser Phe Met Ser Val Ile Pro
      145      150      155      160
Phe Val Phe Leu Ile Leu Arg Leu Pro Phe Cys Gly Asp His Val Ile
      165      170      175
Pro His Thr Asn Cys Glu His Met Gly Leu Ala His Leu Ser Cys Ser
      180      185      190
Ser Ile Lys Ile Asn Ile Ile Tyr Gly Leu Gly Ala Ile Ser Ile Leu
      195      200      205
Val Phe Asp Ile Ile Ala Ile Ala Leu Ser Tyr Val Gln Ile Leu His
      210      215      220
Ala Val Phe His Leu Pro Ser Cys Lys Ala Xaa Leu Lys Ser Leu Ser
      225      230      235      240
Thr Cys Gly Ser His Val Cys Val Ile Leu Ala Phe Tyr Thr Pro Ala
      245      250      255
Leu Phe Ser Phe Val Thr His Arg Phe Gly Gln Asn Val Pro Arg Tyr
      260      265      270
Ile His Ile Leu Leu Ala Asn Leu Tyr Val Val Val Pro Pro Met Leu
      275      280      285
Asn Pro Val Ile Tyr Gly Val Arg Thr Lys Gln Ile Tyr Val Cys Val
      290      295      300
Lys Asn Ile Phe Leu Gln Lys Xaa Glu Ile Glu Lys Lys Ser His Leu
      305      310      315      320
Ile His Ile Arg Arg
      325

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<210> 1238

<211> 319

<212> PRT

<213> Unknown (H38g155 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(319)

<223> Xaa = Any Amino Acid

<400> 1238

```

Met Ser Pro Leu Asn Asp Thr Lys Met Glu Val Leu Arg Phe Leu Leu
 1      5      10      15
Ile Gly Ile Thr Gly Leu Glu Lys Ser Arg Thr Trp Ile Ser Ile Pro
      20      25      30
Phe Leu Ser Val Tyr Leu Leu Ser Trp Met Gly Asn Phe Thr Val Leu
      35      40      45
Phe Phe Ile Lys Thr Glu Gln Ser Leu His Glu Pro Met Tyr Tyr Leu
      50      55      60
Leu Ser Met Leu Ser Ile Ser Asp Leu Gly Leu Ser Leu Ser Ser Leu
      65      70      75      80
Pro Ile Thr Leu Gly Leu Phe Leu Phe Asp Val His Glu Ile His Ala
      85      90      95
Ala Pro Cys Phe Ala Xaa Glu Phe Phe Ile His Leu Phe Thr Val Ser
      100      105      110
Glu Ala Ser Val Leu Ser Val Met Ala Phe Asp Trp Tyr Val Ala Ile
      115      120      125
His Ser Pro Leu Arg Tyr Ser Thr Ile Leu Thr Ser Pro Arg Ala Ile
      130      135      140

```

Lys Thr Gly Val Leu Leu Thr Ser Lys Asn Val Leu Leu Ile Leu Pro
 145 150 155 160
 Leu Pro Phe Leu Leu Gln Arg Leu Arg Tyr Cys His Gln Asn Leu Leu
 165 170 175
 Ser His Ser Tyr Cys Leu His Gln Asp Val Met Lys Leu Met Cys Ser
 180 185 190
 Asp Asn Thr Val Asn Val Val Tyr Gly Leu Cys Ala Gly Leu Ser Thr
 195 200 205
 Met Leu Asp Leu Val Leu Ile Thr Phe Ser Xaa Ile Met Ile Leu Arg
 210 215 220
 Ala Val Leu Gly Ile Ala Thr Pro Arg Gln Gln Phe Lys Ala Leu Asn
 225 230 235 240
 Thr Cys Ile Ser His Ile Cys Ala Val Leu Ile Phe Tyr Val Pro Thr
 245 250 255
 Leu Ser Ala Ala Met Leu His Gln Phe Ala Arg Asp Val Ser Pro Met
 260 265 270
 Ile His Val Leu Met Ala Asp Ile Phe Leu Leu Val Pro Pro Leu Leu
 275 280 285
 Asn Pro Ile Val Tyr Cys Val Lys Thr His Gln Ile Arg Glu Lys Val
 290 295 300
 Val Gly Lys Leu Cys Pro Lys Val Ser Xaa Ser Lys Glu Xaa Glu
 305 310 315

<210> 1239

<211> 313

<212> PRT

<213> Unknown (H38g156 protein)

<220>

<223> Synthetic construct

<400> 1239

Met Ser Ile Ile Asn Thr Ser Tyr Val Glu Ile Thr Thr Phe Phe Leu
 1 5 10 15
 Val Gly Met Pro Gly Leu Glu Tyr Ala His Ile Trp Ile Ser Ile Pro
 20 25 30
 Ile Cys Ser Met Tyr Leu Ile Ala Ile Leu Gly Asn Gly Thr Ile Leu
 35 40 45
 Phe Ile Ile Lys Thr Glu Pro Ser Leu His Glu Pro Met Tyr Tyr Phe
 50 55 60
 Leu Ser Met Leu Ala Met Ser Asp Leu Gly Leu Ser Leu Ser Ser Leu
 65 70 75 80
 Pro Thr Val Leu Ser Ile Phe Leu Phe Asn Ala Pro Glu Ile Ser Ser
 85 90 95
 Asn Ala Cys Phe Ala Gln Glu Phe Phe Ile His Gly Phe Ser Val Leu
 100 105 110
 Glu Ser Ser Val Leu Leu Ile Met Ser Phe Asp Arg Phe Leu Ala Ile
 115 120 125
 His Asn Pro Leu Arg Tyr Thr Ser Ile Leu Thr Thr Val Arg Val Ala
 130 135 140
 Gln Ile Gly Ile Val Phe Ser Phe Lys Ser Met Leu Leu Val Leu Pro
 145 150 155 160
 Phe Pro Phe Thr Leu Arg Asn Leu Arg Tyr Cys Lys Lys Asn Gln Leu
 165 170 175
 Ser His Ser Tyr Cys Leu His Gln Asp Val Met Lys Leu Ala Cys Ser
 180 185 190
 Asp Asn Arg Ile Asp Val Ile Tyr Gly Phe Phe Gly Ala Leu Cys Leu
 195 200 205
 Met Val Asp Phe Ile Leu Ile Ala Val Ser Tyr Thr Leu Ile Leu Lys
 210 215 220
 Thr Val Pro Gly Ile Ala Ser Lys Lys Glu Gln Leu Lys Ala Leu Asn

```

225          230          235          240
Thr Cys Val Ser His Ile Cys Ala Val Ile Ile Phe Tyr Leu Pro Ile
          245          250          255
Ile Asn Leu Ala Val Val His Arg Phe Ala Arg His Val Ser Pro Leu
          260          265          270
Ile Asn Val Leu Met Ala Asn Val Leu Leu Leu Val Pro Pro Leu Thr
          275          280          285
Asn Pro Ile Val Tyr Cys Val Lys Thr Lys Gln Ile Arg Val Arg Val
          290          295          300
Val Ala Lys Leu Cys Gln Arg Lys Ile
305          310

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<210> 1240
<211> 308
<212> PRT
<213> Unknown (H38g157 protein)

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<220>
<223> Synthetic construct

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<400> 1240
Met Val Asn Arg Asn Asn Val Thr Glu Phe Ile Leu Leu Gly Leu Ile
1          5          10          15
Glu Asn Pro Lys Met Gln Lys Ile Ile Phe Val Val Phe Val Ile Tyr
          20          25          30
Ile Thr Thr Met Ile Gly Asn Val Leu Ile Val Val Thr Val Thr Ala
          35          40          45
Ser Pro Ser Leu Arg Ser Pro Met Tyr Phe Tyr Leu Ala Tyr Leu Ser
          50          55          60
Phe Ile Asp Ala Cys Tyr Ser Ser Val Asn Ala Pro Lys Leu Ile Thr
          65          70          75          80
Asp Ser Leu Tyr Glu Asn Lys Thr Ile Leu Leu Asn Gly Cys Met Thr
          85          90          95
Gln Val Phe Gly Glu His Phe Phe Gly Gly Val Glu Val Ile Leu Leu
          100          105          110
Thr Val Met Ala Tyr Asp Arg Tyr Val Val Ile Cys Lys Pro Leu His
          115          120          125
Tyr Thr Thr Ile Met Lys Gln His Val Cys Ser Leu Leu Val Gly Val
          130          135          140
Ser Trp Val Gly Gly Phe Leu His Ala Thr Val Gln Ile Leu Phe Ile
          145          150          155          160
Phe Gln Leu Pro Phe Cys Gly Pro Asn Val Ile Asp His Phe Met Trp
          165          170          175
Asp Leu Asn Pro Leu Leu Asn Leu Val Cys Thr Asn Thr His Thr Leu
          180          185          190
Gly Leu Phe Val Ala Ala Asn Ser Gly Phe Ile Cys Leu Leu Asn Phe
          195          200          205
Leu Leu Leu Leu Val Ser Tyr Met Val Ile Leu Tyr Ser Leu Arg Thr
          210          215          220
His Ser Leu Glu Ala Arg Cys Lys Ala Leu Ser Thr Cys Val Ser His
          225          230          235          240
Ile Thr Val Val Ile Leu Phe Phe Ile Pro Cys Ile Phe Val Tyr Met
          245          250          255
Arg Pro Pro Ala Thr Leu Pro Ile Asp Lys Ala Val Ala Val Phe Tyr
          260          265          270
Thr Met Ile Ala Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn
          275          280          285
Ala Gln Met Lys Asn Ala Ile Arg Lys Leu Cys Ser Arg Lys Ala Ile
          290          295          300
Ser Ser Val Lys
305

```

<210> 1241
 <211> 321
 <212> PRT
 <213> Unknown (H38g158 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(321)
 <223> Xaa = Any Amino Acid

<400> 1241
 Met Ala Tyr His Gly Asn Arg Gly Thr Phe His Pro Ala Thr Phe Phe
 1 5 10 15
 Leu Ile Gly Ile Pro Gly Leu Glu Asp Val His Met Xaa Ile Ser Leu
 20 25 30
 His Phe Cys Ser Val Tyr Leu Leu Ala Leu Leu Gly Asn Ala Thr Ile
 35 40 45
 Leu Leu Val Ile Lys Ala Glu Gln Thr Leu Arg Glu Pro Met Phe Tyr
 50 55 60
 Phe Leu Ala Ile Leu Ser Thr Ile Asp Leu Ala Leu Ser Thr Thr Ser
 65 70 75 80
 Val Pro Arg Thr Leu Gly Ile Phe Trp Phe Asp Ala His Glu Ile Asn
 85 90 95
 Phe Gly Ala Cys Val Ala Gln Met Phe Leu Ile His Ala Phe Thr Gly
 100 105 110
 Met Glu Ala Glu Val Leu Val Ala Met Ala Phe Asp Arg Tyr Val Ala
 115 120 125
 Ile Cys Asn Pro Leu His Tyr Thr Asn Ile Leu Thr Ser Arg Val Leu
 130 135 140
 Val Gly Ile Thr Met Cys Ile Val Ile Arg Pro Val Leu Phe Thr Leu
 145 150 155 160
 Pro Ile Ile Tyr Leu Ile Tyr Arg Leu Pro Phe Cys Gln Gly His Ile
 165 170 175
 Ile Ala His Ser Tyr Tyr Glu His Met Gly Ile Ala Lys Leu Ser Cys
 180 185 190
 Gly Asn Ile Arg Val Asn Ala Ile Tyr Gly Leu Phe Val Val Ser Phe
 195 200 205
 Tyr Leu Leu Asn Leu Val Leu Ile Val Ile Ser Tyr Val Tyr Ile Leu
 210 215 220
 Cys Ala Val Phe Cys Leu Ala Ser His Asp Ala Arg Leu Lys Ala Leu
 225 230 235 240
 Ser Thr Cys Gly Ser His Val Gly Val Ile Cys Val Phe Tyr Ile Pro
 245 250 255
 Ser Asp Phe Ser Phe Leu Thr His Xaa Phe Gly His Asn Ile Pro His
 260 265 270
 Tyr Met His Ile Leu Val Ala Thr Leu Tyr Leu Val Ile Pro Pro Ser
 275 280 285
 Leu Asn Pro Ile Ile Cys Gly Val Arg Thr Lys Trp Lys Arg Glu Arg
 290 295 300
 Val Leu Tyr Val Leu Thr Lys Lys Xaa Asp Ser Asp His Val Leu Leu
 305 310 315 320
 Leu

<210> 1242
 <211> 162
 <212> PRT
 <213> Unknown (H38g159 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(162)

<223> Xaa = Any Amino Acid

<400> 1242

Gly	Thr	Val	Xaa	Ile	Leu	Ser	Pro	Val	Xaa	Leu	Pro	Phe	Tyr	Asp	Pro
1				5					10					15	
Asn	Val	Ile	Ala	His	Phe	Met	Cys	Asp	Leu	Asn	Thr	Leu	Leu	Lys	Leu
			20					25					30		
Leu	Cys	Met	Gly	Thr	Thr	Asn	Thr	Leu	Gly	Phe	Phe	Val	Ala	Ala	Asn
		35					40					45			
Gly	Gly	Phe	Asn	Tyr	Leu	Leu	Asn	Ile	Ile	Phe	Leu	Met	Val	Ser	Xaa
	50					55					60				
Val	Ala	Ile	Leu	Cys	Thr	Leu	Lys	Thr	His	Ser	Leu	Glu	Glu	Arg	Cys
65					70					75				80	
Lys	Ala	Leu	Ser	Thr	Cys	Ile	Ser	His	Thr	Thr	Val	Val	Ile	Leu	Phe
				85					90					95	
Phe	Gly	Phe	Cys	Ile	Ser	Val	Tyr	Leu	Cys	Pro	Val	Thr	Leu	Leu	Pro
			100					105					110		
Ile	Asn	Lys	Ala	Val	Ala	Val	Phe	Tyr	Thr	Met	Ile	Asn	Pro	Met	Leu
		115						120				125			
Lys	Pro	Leu	Val	Tyr	Thr	Leu	Arg	Asn	Ala	Glu	Val	Lys	Ser	Ala	Leu
	130					135					140				
Arg	Lys	Leu	Trp	Val	Lys	Arg	Xaa	Thr	Glu	Glu	Arg	Asn	Asn	Pro	Asn
145					150					155				160	
Ile	Arg														

<210> 1243

<211> 311

<212> PRT

<213> Unknown (H38g160 protein)

<220>

<223> Synthetic construct

<400> 1243

Met	Phe	Tyr	His	Asn	Lys	Ser	Ile	Phe	His	Pro	Val	Thr	Phe	Phe	Leu
1				5				10						15	
Ile	Gly	Ile	Pro	Gly	Leu	Glu	Asp	Phe	His	Met	Trp	Ile	Ser	Gly	Pro
			20					25					30		
Phe	Cys	Ser	Val	Tyr	Leu	Val	Ala	Leu	Leu	Gly	Asn	Ala	Thr	Ile	Leu
		35					40				45				
Leu	Val	Ile	Lys	Val	Glu	Gln	Thr	Leu	Arg	Glu	Pro	Met	Phe	Tyr	Phe
	50					55				60					
Leu	Ala	Ile	Leu	Ser	Thr	Ile	Asp	Leu	Ala	Leu	Ser	Ala	Thr	Ser	Val
65					70					75				80	
Pro	Arg	Met	Leu	Gly	Ile	Phe	Trp	Phe	Asp	Ala	His	Glu	Ile	Asn	Tyr
				85				90						95	
Gly	Ala	Cys	Val	Ala	Gln	Met	Phe	Leu	Ile	His	Ala	Phe	Thr	Gly	Met
			100					105					110		
Glu	Ala	Glu	Val	Leu	Leu	Ala	Met	Ala	Phe	Asp	Arg	Tyr	Val	Ala	Ile
		115					120					125			
Cys	Ala	Pro	Leu	His	Tyr	Ala	Thr	Ile	Leu	Thr	Ser	Leu	Val	Leu	Val
	130					135					140				
Gly	Ile	Ser	Met	Cys	Ile	Val	Ile	Arg	Pro	Val	Leu	Leu	Thr	Leu	Pro
145					150					155				160	

Met Val Tyr Leu Ile Tyr Arg Leu Pro Phe Cys Gln Ala His Ile Ile
 165 170 175
 Ala His Ser Tyr Cys Glu His Met Gly Ile Ala Lys Leu Ser Cys Gly
 180 185 190
 Asn Ile Arg Ile Asn Gly Ile Tyr Gly Leu Phe Val Val Ser Phe Phe
 195 200 205
 Val Leu Asn Leu Val Leu Ile Gly Ile Ser Tyr Val Tyr Ile Leu Arg
 210 215 220
 Ala Val Phe Arg Leu Pro Ser His Asp Ala Gln Leu Lys Ala Leu Ser
 225 230 235 240
 Thr Cys Gly Ala His Val Gly Val Ile Cys Val Phe Tyr Ile Pro Ser
 245 250 255
 Val Phe Ser Phe Leu Thr His Arg Phe Gly His Gln Ile Pro Gly Tyr
 260 265 270
 Ile His Ile Leu Val Ala Asn Leu Tyr Leu Ile Ile Pro Pro Ser Leu
 275 280 285
 Asn Pro Ile Ile Tyr Gly Val Arg Thr Lys Gln Ile Arg Glu Arg Val
 290 295 300
 Leu Tyr Val Phe Thr Lys Lys
 305 310

<210> 1244

<211> 315

<212> PRT

<213> Unknown (H38g161 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(315)

<223> Xaa = Any Amino Acid

<400> 1244

Met Glu Asn Arg Asn Asn Val Thr Glu Phe Val Leu Leu Gly Leu Thr
 1 5 10 15
 Glu Asn Pro Lys Met Gln Lys Ile Ile Phe Val Val Phe Phe Val Ile
 20 25 30
 Tyr Ile Ile Thr Val Val Gly Asn Ala Leu Ile Val Val Thr Ile Thr
 35 40 45
 Ala Ser Pro Ser Leu Gly Ser Pro Met Tyr Leu Phe Leu Ala Tyr Leu
 50 55 60
 Ser Phe Ile Asp Ala Cys Tyr Ser Ser Val Asn Thr Pro Lys Leu Ile
 65 70 75 80
 Thr Asp Ser Leu Tyr Gly Lys Asn Thr Ile Leu Phe Asn Gly Cys Met
 85 90 95
 Thr Gln Val Phe Gly Glu His Phe Phe Gly Gly Ala Glu Gly Ile Leu
 100 105 110
 Leu Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu
 115 120 125
 His Tyr Met Thr Ile Met Asn Gln Cys Val Tyr Ala Leu Leu Met Gly
 130 135 140
 Val Val Trp Met Gly Gly Phe Leu His Ala Thr Ile Gln Ile Leu Phe
 145 150 155 160
 Ile Phe Gln Leu Pro Phe Cys Gly Pro Asn Val Ile Asp His Phe Met
 165 170 175
 Cys Asp Leu Asn Pro Leu Leu Asn Leu Ala Cys Thr Asp Thr His Met
 180 185 190
 Leu Gly Leu Phe Ile Ala Ala Asn Ser Gly Phe Ile Cys Leu Leu Asn
 195 200 205
 Phe Val Leu Leu Leu Val Ser Tyr Val Val Ile Leu Arg Ser Leu Arg

210	215	220
Thr His Ser Leu Glu Ala Arg His Lys Ala Leu Ser Thr Cys Val Ser		
225	230	235
His Ile Thr Val Val Ile Leu Phe Phe Val Pro Cys Ile Phe Val Tyr		240
	245	250
Met Arg Pro Ala Ala Thr Leu Pro Ile Asp Lys Ala Val Ala Ile Phe		255
	260	265
Tyr Thr Met Ile Thr Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg		270
	275	280
Asn Ala Gln Met Lys Asn Ala Ile Arg Lys Leu Cys Ser Arg Lys Asp		285
	290	295
Ile Ser Gly Asn Lys Xaa Met Xaa Leu Glu Leu		300
305	310	315

<210> 1245

<211> 322

<212> PRT

<213> Unknown (H38g162 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(322)

<223> Xaa = Any Amino Acid

<400> 1245

Ser Asn Thr Gly Met Ser Ile Leu Asn Thr Ser Glu Met Glu Ile Ser		
1	5	10
Ile Phe Tyr Leu Val Gly Ile Pro Gly Leu Glu His Ala Asn Ile Trp		15
	20	25
Ile Ser Ile Pro Ile Cys Leu Met Tyr Thr Val Ala Ile Leu Gly Asn		30
	35	40
Cys Thr Ile Leu Phe Phe Ile Lys Thr Glu Pro Ser Leu His Glu Pro		45
	50	55
Met Tyr Tyr Phe Leu Ser Met Leu Ala Leu Ser Asp Leu Gly Leu Ser		60
	65	70
Leu Ser Ser Leu Pro Thr Met Leu Arg Ile Phe Leu Phe Asn Ala Pro		75
	85	90
Gly Ile Ser Pro Asp Ala Cys Ile Ala Gln Glu Phe Phe Ile His Gly		95
	100	105
Phe Ser Ala Met Glu Ser Ser Val Leu Leu Ile Met Ser Phe Asp Arg		110
	115	120
Phe Ile Ala Ile Cys Asn Pro Leu Arg Tyr Thr Ser Ile Leu Thr Ser		125
	130	135
Ala Arg Val Ile Gln Ile Gly Leu Ala Phe Ser Leu Lys Asn Val Leu		140
	145	150
Leu Ile Leu Pro Phe Pro Phe Thr Leu Lys His Leu Lys Tyr Cys Lys		155
	165	170
Lys Asn Leu Leu Ser Gln Ser Tyr Cys Leu His Gln Asp Val Met Lys		175
	180	185
Leu Ala Cys Thr Asp Asn Lys Val Asn Ile Ile Tyr Gly Leu Phe Val		190
	195	200
Ala Leu Thr Gly Ile Leu Asp Leu Thr Phe Ile Phe Met Ser Tyr Met		205
	210	215
Leu Ile Leu Lys Ala Val Leu Ser Ile Ala Ser Xaa Lys Lys Arg Leu		220
	225	230
Lys Val Leu Asn Thr Cys Val Ser His Ile Cys Ala Val Leu Ile Phe		235
	245	250
Tyr Val Pro Ile Ser Leu Ala Val Ile Tyr Arg Phe Ala Lys His		255
	260	265
		270

Ser Phe Pro Ile Thr Arg Ile Leu Ile Ala Asp Ala Phe Leu Leu Val
 275 280 285
 Pro Pro Leu Met Asn Pro Ile Val Tyr Cys Val Lys Ser Gln Gln Ile
 290 295 300
 Arg Asn Leu Val Leu Glu Lys Leu Cys Gln Lys Gln Ser Xaa Ser Gly
 305 310 315 320
 Cys Leu

<210> 1246

<211> 319

<212> PRT

<213> Unknown (H38g163 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(319)

<223> Xaa = Any Amino Acid

<400> 1246

Ser His Thr Glu Pro Gln Asn Leu Thr Gly Val Ser Glu Phe Leu Leu
 1 5 10 15
 Leu Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Leu Leu Ala Gly Leu
 20 25 30
 Phe Leu Ser Met Cys Leu Val Thr Met Leu Arg Glu Leu Leu Ile Ile
 35 40 45
 Leu Ala Val Thr Ser Asp Ser His Leu His Ile Pro Met Tyr Phe Phe
 50 55 60
 Leu Ser Asn Leu Val Leu Gly His Asp Ile Gly Phe Thr Xaa Ala Thr
 65 70 75 80
 Val Pro Lys Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser
 85 90 95
 His Ala Gly Cys Leu Thr Gln Ile Pro Phe Phe Val Leu Phe Val Cys
 100 105 110
 Ile Asp Asp Met Leu Leu Thr Val Met Ala Tyr Asp Xaa Phe Val Ala
 115 120 125
 Ile Cys His Pro Leu His Tyr Pro Val Ile Met Asn Pro His Leu Cys
 130 135 140
 Val Phe Leu Val Leu Met Phe Phe Leu Ser Leu Leu Asp Ser Xaa Leu
 145 150 155 160
 His Asn Trp Ile Val Gln Phe Thr Cys Phe Lys Asn Val Glu Ile Ser
 165 170 175
 Asn Phe Phe Cys Asp Xaa Ser Gln Leu Leu Asn Leu Ala Cys Ser Asp
 180 185 190
 Val Ile Ser Asn Ile Phe Ile His Leu Asp Ser Thr Ile Phe Gly Phe
 195 200 205
 Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys Ile Val Pro Ser
 210 215 220
 Ile Leu Arg Ile Pro Leu Ser Asp Gly Lys Tyr Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Gly Ser His Leu Ala Ile Val Cys Leu Phe Tyr Gly Thr Gly Ile
 245 250 255
 Gly Met Tyr Leu Thr Ser Ala Val Ser Pro Ala Pro Arg Asn Gly Val
 260 265 270
 Val Ala Ser Val Leu Tyr Ala Ile Val Thr Pro Met Leu Asn Pro Phe
 275 280 285
 Ile Cys Ser Leu Arg Asn Arg Gly Ile Gln Ser Ala Leu Trp Arg Leu
 290 295 300
 Cys Arg Arg Lys Val Xaa Ser His Asp Leu Phe His Pro Phe Ser

305

310

315

<210> 1247

<211> 320

<212> PRT

<213> Unknown (H38g164 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(320)

<223> Xaa = Any Amino Acid

<400> 1247

Met	Arg	Leu	Ile	Xaa	Asp	Glu	Glu	Met	Ser	Arg	Arg	Asn	Tyr	Thr	Glu
1				5					10					15	
Leu	Thr	Glu	Phe	Val	Leu	Leu	Gly	Leu	Thr	Ser	Arg	Pro	Glu	Leu	Arg
			20					25					30		
Val	Ala	Phe	Leu	Ala	Leu	Phe	Leu	Phe	Val	Tyr	Ile	Ala	Thr	Val	Val
		35					40					45			
Gly	Asn	Leu	Gly	Met	Ile	Ile	Leu	Ile	Lys	Val	Asp	Ser	Arg	Leu	His
	50				55					60					
Thr	Pro	Met	Xaa	Phe	Phe	Leu	Ser	Ser	Leu	Ser	Ile	Leu	Asp	Leu	Cys
65				70					75					80	
Phe	Ser	Thr	Asn	Phe	Thr	Pro	Lys	Met	Leu	Glu	Asn	Phe	Leu	Ser	Glu
			85					90					95		
Lys	Lys	Thr	Ile	Ser	Tyr	Ala	Gly	Cys	Leu	Met	Gln	Cys	Tyr	Val	Val
		100					105					110			
Ile	Ala	Val	Val	Leu	Ala	Glu	His	Cys	Met	Leu	Ala	Val	Met	Ala	Tyr
	115				120					125					
Asp	Arg	Tyr	Met	Ala	Ile	Cys	Asn	Pro	Leu	Leu	Tyr	Ser	Ser	Lys	Met
	130				135					140					
Ser	Gln	Gly	Val	Cys	Val	His	Leu	Val	Ile	Val	Pro	Tyr	Val	Tyr	Gly
145				150					155					160	
Phe	Leu	Leu	Ser	Val	Met	Glu	Thr	Leu	Arg	Thr	Tyr	Asn	Leu	Ser	Phe
			165					170					175		
Cys	Gly	Thr	Asn	Glu	Ile	Asn	His	Phe	Tyr	Cys	Ala	Asp	Pro	Pro	Leu
	180					185						190			
Ile	Lys	Leu	Ala	Cys	Ser	Asp	Thr	Tyr	Ser	Lys	Glu	Leu	Ser	Met	Tyr
	195					200					205				
Ile	Val	Ala	Gly	Tyr	Ser	Asn	Val	Gln	Ser	Leu	Leu	Ile	Ile	Leu	Thr
	210				215					220					
Ser	Tyr	Met	Phe	Ile	Leu	Val	Ala	Ile	Leu	Arg	Ser	His	Ser	Ala	Glu
225				230					235					240	
Gly	Arg	Lys	Lys	Ala	Phe	Ser	Thr	Cys	Gly	Ser	His	Leu	Thr	Val	Val
			245					250					255		
Thr	Ile	Phe	Tyr	Gly	Thr	Leu	Phe	Cys	Met	His	Leu	Arg	Arg	Pro	Thr
		260					265					270			
Asp	Glu	Ser	Val	Glu	Gln	Gly	Lys	Met	Val	Ala	Val	Phe	Tyr	Thr	Thr
	275					280				285					
Val	Ile	Leu	Met	Leu	Asn	Ser	Met	Ile	Tyr	Gly	Leu	Arg	Asn	Lys	Asp
	290				295					300					
Val	Lys	Glu	Ala	Leu	Lys	Lys	Ala	Ile	Gly	Lys	Gln	Thr	Leu	Gly	Lys
305				310					315					320	

<210> 1248

<211> 316

<212> PRT

<213> Unknown (H38g165 protein)

<220>

<223> Synthetic construct

<400> 1248

```

Arg Arg Met Gly Asn His Thr Ala Val Ser Leu Phe Leu Leu Trp Gly
 1      5      10      15
Phe Ser Ser Phe Ser Asp Leu Gln Ser Leu Leu Phe Val Val Ile Leu
 20      25      30
Leu Leu His Val Thr Ile Leu Ala Ala Asn Val Ser Ile Met Gly Ala
 35      40      45
Ile Lys Leu Ser His Asn Leu His Thr Pro Met Tyr Phe Phe Leu Cys
 50      55      60
Gly Leu Ser Phe Ser Glu Thr Cys Thr Thr Val Val Val Ile Pro Arg
 65      70      75      80
Met Leu Val Asp Phe Leu Ser Glu Ser Lys Thr Ile Ser Leu Pro Glu
 85      90      95
Cys Ala Thr Gln Met Phe Phe Phe Leu Gly Phe Ala Ser Asn Asn Cys
 100     105     110
Phe Ile Met Ala Ala Met Ser Tyr Asp Arg Tyr Thr Ala Ile His Asn
 115     120     125
Pro Leu Gln Tyr His Thr Leu Met Thr Arg Lys Ile Cys Leu Gln Met
 130     135     140
Met Met Ala Ser Trp Met Val Gly Phe Leu Phe Ser Leu Cys Ile Ile
 145     150     155     160
Val Thr Val Phe Asn Leu Ser Leu Cys Asp Leu Asn Thr Ile Gln His
 165     170     175
Tyr Phe Cys Asp Ile Ser Pro Val Val Ser Leu Ala Cys Asn Tyr Thr
 180     185     190
Phe Tyr His Glu Met Ala Ile Phe Val Leu Ser Ala Phe Val Leu Val
 195     200     205
Gly Ser Cys Ile Leu Ile Met Ile Ser Tyr Val Phe Ile Val Phe Ile
 210     215     220
Val Ile Lys Met Pro Ser Ala Lys Gly Arg Ser Lys Ala Phe Ser Thr
 225     230     235     240
Cys Ser Ser His Leu Thr Val Val Ser Ile His Tyr Gly Phe Ala Cys
 245     250     255
Phe Val Tyr Leu Arg Pro Lys Asn Ser Asn Ser Phe Asp Glu Asp Met
 260     265     270
Leu Thr Ala Met Ile Tyr Thr Ile Leu Met Pro Leu Leu Asn Pro Ile
 275     280     285
Val Tyr Ser Leu Arg Asn Lys Glu Met Gln Ile Ala Leu Arg Lys Thr
 290     295     300
Leu Gly Ser Val Phe Gly Val Phe Pro Gln Lys Thr
 305     310     315

```

<210> 1249

<211> 319

<212> PRT

<213> Unknown (H38g166 protein)

<220>

<223> Synthetic construct

<400> 1249

```

Met Ser Ala Tyr Asn Asn Thr Asn Ala Arg Pro Ser Thr Phe Ile Leu
 1      5      10      15
Ile Gly Ile Pro Gly Leu Glu Ala Ala His Ile Trp Ile Ser Ile Pro
 20      25      30
Phe Cys Val Val Tyr Leu Leu Ala Leu Leu Gly Asn Gly Ser Leu Leu
 35      40      45
Phe Ile Ile Lys Thr Glu Pro Ser Leu His Glu Pro Met Tyr Leu Phe

```

50	55	60
Leu Cys Met Leu Ala Val	Val Asp Leu Val Val Cys Ser Thr Ala Val	
65	70	75
Pro Lys Leu Leu Ser Leu Phe Trp Phe	His Asp Gly Glu Ile Arg Phe	80
	85	90
Glu Thr Cys Leu Thr Gln Met Phe	Leu Ile His Ser Cys Ser Thr Met	95
	100	105
Glu Ser Gly Phe Phe Leu Ala Met	Ala Phe Asp Arg Tyr Val Ala Ile	110
	115	120
Cys Asn Pro Leu Arg His Ser	Ala Ile Leu Thr Arg Ala Val Ile Gly	125
	130	135
Arg Val Gly Leu Ala Ile Val	Leu Arg Gly Ile Ala Leu Leu Ser Pro	140
	145	150
His Ser Phe Leu Leu Arg Trp	Leu Pro Tyr Cys Arg Thr His Ile Ile	155
	165	170
Ser His Thr Tyr Cys Glu Phe Met	Ala Leu Ile Arg Ile Ala Cys Ala	175
	180	185
Glu Thr Lys Phe Arg Arg Ala Tyr	Ser Leu Ile Val Ala Phe Leu Thr	190
	195	200
Gly Val Val Asp Phe Ile Leu Ile	Ile Tyr Ser Tyr Val Leu Ile Leu	205
	210	215
His Thr Val Phe Gln Leu Pro Ser	Lys Asp Ala Arg Leu Lys Ser Leu	220
	225	230
Gly Thr Cys Gly Ser His Val Cys	Val Ile Leu Val Ser Tyr Thr Pro	235
	245	250
Ala Phe Phe Ser Phe Leu Thr His	Arg Phe Gly His His Val Ala Pro	255
	260	265
His Phe His Ile Phe Val Ala Asn	Ile Tyr Leu Leu Val Pro Pro Met	270
	275	280
Val Asn Pro Ile Ile Tyr Gly Val	Arg Thr Lys Arg Ile Trp Asp Arg	285
	290	295
Phe Leu Lys Val Phe Ser Phe Ser	Lys Pro Leu Ser Lys Ser Phe	300
	305	310
		315

<210> 1250

<211> 307

<212> PRT

<213> Unknown (H38g167 protein)

<220>

<223> Synthetic construct

<400> 1250

Met Leu Asn Phe Thr Asp Val Thr Glu Phe Ile Leu Leu Gly Leu Thr	
1	5
Ser Arg Arg Glu Trp Gln Val Leu Phe Phe Ile Ile Phe Leu Val Val	10
	15
	20
Tyr Ile Ile Thr Met Val Gly Asn Ile Gly Met Met Val Leu Ile Lys	25
	30
	35
Val Ser Pro Gln Leu Asn Asn Pro Met Tyr Phe Phe Leu Ser His Leu	40
	45
	50
Ser Phe Val Asp Val Trp Phe Ser Ser Asn Val Thr Pro Lys Met Leu	55
	60
	65
Glu Asn Leu Leu Ser Asp Lys Lys Thr Ile Thr Tyr Ala Gly Cys Leu	70
	75
	80
	85
Val Gln Cys Phe Phe Phe Ile Ala Leu Val His Val Glu Ile Phe Ile	90
	95
	100
Leu Ala Ala Met Ala Phe Asp Arg Tyr Met Ala Ile Gly Asn Pro Leu	105
	110
	115
Leu Tyr Gly Ser Lys Met Ser Arg Val Val Cys Ile Arg Leu Ile Thr	120
	125
	130
	135
	140

Phe Pro Tyr Ile Tyr Gly Phe Leu Thr Ser Leu Ala Ala Thr Leu Trp
 145 150 155 160
 Thr Tyr Gly Leu Tyr Phe Cys Gly Lys Ile Glu Ile Asn His Phe Tyr
 165 170 175
 Cys Ala Asp Pro Pro Leu Ile Lys Met Ala Cys Ala Gly Thr Phe Val
 180 185 190
 Lys Glu Tyr Thr Met Ile Ile Leu Ala Gly Ile Asn Phe Thr Tyr Ser
 195 200 205
 Leu Thr Val Ile Ile Ile Ser Tyr Leu Phe Ile Leu Ile Ala Ile Leu
 210 215 220
 Arg Met Arg Ser Ala Glu Gly Arg Gln Lys Ala Phe Ser Thr Cys Gly
 225 230 235 240
 Ser His Leu Thr Ala Val Ile Ile Phe Tyr Gly Thr Leu Ile Phe Met
 245 250 255
 Tyr Leu Arg Arg Pro Thr Glu Glu Ser Val Glu Gln Gly Lys Met Val
 260 265 270
 Ala Val Phe Tyr Thr Thr Val Ile Pro Met Leu Asn Pro Met Ile Tyr
 275 280 285
 Ser Leu Arg Asn Lys Asp Val Lys Lys Ala Met Met Lys Val Ile Ser
 290 295 300
 Arg Ser Cys
 305

<210> 1251

<211> 322

<212> PRT

<213> Unknown (H38g168 protein)

<220>

<223> Synthetic construct

<400> 1251

Met Thr Met Thr Thr Glu Asn Pro Asn Gln Thr Val Val Ser His Phe
 1 5 10 15
 Phe Leu Glu Gly Leu Arg Tyr Thr Ala Lys His Ser Ser Leu Phe Phe
 20 25 30
 Leu Leu Phe Leu Leu Ile Tyr Ser Ile Thr Val Ala Gly Asn Leu Leu
 35 40 45
 Ile Leu Leu Thr Val Gly Ser Asp Ser His Leu Ser Leu Pro Met Tyr
 50 55 60
 His Phe Leu Gly His Leu Ser Phe Leu Asp Ala Trp Leu Ser Thr Val
 65 70 75 80
 Thr Val Pro Lys Val Met Ala Gly Leu Leu Thr Leu Asp Gly Lys Val
 85 90 95
 Ile Ser Phe Glu Gly Cys Ala Val Gln Leu Tyr Cys Phe His Phe Leu
 100 105 110
 Ala Ser Thr Glu Cys Phe Leu Tyr Thr Val Met Ala Tyr Asp Arg Tyr
 115 120 125
 Leu Ala Ile Cys Gln Pro Leu His Tyr Pro Val Ala Met Asn Arg Arg
 130 135 140
 Met Cys Ala Glu Met Ala Gly Ile Thr Trp Ala Ile Gly Ala Thr His
 145 150 155 160
 Ala Ala Ile His Thr Ser Leu Thr Phe Arg Leu Leu Tyr Cys Gly Pro
 165 170 175
 Cys His Ile Ala Tyr Phe Phe Cys Asp Ile Pro Pro Val Leu Lys Leu
 180 185 190
 Ala Cys Thr Asp Thr Thr Ile Asn Glu Leu Val Met Leu Ala Ser Ile
 195 200 205
 Gly Ile Val Ala Ala Gly Cys Leu Ile Leu Ile Val Ile Ser Tyr Ile
 210 215 220
 Phe Ile Val Ala Ala Val Leu Arg Ile Arg Thr Ala Gln Gly Arg Gln

```

225          230          235          240
Arg Ala Phe Ser Pro Cys Thr Ala Gln Leu Thr Gly Val Leu Leu Tyr
          245          250          255
Tyr Val Pro Pro Val Cys Ile Tyr Leu Gln Pro Arg Ser Ser Glu Ala
          260          265          270
Gly Ala Gly Ala Pro Ala Val Phe Tyr Thr Ile Val Thr Pro Met Leu
          275          280          285
Asn Pro Phe Ile Tyr Thr Leu Arg Asn Lys Glu Val Lys His Ala Leu
          290          295          300
Gln Arg Leu Leu Cys Ser Ser Phe Arg Glu Ser Thr Ala Gly Ser Pro
305          310          315          320
Pro Pro

```

<210> 1252

<211> 322

<212> PRT

<213> Unknown (H38g169 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(322)

<223> Xaa = Any Amino Acid

<400> 1252

```

Lys Met Leu Asn Phe Thr Asp Val Thr Glu Phe Ile Leu Leu Gly Leu
 1          5          10          15
Thr Ser Arg Arg Glu Trp Gln Val Leu Phe Phe Ile Val Phe Leu Val
          20          25          30
Val Tyr Ile Ile Thr Val Val Gly Asn Ile Gly Met Met Leu Leu Ile
          35          40          45
Lys Val Ser Pro Gln Leu Asn Ser Pro Met Tyr Phe Phe Leu Ser His
          50          55          60
Leu Ser Phe Val Asp Val Trp Phe Ser Ser Asn Val Thr Pro Lys Met
          65          70          75          80
Leu Glu Asn Leu Leu Ser Asp Lys Lys Lys Thr Ile Ser Tyr Ala Gly
          85          90          95
Cys Leu Ala Gln Cys Phe Phe Phe Ile Ala Leu Val His Val Glu Ile
          100          105          110
Phe Ile Leu Ala Ala Ile Ala Phe Asp Arg Tyr Thr Val Ile Gly Asn
          115          120          125
Pro Leu Leu Tyr Gly Ser Lys Met Ser Arg Asp Val Cys Ile Arg Leu
          130          135          140
Ile Thr Phe Pro Tyr Ile Tyr Gly Phe Leu Thr Ser Leu Thr Ala Thr
          145          150          155          160
Leu Trp Thr Tyr Gly Leu Tyr Phe Cys Gly Lys Ile Glu Ile Asn His
          165          170          175
Phe Tyr Cys Ala Asp Pro Pro Leu Ile Lys Met Ala Cys Ala Gly Thr
          180          185          190
Phe Val Lys Glu Tyr Thr Met Leu Ile Leu Ala Gly Ile Asn Phe Thr
          195          200          205
Tyr Ser Leu Thr Val Ile Ile Ile Ser Tyr Leu Phe Ile Leu Ile Ala
          210          215          220
Ile Leu Arg Met Arg Ser Ala Glu Gly Arg Gln Lys Ala Phe Ser Thr
          225          230          235          240
Cys Gly Ser His Leu Thr Ala Val Ile Ile Phe Tyr Gly Thr Leu Ile
          245          250          255
Phe Met Tyr Leu Arg Arg Pro Thr Glu Glu Ser Val Glu Gln Gly Lys
          260          265          270

```

Met Val Ala Val Phe Tyr Thr Thr Val Ile Pro Met Leu Asn Pro Met
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Lys Ala Met Met Lys Val
 290 295 300
 Ile Ser Arg Ser Cys Xaa Thr Lys Xaa Asn Gln Val Xaa Ile Asn Phe
 305 310 315 320
 Val Phe

<210> 1253

<211> 311

<212> PRT

<213> Unknown (H38g170 protein)

<220>

<223> Synthetic construct

<400> 1253

Met Ser Asn Ala Ser Leu Val Thr Ala Phe Ile Leu Thr Gly Leu Pro
 1 5 10 15
 His Ala Pro Gly Leu Asp Ala Leu Leu Phe Gly Ile Phe Leu Val Val
 20 25 30
 Tyr Val Leu Thr Val Leu Gly Asn Leu Leu Ile Leu Leu Val Ile Arg
 35 40 45
 Val Asp Ser His Leu His Thr Pro Met Tyr Tyr Phe Leu Thr Asn Leu
 50 55 60
 Ser Phe Ile Asp Met Trp Phe Ser Thr Val Thr Val Pro Lys Met Leu
 65 70 75 80
 Met Thr Leu Val Ser Pro Ser Gly Arg Ala Ile Ser Phe His Ser Cys
 85 90 95
 Val Ala Gln Leu Tyr Phe Phe His Phe Leu Gly Ser Thr Glu Cys Phe
 100 105 110
 Leu Tyr Thr Val Met Ser Tyr Asp Arg Tyr Leu Ala Ile Ser Tyr Pro
 115 120 125
 Leu Arg Tyr Thr Ser Met Met Ser Gly Ser Arg Cys Ala Leu Leu Ala
 130 135 140
 Thr Gly Thr Trp Leu Ser Gly Ser Leu His Ser Ala Val Gln Thr Ile
 145 150 155 160
 Leu Thr Phe His Leu Pro Tyr Cys Gly Pro Asn Gln Ile Gln His Tyr
 165 170 175
 Phe Cys Asp Ala Pro Pro Ile Leu Lys Leu Ala Cys Ala Asp Thr Ser
 180 185 190
 Ala Asn Val Met Val Ile Phe Val Asp Ile Gly Ile Val Ala Ser Gly
 195 200 205
 Cys Phe Val Leu Ile Val Leu Ser Tyr Val Ser Ile Val Cys Ser Ile
 210 215 220
 Leu Arg Ile Arg Thr Ser Asp Gly Arg Arg Arg Ala Phe Gln Thr Cys
 225 230 235 240
 Ala Ser His Cys Ile Val Val Leu Cys Phe Phe Val Pro Cys Val Val
 245 250 255
 Ile Tyr Leu Arg Pro Gly Ser Met Asp Ala Met Asp Gly Val Val Ala
 260 265 270
 Ile Phe Tyr Thr Val Leu Thr Pro Leu Leu Asn Pro Val Val Tyr Thr
 275 280 285
 Leu Arg Asn Lys Glu Val Lys Lys Ala Val Leu Lys Leu Arg Asp Lys
 290 295 300
 Val Ala His Pro Gln Arg Lys
 305 310

<210> 1254

<211> 320

<212> PRT
 <213> Unknown (H38g171 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(320)

<223> Xaa = Any Amino Acid

<400> 1254

Gly	Val	Gly	Leu	Xaa	Lys	Leu	Xaa	Trp	Gln	Ile	Ile	Phe	Ser	Gly	Asp	1	5	10	15
Ser	Phe	Ser	Thr	Trp	Glu	Met	Phe	Ser	Leu	Ser	Ile	Leu	Gln	Leu	Pro	20	25	30	
Xaa	Met	Tyr	Thr	Val	Ala	Leu	Ser	Gly	Thr	Ser	Ile	Leu	Ile	Phe	Leu	35	40	45	
Ile	Xaa	Thr	Asp	Phe	Xaa	Val	His	Thr	Ser	Leu	Tyr	Ser	Phe	Xaa	Val	50	55	60	
Leu	Ile	Asp	Ile	Ala	Ile	Ser	Val	Val	Lys	Ile	Gly	Ile	Glu	Val	Phe	65	70	75	80
Ser	Gly	Lys	Ile	Asn	Phe	Ser	His	Thr	Gly	Cys	Gly	Thr	Gln	Ile	Phe	85	90	95	
Phe	Phe	Leu	Thr	Ala	Gly	Ile	Phe	Lys	Tyr	Val	Leu	Leu	Thr	Tyr	Met	100	105	110	
Ala	Tyr	Asp	His	Asn	Val	Ala	Ile	Cys	Asp	Leu	Arg	Xaa	Pro	Thr	Phe	115	120	125	
Met	Ser	Asp	Gln	Val	Phe	Xaa	Gln	Trp	Ala	Val	Glu	Ser	Trp	Ile	Gly	130	135	140	
Gly	Lys	Leu	Ser	Ser	Leu	Ala	His	Thr	Ile	Tyr	Ile	Phe	His	Leu	Phe	145	150	155	160
Ser	Tyr	Lys	Ala	Lys	Glu	Ile	Ser	His	Leu	Trp	Pro	Lys	Leu	Phe	Xaa	165	170	175	
Ser	Ser	Ser	Val	Gly	Ile	Pro	Tyr	Ile	Gln	Asn	Asp	Val	Phe	Phe	Thr	180	185	190	
Ile	Ile	Thr	Phe	Leu	Phe	Thr	Leu	Leu	Pro	Leu	Thr	Leu	Thr	Leu	Ser	195	200	205	
Ser	Lys	Leu	Ile	Val	Phe	Thr	Ile	Leu	His	Met	Asn	Ser	Ser	Asn	Gly	210	215	220	
Gly	Ala	Lys	Ser	Trp	His	Thr	Tyr	Cys	Phe	His	Leu	Ser	Val	Leu	Ile	225	230	235	240
Pro	Cys	Cys	Gly	Gln	Ala	Ile	Phe	Val	Tyr	Met	Thr	Ser	Ser	Ser	Phe	245	250	255	
Xaa	Thr	Val	Asn	Lys	Tyr	Gln	Thr	Met	Ser	Val	Leu	Thr	Ala	Xaa	Leu	260	265	270	
Tyr	Pro	Leu	Leu	Lys	Pro	Leu	Ile	Asp	Ile	Leu	Lys	Asn	Ala	Glu	Val	275	280	285	
Ala	Gly	Ala	Trp	Ser	Lys	Phe	Leu	Xaa	Lys	Lys	Ala	Leu	Lys	Ser	Gln	290	295	300	
His	Leu	Ile	Thr	Arg	Ser	Cys	Glu	Asn	Lys	Xaa	Thr	Thr	Glu	Gln	Ser	305	310	315	320

<210> 1255

<211> 320

<212> PRT

<213> Unknown (H38g172 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(320)

<223> Xaa = Any Amino Acid

<400> 1255

```

Met Leu Val Pro Lys Lys Met Val Arg Gly Asn Ser Thr Leu Val Thr
 1           5           10           15
Glu Phe Ile Leu Leu Gly Leu Lys Asp Leu Pro Glu Leu Gln Pro Ile
      20           25           30
Leu Phe Val Leu Phe Leu Leu Ile Tyr Leu Ile Thr Val Gly Gly Asn
      35           40           45
Leu Gly Met Leu Val Leu Ile Arg Ile Asp Ser Arg Leu His Thr Pro
      50           55           60
Met Tyr Phe Phe Leu Ala Ser Leu Ser Cys Leu Asp Leu Tyr Tyr Ser
      65           70           75           80
Thr Asn Val Thr Pro Lys Met Leu Val Asn Phe Phe Ser Asp Lys Lys
      85           90           95
Ala Ile Ser Tyr Ala Ala Cys Leu Val Gln Cys Tyr Phe Phe Ile Ala
      100          105          110
Val Val Ile Thr Glu Tyr Tyr Met Leu Ala Val Met Ala Tyr Asp Arg
      115          120          125
Tyr Val Ala Ile Cys Asn Pro Leu Leu Tyr Ser Ser Lys Met Ser Lys
      130          135          140
Gly Leu Cys Ile Arg Leu Ile Ala Gly Pro Tyr Val Tyr Gly Phe Leu
      145          150          155          160
Ser Gly Leu Met Glu Thr Met Trp Thr Tyr His Leu Thr Phe Cys Gly
      165          170          175
Ser Asn Ile Ile Asn His Phe Tyr Cys Ala Asp Pro Pro Leu Ile Arg
      180          185          190
Leu Ser Cys Ser Asp Thr Phe Ile Lys Glu Thr Ser Met Phe Val Val
      195          200          205
Ala Xaa Phe Asn Leu Ser Ser Ser Leu Ile Ile Ile Leu Ile Ser Tyr
      210          215          220
Ile Phe Ile Leu Ile Ala Ile Leu Arg Met Arg Ser Ala Glu Ser Arg
      225          230          235          240
Arg Lys Ala Phe Ser Thr Cys Gly Ser His Leu Val Ala Val Thr Val
      245          250          255
Phe Tyr Gly Thr Leu Phe Cys Met Tyr Val Arg Pro Pro Thr Asp Arg
      260          265          270
Ser Val Glu Gln Ser Lys Val Ile Ala Val Phe Tyr Thr Phe Val Ser
      275          280          285
Pro Met Leu Asn Pro Ile Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys
      290          295          300
Gln Ala Phe Trp Lys Leu Ile Arg Arg Asn Val Leu Leu Lys Xaa Asn
      305          310          315          320

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<210> 1256

<211> 235

<212> PRT

<213> Unknown (H38g173 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(235)

<223> Xaa = Any Amino Acid

<400> 1256

```

Met Leu Phe Ile Ser Gln Trp Gly Glu Arg Xaa Arg Val Arg Arg Asn
 1           5           10           15
Val Gln Leu Met Thr Ala Phe Ile Leu Met Asp Leu Pro His Val Pro

```

```

      20      25      30
Ala Leu Asp Ala Pro Leu Phe Gly Val Phe Leu Val Val Tyr Val Leu
  35      40      45
Thr Val Leu Gly Asn Leu Leu Ile Leu Leu Val Ile Arg Val Tyr Ser
  50      55      60
His Leu His Thr Pro Lys Tyr Tyr Phe Leu Thr Asn Leu Ser Phe Ile
  65      70      75      80
Asp Leu Trp Phe Phe Thr Val Met Val Pro Lys Met Pro Arg Thr Leu
      85      90      95
Leu Ser Leu Cys Gly Lys Ala Val Ser Phe His Ser Cys Met Thr Gln
      100      105      110
Leu Tyr Phe Phe Tyr Phe Leu Gly Ser Thr Glu Cys Leu Leu Tyr Thr
      115      120      125
Val Met Ser Tyr Asp Arg Tyr Arg Gly Asn Thr Gln His Phe Pro Gly
      130      135      140
Ser Glu Asn Leu Pro Thr Lys Xaa Ala Lys Cys Xaa Trp Pro Gly Gly
      145      150      155      160
His Thr Gly Leu Pro Leu Ile Ile Leu Ala Asp Leu Ser Gly Xaa Leu
      165      170      175
Arg Val Asp Ser Ser Xaa Trp Ala Ile Gln Asn Xaa Xaa Tyr Asn Leu
      180      185      190
Val Ile Gln Val Lys Phe Ile Thr Cys Ile Gly Leu Ser Ile Lys His
      195      200      205
Tyr Ser Lys Gln Leu Ala Gln Leu Xaa Phe Phe His Arg Leu Ser Lys
      210      215      220
Thr Phe Leu Asn Ser Gln Leu Asp Phe Tyr Leu
      225      230      235

```

<210> 1257

<211> 307

<212> PRT

<213> Unknown (H38g174 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(307)

<223> Xaa = Any Amino Acid

<400> 1257

```

Met Ile Thr Glu Phe Ile Leu Ile Gly Phe Ser Asn Leu Gly Asp Leu
  1      5      10      15
Gln Ile Leu Leu Phe Phe Ile Phe Leu Leu Val Tyr Leu Thr Thr Leu
      20      25      30
Met Ala Asn Thr Thr Ile Met Thr Val Ile His Leu Asp Arg Ala Leu
      35      40      45
His Thr Pro Met Tyr Phe Phe Leu Phe Val Leu Ser Cys Ser Glu Thr
      50      55      60
Cys Tyr Thr Leu Val Ile Val Pro Lys Met Leu Thr Asn Leu Leu Ser
      65      70      75      80
Ala Ile Pro Thr Ile Ser Phe Ser Gly Cys Val Val Gln Leu Tyr Leu
      85      90      95
Phe Val Gly Leu Ala Cys Thr Asn Cys Phe Leu Ile Ala Val Met Gly
      100      105      110
Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro Leu Asn Tyr Thr Leu Ile
      115      120      125
Val Ser Xaa Ala Thr Cys Met Gln Leu Val Leu Ala Ser Ser Phe Cys
      130      135      140
Gly Phe Leu Thr Ser Val Ile Val Asn Ile Leu Val Phe Ser Val Leu
      145      150      155      160

```

Leu Cys Ala Ser Asn Arg Ile Asn His Phe Phe Cys Asp Ile Ser Pro
 165 170 175
 Val Ile Lys Leu Gly Cys Thr Asp Thr Asn Leu Lys Glu Met Val Ile
 180 185 190
 Phe Phe Leu Ser Ile Leu Val Leu Leu Val Pro Leu Val Leu Ile Phe
 195 200 205
 Ile Ser Tyr Ile Phe Ile Val Ser Thr Ile Leu Lys Ile Ser Ser Val
 210 215 220
 Glu Gly Gln Cys Lys Ala Phe Ala Thr Cys Ala Ser His Leu Thr Val
 225 230 235 240
 Val Val Val His Tyr Gly Cys Ala Ser Phe Ile Tyr Leu Arg Pro Thr
 245 250 255
 Ser Leu Tyr Ser Ser Asp Lys Asp Arg Leu Val Ala Val Thr Tyr Thr
 260 265 270
 Val Ile Thr Pro Leu Leu Asn Pro Leu Val Tyr Thr Leu Arg Asn Lys
 275 280 285
 Glu Val Lys Met Ala Leu Arg Lys Val Leu Gly Arg Cys Leu Asn Ser
 290 295 300
 Lys Thr Val
 305

<210> 1258

<211> 157

<212> PRT

<213> Unknown (H38g175 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(157)

<223> Xaa = Any Amino Acid

<400> 1258

Ile Cys His Asn Arg Lys Val Ile Pro Ala Ser Met Xaa Asn Met Cys
 1 5 10 15
 Xaa Phe Leu Leu Lys Val Ala Xaa Asp Asn Phe Leu His Val Leu Phe
 20 25 30
 Ile Leu Ala Lys Thr Ala Pro Pro Leu Leu Phe Leu Xaa Glu Ile Pro
 35 40 45
 Ser Tyr Phe Ser Ser Pro Ser Xaa Ile Ile Val Leu Xaa Cys Leu Pro
 50 55 60
 Xaa Phe Leu Lys Gln Leu Val Ile Leu Phe Val Phe Leu Leu Leu Asn
 65 70 75 80
 Xaa Ser Tyr Leu Thr Leu Ile Phe Met Leu Leu Thr Met Lys Ile Thr
 85 90 95
 Ser Ser Phe Lys Ala Ser Thr Val Ile Ser Cys Leu Gln Phe Pro Ser
 100 105 110
 Lys Ala Thr Cys Met His Gly Val Phe Ser Ala Val Cys Ala Gln Met
 115 120 125
 Xaa Pro Tyr Tyr Asn Gly Xaa Ile Ile Xaa His Pro Glu Ser Ile Thr
 130 135 140
 Glu Ser Lys Xaa Leu Thr Cys Val Asn Pro Xaa Phe Asn
 145 150 155

<210> 1259

<211> 321

<212> PRT

<213> Unknown (H38g176 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(321)

<223> Xaa = Any Amino Acid

<400> 1259

```

Gly Thr Lys Ser Ile Lys Leu Thr Ser Leu Ser Glu Phe Leu Leu Leu
 1           5           10           15
Glu Phe Ser Ser Leu Glu Glu Ile Gln Gln Ile Leu Phe Leu Val Cys
      20           25           30
Leu Trp Leu Tyr Leu Ile Val Leu Ser Gly Asn Ile Thr Thr Val Thr
      35           40           45
Val Ile Arg Leu Asp Gln Ser Leu His Ile Pro Val Tyr Leu Phe Leu
      50           55           60
Gly Ile Leu Ser Ile Ser Gly Thr Cys Tyr Thr Phe Val Ile Leu Pro
65           70           75           80
Lys Met Leu Ile Asp Leu Leu Ser Leu Leu Arg Thr Ile Ser Phe Ile
      85           90           95
Asn Cys Ala Leu Gln Met Phe Phe Phe Leu Gly Phe Ala Val Thr Asn
      100          105          110
Phe Met Phe Leu Gly Met Thr Val Tyr Asp Ser Tyr Val Ala Ile Cys
      115          120          125
His Pro Leu His Tyr Pro Val Leu Thr Ser Trp Gln Ile Cys Lys Gln
130          135          140
Leu Ala Ala Thr Cys Ala Val Ile Val Phe Phe Cys Leu Phe Val Phe
145          150          155          160
Thr Asp Arg Leu Leu Leu Arg Phe Ser Leu Leu Phe Cys Gly Pro Asn
      165          170          175
Lys Ile Asn His Tyr Phe Cys Asp Ile Ser Leu Leu Ile Gln Leu Ala
      180          185          190
Cys Thr Asp Thr Tyr Ile Arg Glu Leu Val Ile Phe Ile Gly Gly Ile
      195          200          205
Leu Ala Leu Thr Val Pro Leu Met Phe Ile Cys Ile Ser Tyr Gly Phe
210          215          220
Ile Val His Thr Ile Leu Arg Ile Pro Ser Cys Glu Ser Lys Gln Lys
225          230          235          240
Ala Ile Ser Thr Cys Ala Ser His Leu Ile Met Val Val Val His Tyr
      245          250          255
Gly Cys Ala Ser Phe Val Asn Leu Xaa Pro Ser Ala Lys Xaa Ser Ser
      260          265          270
Ser Lys Xaa Pro Ser Ser Lys Asn Arg Leu Val Thr Val Thr Tyr Thr
      275          280          285
Val Val Thr Pro Leu Leu Asn Pro Met Val Tyr Ser Phe Lys Asn Lys
290          295          300
Asn Val Gln Met Ala Ile Trp Lys Val Ile Cys Gln Gly Gly Phe Pro
305          310          315          320
Pro

```

<210> 1260

<211> 317

<212> PRT

<213> Unknown (H38g177 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(317)

<223> Xaa = Any Amino Acid

<400> 1260
 Met Arg Arg Asn Cys Thr Leu Val Thr Glu Phe Ile Leu Leu Gly Leu
 1 5 10 15
 Ala Asn His Arg Glu Leu Gln Ile Phe Leu Phe Thr Leu Phe Leu Thr
 20 25 30
 Ile Tyr Met Val Thr Val Ala Gly Asn Leu Gly Met Ile Ala Leu Ile
 35 40 45
 Gln Ala Asn Ala Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser Asn
 50 55 60
 Leu Ser Phe Val Asp Leu Cys Phe Ser Ser Asn Val Thr Pro Arg Met
 65 70 75 80
 Leu Glu Ile Phe Leu Ser Glu Lys Lys Ser Ile Ser Tyr Pro Ala Arg
 85 90 95
 Leu Val Gln Cys Tyr Leu Phe Ile Thr Leu Val His Val Glu Leu Tyr
 100 105 110
 Ile Leu Ala Val Met Ala Phe Asp Arg Tyr Met Ala Ile Cys Asn Pro
 115 120 125
 Leu Leu Tyr Gly Ser Arg Met Ser Lys Ser Val Cys Ser Phe Leu Ile
 130 135 140
 Thr Val Leu Tyr Val Tyr Gly Ala Leu Thr Gly Leu Met Glu Thr Met
 145 150 155 160
 Trp Thr Tyr Asn Leu Ala Phe Cys Gly Pro Ser Glu Ile Asn His Phe
 165 170 175
 Tyr Cys Val Asp Pro Pro Leu Ile Lys Leu Ala Cys Ser Asp Thr Tyr
 180 185 190
 Asn Lys Glu Val Ser Met Phe Val Val Ala Gly Phe Asn Phe Thr Tyr
 195 200 205
 Pro Leu Leu Ile Ile Leu Ile Ser Tyr Leu Tyr Ile Phe Pro Ala Thr
 210 215 220
 Leu Arg Ile Cys Ser Thr Glu Gly Arg His Lys Ala Phe Ser Thr Cys
 225 230 235 240
 Gly Ser His Leu Thr Ala Val Thr Ile Phe Tyr Ser Ala Leu Phe Phe
 245 250 255
 Met Tyr Leu Arg Arg Pro Ser Glu Glu Ser Met Glu Gln Gly Lys Met
 260 265 270
 Val Ala Val Phe Tyr Thr Thr Val Ile Pro Met Leu Asn Pro Met Ile
 275 280 285
 Tyr Ser Leu Arg Asn Lys Asp Val Lys Glu Ala Leu Cys Lys Glu Leu
 290 295 300
 Phe Lys Arg Lys Leu Phe Ser Lys Xaa Thr Leu Leu Leu
 305 310 315

<210> 1261

<211> 317

<212> PRT

<213> Unknown (H38g178 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(317)

<223> Xaa = Any Amino Acid

<400> 1261

Thr Asp Val Xaa Glu Phe Leu Leu Leu Gly Leu Ser Glu Asp Pro Glu
 1 5 10 15
 Leu Gln Pro Val Leu Ala Leu Leu Ser Leu Ser Leu Ser Met Tyr Leu
 20 25 30
 Val Thr Val Leu Arg Asn Leu Leu Ser Ile Leu Ala Val Ser Ser Asp

<400> 1262															
Met	Arg	Gly	Phe	Asn	Lys	Thr	Thr	Val	Val	Thr	Gln	Phe	Ile	Leu	Val
1				5					10					15	
Gly	Phe	Ser	Ser	Leu	Gly	Glu	Leu	Gln	Leu	Leu	Leu	Phe	Val	Ile	Phe
			20					25					30		
Leu	Leu	Leu	Tyr	Leu	Thr	Ile	Leu	Val	Ala	Asn	Val	Thr	Ile	Met	Ala
			35				40					45			
Val	Ile	Arg	Phe	Ser	Trp	Thr	Leu	His	Thr	Pro	Met	Tyr	Gly	Phe	Leu
	50					55					60				
Phe	Ile	Leu	Ser	Phe	Ser	Glu	Ser	Cys	Tyr	Thr	Phe	Val	Ile	Ile	Pro
65					70					75					80
Gln	Leu	Leu	Val	His	Leu	Leu	Ser	Asp	Thr	Lys	Thr	Ile	Ser	Phe	Met
				85					90					95	
Ala	Cys	Ala	Thr	Gln	Leu	Phe	Phe	Phe	Leu	Gly	Phe	Ala	Cys	Thr	Asn
			100					105					110		
Cys	Leu	Leu	Ile	Ala	Val	Met	Gly	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Cys
			115				120					125			

His Pro Leu Arg Tyr Thr Leu Ile Ile Asn Lys Arg Leu Gly Leu Glu
 130 135 140
 Leu Ile Ser Leu Ser Gly Ala Thr Gly Phe Phe Ile Ala Leu Val Ala
 145 150 155 160
 Thr Asn Leu Ile Cys Asp Met Arg Phe Cys Gly Pro Asn Arg Val Asn
 165 170 175
 His Tyr Phe Cys Asp Met Ala Pro Val Ile Lys Leu Ala Cys Thr Asp
 180 185 190
 Thr His Val Lys Glu Leu Ala Leu Phe Ser Leu Ser Ile Leu Val Ile
 195 200 205
 Met Val Pro Phe Leu Leu Ile Leu Ile Ser Tyr Gly Phe Ile Val Asn
 210 215 220
 Thr Ile Leu Lys Ile Pro Ser Ala Glu Gly Lys Lys Ala Phe Val Thr
 225 230 235 240
 Cys Ala Ser His Leu Thr Val Val Phe Val His Tyr Gly Cys Ala Ser
 245 250 255
 Ile Ile Tyr Leu Arg Pro Lys Ser Lys Ser Ala Ser Asp Lys Asp Gln
 260 265 270
 Leu Val Ala Val Thr Tyr Thr Val Val Thr Pro Leu Leu Asn Pro Leu
 275 280 285
 Val Tyr Ser Leu Arg Asn Lys Glu Val Lys Thr Ala Leu Lys Arg Val
 290 295 300
 Leu Gly Met Pro Val Ala Thr Lys Met Ser
 305 310

<210> 1263

<211> 314

<212> PRT

<213> Unknown (H38g180 protein)

<220>

<223> Synthetic construct

<400> 1263

Met Met Gly Gln Asn Gln Thr Ser Ile Ser Asp Phe Leu Leu Leu Gly
 1 5 10 15
 Leu Pro Ile Gln Pro Glu Gln Gln Asn Leu Cys Tyr Ala Leu Phe Leu
 20 25 30
 Ala Met Tyr Leu Thr Thr Leu Leu Gly Asn Leu Leu Ile Ile Val Leu
 35 40 45
 Ile Arg Leu Asp Ser His Leu His Thr Pro Met Tyr Leu Phe Leu Ser
 50 55 60
 Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Ile Pro Lys
 65 70 75 80
 Leu Leu Gln Asn Met Gln Asn Gln Asp Pro Ser Ile Pro Tyr Ala Asp
 85 90 95
 Cys Leu Thr Gln Met Tyr Phe Phe Leu Leu Phe Gly Asp Leu Glu Ser
 100 105 110
 Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe
 115 120 125
 Pro Leu His Tyr Thr Ala Ile Met Ser Pro Met Leu Cys Leu Ala Leu
 130 135 140
 Val Ala Leu Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr
 145 150 155 160
 Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp Asn Val Ile Pro His
 165 170 175
 Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu Ala Phe Ser Asp Thr
 180 185 190
 Arg Val Asn Glu Trp Val Ile Phe Met Gly Gly Leu Ile Leu Val
 195 200 205
 Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala Arg Ile Val Ser Ser

```

      210              215              220
Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys Lys Ala Phe Ser Thr
225              230              235              240
Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Val Ile
      245              250              255
Gly Leu Tyr Leu Cys Ser Ser Ala Asn Ser Ser Thr Leu Lys Asp Thr
      260              265              270
Val Met Ala Met Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe
      275              280              285
Ile Tyr Ser Leu Arg Asn Arg Asp Met Lys Gly Ala Leu Ser Arg Val
      290              295              300
Ile His Gln Lys Lys Thr Phe Phe Ser Leu
305              310

```

<210> 1264

<211> 275

<212> PRT

<213> Unknown (H38g181 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(275)

<223> Xaa = Any Amino Acid

<400> 1264

```

Thr Ile Ile Asn Val Asn Ile Ser Pro Glu Phe Val Leu Val Gly Phe
1              5              10              15
Ser Ser Asp Ala Glu Ile Gln Ile Met Leu Phe Val Leu Ile Leu Val
      20              25              30
Ile His Leu Leu Thr Leu Thr Gly Lys Leu Val Met Ile Leu Glu Ile
      35              40              45
Arg Ala Asp Ser His Leu Gln Arg Pro Met Tyr Phe Phe Leu Xaa His
      50              55              60
Leu Ser Phe Leu Asp Leu Ser Tyr Ser Ser Val Thr Val Pro Arg Met
      65              70              75              80
Leu Gln Asn Phe Leu Ser Gly Arg Lys Ala Ser Gln Cys Gly Ala Ala
      85              90              95
Ser Pro Ser Phe Phe Phe Thr Leu Ser Gly Gly Thr Glu Ala Cys Leu
      100              105              110
Phe Ser Ala Met Ala Tyr Asp His Tyr Ala Thr Ile Arg His Pro Val
      115              120              125
Val Tyr Thr Met Val Met Asn Arg Ser Leu Cys Met Val Ile Leu Arg
      130              135              140
Ile Ala Trp Ala Ala Gly Phe Leu Ile Ser Leu Met Asp Ser Leu Phe
      145              150              155              160
Thr His Lys Leu His Phe Cys Gly Pro Asp Ile Ile Pro Tyr Phe Arg
      165              170              175
Cys Lys Leu Pro Pro Phe Phe Pro Leu Ser Tyr Ile Asp Pro Thr Val
      180              185              190
Asn Glu Ile Leu Leu Ala Val Ser Gln Ala Phe Trp Gly Leu Leu Thr
      195              200              205
Leu Ser Leu Ile Phe Phe Ser Tyr Ser Arg Ile Thr Ser Val Ile Leu
      210              215              220
Ser Ile Cys Ser Ser Glu Gly Gln Gly Lys Ala Phe Ser Ala Cys Pro
      225              230              235              240
Ser His Leu Ala Val Val Leu Ser Phe Tyr Gly Thr Ala Phe Phe Arg
      245              250              255
Tyr Pro Gly Ser Thr Ser Gly Ser Val Leu Gly Gln Val Val Ser Val
      260              265              270

```

Gln Tyr Ser
275

<210> 1265
<211> 312
<212> PRT
<213> Unknown (H38g182 protein)

<220>
<223> Synthetic construct

<221> VARIANT
<222> (1)...(312)
<223> Xaa = Any Amino Acid

<400> 1265
Met Arg Arg Asn Phe Thr Leu Val Thr Glu Phe Ile Leu Leu Gly Leu
1 5 10 15
Thr Asn His Gln Glu Leu Gln Ile Leu Leu Phe Met Leu Phe Leu Ala
20 25 30
Ile Tyr Met Val Thr Val Ala Gly Asn Leu Ser Met Ile Ala Leu Ile
35 40 45
Gln Ala Asn Ala Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser His
50 55 60
Leu Ser Phe Leu Asp Leu Cys Phe Ser Ser Asn Val Thr Pro Lys Met
65 70 75 80
Leu Glu Ile Phe Leu Ser Glu Lys Lys Ser Ile Ser Tyr Pro Ala Cys
85 90 95
Leu Val Gln Cys Tyr Leu Tyr Ile Ile Leu Val His Val Glu Ile Tyr
100 105 110
Ile Leu Ala Val Met Ala Phe Asp Xaa Tyr Met Ala Ile Xaa Asn Pro
115 120 125
Leu Leu Tyr Gly Ser Lys Met Ser Lys Ser Val Cys Ser Phe Leu Ile
130 135 140
Thr Val Pro Tyr Val Tyr Gly Ala Leu Thr Gly Leu Met Glu Thr Met
145 150 155 160
Trp Thr Tyr Asn Leu Ala Phe Cys Gly Pro Asn Glu Ile Asn His Phe
165 170 175
Tyr Cys Ala Asp Pro Pro Leu Ile Lys Leu Ala Cys Ser Asp Thr Tyr
180 185 190
Asn Lys Glu Leu Ser Met Phe Val Val Ala Gly Trp Asn Leu Ser Phe
195 200 205
Ser Leu Phe Ile Ile Phe Ile Ser Tyr Phe Tyr Ile Phe Pro Ala Ile
210 215 220
Leu Arg Ile Arg Ser Thr Glu Gly Arg Gln Lys Ala Phe Ser Thr Cys
225 230 235 240
Gly Ser His Leu Thr Ala Val Thr Ile Phe Tyr Ala Thr Leu Phe Phe
245 250 255
Met Cys Leu Arg Pro Pro Ser Glu Glu Ser Met Glu Gln Gly Gln Met
260 265 270
Val Ala Val Leu Tyr Thr Thr Val Ile Pro Met Leu Asn Pro Met Ile
275 280 285
Tyr Ser Leu Arg Asn Lys Asp Val Lys Lys Ala Leu Ser Lys Glu Leu
290 295 300
Phe Lys Arg Lys Leu Phe Pro Lys
305 310

<210> 1266
<211> 315
<212> PRT
<213> Unknown (H38g183 protein)

<220>

<223> Synthetic construct

<400> 1266

```

Met Glu Pro Glu Ala Gly Thr Asn Arg Thr Ala Val Ala Glu Phe Ile
 1          5          10          15
Leu Leu Gly Leu Val Gln Thr Glu Glu Met Gln Pro Val Val Phe Val
          20          25          30
Leu Leu Leu Phe Ala Tyr Leu Val Thr Ile Gly Gly Asn Leu Ser Ile
          35          40          45
Leu Ala Ala Val Leu Val Glu Pro Lys Leu His Ala Pro Met Tyr Phe
          50          55          60
Phe Leu Gly Asn Leu Ser Val Leu Asp Val Gly Cys Ile Thr Val Thr
65          70          75          80
Val Pro Ala Met Leu Gly Arg Leu Leu Ser His Lys Ser Thr Ile Ser
          85          90          95
Tyr Asp Ala Cys Leu Ser Gln Leu Phe Phe His Leu Leu Ala Gly
          100          105          110
Met Asp Cys Phe Leu Leu Thr Ala Met Ala Tyr Asp Arg Leu Leu Ala
          115          120          125
Ile Cys Gln Pro Leu Thr Tyr Ser Thr Arg Met Ser Gln Thr Val Gln
          130          135          140
Arg Met Leu Val Ala Ala Ser Trp Ala Cys Ala Phe Thr Asn Ala Leu
145          150          155          160
Thr His Thr Val Ala Met Ser Thr Leu Asn Phe Cys Gly Pro Asn Glu
          165          170          175
Val Asn His Phe Tyr Cys Asp Leu Pro Gln Leu Phe Gln Leu Ser Cys
          180          185          190
Ser Ser Thr Gln Leu Asn Glu Leu Leu Leu Phe Val Ala Ala Ala Phe
          195          200          205
Met Ala Val Ala Pro Leu Val Phe Ile Ser Val Ser Tyr Ala His Val
          210          215          220
Val Ala Ala Val Leu Gln Ile Arg Ser Ala Glu Gly Arg Lys Lys Ala
225          230          235          240
Phe Ser Thr Cys Gly Ser His Leu Thr Val Val Gly Ile Phe Tyr Gly
          245          250          255
Thr Gly Val Phe Ser Tyr Met Arg Leu Gly Ser Val Glu Ser Ser Asp
          260          265          270
Lys Asp Lys Gly Val Gly Val Phe Met Thr Val Ile Asn Pro Met Leu
          275          280          285
Asn Pro Leu Ile Tyr Ser Leu Arg Asn Thr Asp Val Gln Gly Ala Leu
          290          295          300
Trp Gln Leu Leu Val Gly Glu Arg Ser Leu Thr
305          310          315

```

<210> 1267

<211> 317

<212> PRT

<213> Unknown (H38g184 protein)

<220>

<223> Synthetic construct

<400> 1267

```

Met Leu Arg Asn Gly Ser Ile Val Thr Glu Phe Ile Leu Val Gly Phe
 1          5          10          15
Gln Gln Ser Ser Thr Ser Thr Arg Ala Leu Leu Phe Ala Leu Phe Leu
          20          25          30
Ala Leu Tyr Ser Leu Thr Met Ala Met Asn Gly Leu Ile Ile Phe Ile
          35          40          45

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Thr Ser Trp Thr Asp Pro Lys Leu Asn Ser Pro Met Tyr Phe Phe Leu
  50                      55                      60
Gly His Leu Ser Leu Leu Asp Val Cys Phe Ile Thr Thr Thr Ile Pro
  65                      70                      75                      80
Gln Met Leu Ile His Leu Val Val Arg Asp His Ile Val Ser Phe Val
                      85                      90                      95
Cys Cys Met Thr Gln Thr Tyr Phe Val Phe Cys Val Gly Val Ala Glu
          100                      105                      110
Cys Ile Leu Leu Ala Phe Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys
          115                      120                      125
Tyr Pro Leu Asn Tyr Val Pro Ile Ile Ser Gln Lys Val Cys Val Arg
          130                      135                      140
Leu Val Gly Thr Ala Trp Phe Phe Gly Leu Ile Asn Gly Ile Phe Leu
          145                      150                      155                      160
Glu Tyr Ile Ser Phe Arg Glu Pro Phe Arg Arg Asp Asn His Ile Glu
          165                      170                      175
Ser Phe Phe Cys Glu Ala Pro Ile Val Ile Gly Leu Ser Cys Gly Asp
          180                      185                      190
Pro Gln Phe Ser Leu Trp Ala Ile Phe Ala Asp Ala Ile Val Val Ile
          195                      200                      205
Leu Ser Pro Met Val Leu Thr Val Thr Ser Tyr Val His Ile Leu Ala
          210                      215                      220
Thr Ile Leu Ser Lys Ala Ser Ser Ser Gly Arg Gly Lys Thr Phe Ser
          225                      230                      235                      240
Thr Cys Ala Ser His Leu Thr Val Val Ile Phe Leu Tyr Thr Ser Ala
          245                      250                      255
Met Phe Ser Tyr Met Asn Pro His Ser Thr His Gly Pro Asp Lys Asp
          260                      265                      270
Lys Pro Phe Ser Leu Leu Tyr Thr Ile Ile Thr Pro Met Cys Asn Pro
          275                      280                      285
Ile Ile Tyr Ser Phe Arg Asn Lys Glu Ile Lys Glu Ala Met Val Arg
          290                      295                      300
Ala Leu Gly Arg Thr Arg Leu Ala Gln Pro Gln Ser Val
          305                      310                      315

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<210> 1268

<211> 324

<212> PRT

<213> Unknown (H38g185 protein)

<220>

<223> Synthetic construct

<400> 1268

```

Met Phe Tyr Phe Phe Pro Pro Leu Gln Ile Leu Ala Glu Asn Leu Thr
  1                      5                      10                      15
Met Val Thr Glu Phe Leu Leu Leu Gly Phe Ser Ser Leu Gly Glu Ile
          20                      25                      30
Gln Leu Ala Leu Phe Val Val Phe Leu Phe Leu Tyr Leu Val Ile Leu
          35                      40                      45
Ser Gly Asn Val Thr Ile Ile Ser Val Ile His Leu Asp Lys Ser Leu
          50                      55                      60
His Thr Pro Met Tyr Phe Phe Leu Gly Ile Leu Ser Thr Ser Glu Thr
          65                      70                      75                      80
Phe Tyr Thr Phe Val Ile Leu Pro Lys Met Leu Ile Asn Leu Leu Ser
          85                      90                      95
Val Ala Arg Thr Ile Ser Phe Asn Cys Cys Ala Leu Gln Met Phe Phe
          100                      105                      110
Phe Leu Gly Phe Ala Ile Thr Asn Cys Leu Leu Leu Gly Val Met Gly
          115                      120                      125
Tyr Asp Arg Tyr Ala Ala Ile Cys His Pro Leu His Tyr Pro Thr Leu

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      130              135              140
Met Ser Trp Gln Val Cys Gly Lys Leu Ala Ala Cys Ala Ile Gly
145              150              155              160
Gly Phe Leu Ala Ser Leu Thr Val Val Asn Leu Val Phe Ser Leu Pro
      165              170              175
Phe Cys Ser Ala Asn Lys Val Asn His Tyr Phe Cys Asp Ile Ser Ala
      180              185              190
Val Ile Leu Leu Ala Cys Thr Asn Thr Asp Val Asn Glu Phe Val Ile
      195              200              205
Phe Ile Cys Gly Val Leu Val Leu Val Val Pro Phe Leu Phe Ile Cys
      210              215              220
Val Ser Tyr Leu Cys Ile Leu Arg Thr Ile Leu Lys Ile Pro Ser Ala
225              230              235              240
Glu Gly Arg Arg Lys Ala Phe Ser Thr Cys Ala Ser His Leu Ser Val
      245              250              255
Val Ile Val His Tyr Gly Cys Ala Ser Phe Ile Tyr Leu Arg Pro Thr
      260              265              270
Ala Asn Tyr Val Ser Asn Lys Asp Arg Leu Val Thr Val Thr Tyr Thr
      275              280              285
Ile Val Thr Pro Leu Leu Asn Pro Met Val Tyr Ser Leu Arg Asn Lys
      290              295              300
Asp Val Gln Leu Ala Ile Arg Lys Val Leu Gly Lys Lys Gly Ser Leu
305              310              315              320
Lys Leu Tyr Asn

```

<210> 1269

<211> 327

<212> PRT

<213> Unknown (H38g186 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(327)

<223> Xaa = Any Amino Acid

<400> 1269

```

Lys Leu Gln Leu Asn Asn Phe Thr Glu Val Thr Met Phe Ile Leu Ile
 1              5              10              15
Ser Phe Thr Glu Glu Phe Asp Val Gln Val Phe Leu Phe Leu Leu Phe
      20              25              30
Leu Ala Ile Tyr Leu Phe Thr Leu Ile Gly Asn Leu Gly Leu Val Val
      35              40              45
Pro Ile Ile Gly Asp Phe Trp Leu His Ser Pro Met Tyr Tyr Phe Leu
      50              55              60
Gly Val Leu Ser Phe Leu Asp Val Cys Tyr Ser Thr Val Val Thr Pro
      65              70              75              80
Lys Met Leu Val Asn Phe Leu Ala Lys Asn Lys Ser Ile Ser Phe Leu
      85              90              95
Gly Cys Ala Thr Gln Met Phe Leu Ala Cys Thr Phe Gly Thr Thr Glu
      100              105              110
Cys Phe Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Tyr
      115              120              125
Asn Pro Leu Leu Tyr Ser Val Ser Met Ser Pro Arg Val Tyr Val Pro
      130              135              140
Leu Ile Thr Ala Ser Tyr Val Ala Ser Ile Leu His Ala Thr Ile His
      145              150              155              160
Thr Val Ala Thr Phe Ser Leu Ser Phe Cys Gly Ser Asn Glu Ile Arg
      165              170              175

```

His Val Phe Cys Asn Met Pro Pro Leu Leu Ala Ile Ser Cys Ser Asp
 180 185 190
 Thr His Val Ile Gln Leu Leu Phe Phe Tyr Phe Val Gly Ser Ile Glu
 195 200 205
 Ile Val Thr Ile Leu Ile Val Leu Ile Ser Tyr Gly Phe Ile Leu Leu
 210 215 220
 Ala Ile Leu Lys Met Gln Ser Ala Glu Gly Arg Arg Lys Val Phe Ser
 225 230 235 240
 Thr Cys Gly Ala His Leu Thr Gly Val Thr Ile Tyr His Gly Thr Ile
 245 250 255
 Leu Phe Met Tyr Val Arg Pro Ser Ser Ser Tyr Thr Ser Asp Asn Asp
 260 265 270
 Met Ile Val Ser Ile Phe Tyr Thr Ile Val Ile Pro Met Leu Asn Pro
 275 280 285
 Ile Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Glu Ala Ile Lys Arg
 290 295 300
 Leu Leu Val Arg Asn Trp Phe Ile Asn Lys Leu Xaa Phe Xaa Asn Xaa
 305 310 315 320
 Val Lys Leu Gln Ile Ile Leu
 325

<210> 1270

<211> 319

<212> PRT

<213> Unknown (H38g187 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(319)

<223> Xaa = Any Amino Acid

<400> 1270

Met Asp Arg Val Asn Asn Ser Ala Val Ser Lys Phe Val Leu Ile Gly
 1 5 10 15
 Leu Ser Lys Pro Trp Glu Met His Leu Phe Leu Phe Trp Phe Phe
 20 25 30
 Ser Val Phe Tyr Met Gly Ile Ile Leu Glu Asn Leu Phe Ile Val Phe
 35 40 45
 Thr Val Ile Ile Asp Ser His Leu Asn Ser Pro Val Tyr Cys Leu Leu
 50 55 60
 Ala Asn Ile Tyr Leu Leu Asp Leu Val Phe Ser Tyr Ser Ser Asp Phe
 65 70 75 80
 Phe Thr Asn Cys Ser Ile Ile Ser Phe Pro Arg Cys Ile Ile Gln Ile
 85 90 95
 Phe Phe Ile Cys Val Met Arg Lys Ile Glu Met Val Leu Leu Ile Thr
 100 105 110
 Met Ala Xaa Ser Arg Tyr Thr Ala Ile Cys Lys Pro Pro His Tyr Leu
 115 120 125
 Thr Thr Met Asn Pro Lys Met Cys Val Ser Leu Leu Glu Ala Ser Trp
 130 135 140
 Ile Val Arg Ile Ile His Ala Val Ser Gln Phe Val Phe Ala Ile Asn
 145 150 155 160
 Leu Pro Phe Cys Gly Pro Asn Arg Val Gly Ser Phe His Cys Asp Phe
 165 170 175
 Pro Tyr Val Met Lys Leu Ala Cys Val Asp Thr Tyr Lys Leu Glu Val
 180 185 190
 Val Val Thr Ala Asn Ser Gly Leu Ile Ser Ile Ala Thr Cys Phe Leu
 195 200 205
 Leu Ile Ile Ser Tyr Ile Phe Ile Ser Val Thr Val Xaa Asn Pro Ser

210		215		220
Ser Gly Asp Leu Ser	Lys Ala Phe Val Ser Cys Ser Asp His Ile Thr			
225	230	235		240
Val Gly Ile Leu Phe	Met Pro Cys Ile Phe Leu Tyr Val Xaa Pro			
	245	250		255
Leu Pro Lys Thr Thr	His Asp Xaa Tyr Leu Phe Ile Val Pro Leu Leu			
	260	265		270
Ser Pro Leu Ser Arg	Ile Tyr Thr Leu Arg Asn Lys Asp Met Asn Val			
	275	280		285
Ser Met Glu Arg Leu	Gly Lys Trp Ile Ala Gly Ser Ser Arg Met Ser			
	290	295		300
Xaa Xaa Met Val Leu	Ser Arg Val Gln Asp Asp Ser Val Ser Pro			
305	310	315		

<210> 1271

<211> 324

<212> PRT

<213> Unknown (H38g188 protein)

<220>

<223> Synthetic construct

<400> 1271

Met Thr Thr Ile Ile	Leu Glu Val Asp Asn His Thr Val Thr Thr Arg
1	5 10 15
Phe Ile Leu Leu Gly	Phe Pro Thr Arg Pro Ala Phe Gln Leu Leu Phe
	20 25 30
Phe Ser Ile Phe Leu	Ala Thr Tyr Leu Leu Thr Leu Leu Glu Asn Leu
	35 40 45
Leu Ile Ile Leu Ala	Ile His Ser Asp Gly Gln Leu His Lys Pro Met
	50 55 60
Tyr Phe Phe Leu Ser	His Leu Ser Phe Leu Glu Met Trp Tyr Val Thr
65	70 75 80
Val Ile Ser Pro Lys	Met Leu Val Asp Phe Leu Ser His Asp Lys Ser
	85 90 95
Ile Ser Phe Asn Gly	Cys Met Thr Gln Leu Tyr Phe Phe Val Thr Phe
	100 105 110
Val Cys Thr Glu Tyr	Ile Leu Leu Ala Ile Met Ala Phe Asp Arg Tyr
	115 120 125
Val Ala Ile Cys Asn	Pro Leu Arg Tyr Pro Val Ile Met Thr Asn Gln
	130 135 140
Leu Cys Gly Thr Leu	Ala Gly Gly Cys Trp Phe Cys Gly Leu Met Thr
145	150 155 160
Ala Met Ile Lys Met	Val Phe Ile Ala Gln Leu His Tyr Cys Gly Met
	165 170 175
Pro Gln Ile Asn His	Tyr Phe Cys Asp Ile Ser Pro Leu Leu Asn Val
	180 185 190
Ser Cys Glu Asp Ala	Ser Gln Ala Glu Met Val Asp Phe Phe Leu Ala
	195 200 205
Leu Met Val Ile Ala	Ile Pro Leu Cys Val Val Val Ala Ser Tyr Ala
	210 215 220
Ala Ile Leu Ala Thr	Ile Leu Arg Ile Pro Ser Ala Gln Gly Arg Gln
225	230 235 240
Lys Ala Phe Ser Thr	Cys Ala Ser His Leu Thr Val Val Ile Leu Phe
	245 250 255
Tyr Ser Met Thr Leu	Phe Thr Tyr Ala Arg Pro Lys Leu Met Tyr Ala
	260 265 270
Tyr Asn Ser Asn Lys	Val Val Ser Val Leu Tyr Thr Val Ile Val Pro
	275 280 285
Leu Leu Asn Pro Ile	Ile Tyr Cys Leu Arg Asn His Glu Val Lys Ala
290	295 300

Ala Leu Arg Lys Thr Ile His Cys Arg Gly Ser Gly Pro Gln Gly Asn
 305 310 315 320
 Gly Ala Phe Ser

<210> 1272

<211> 323

<212> PRT

<213> Unknown (H38g189 protein)

<220>

<223> Synthetic construct

<400> 1272

Met Met Gly Gln Asn Gln Thr Ser Ile Ser Asp Phe Leu Leu Leu Gly
 1 5 10 15
 Leu Pro Ile Gln Pro Glu Gln Gln Asn Leu Cys Tyr Ala Leu Phe Leu
 20 25 30
 Ala Met Tyr Leu Thr Thr Leu Leu Gly Asn Leu Leu Ile Ile Val Leu
 35 40 45
 Ile Arg Leu Asp Ser His Leu His Thr Pro Val Tyr Leu Phe Leu Ser
 50 55 60
 Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys
 65 70 75 80
 Leu Leu Gln Asn Met Gln Asn Gln Asp Pro Ser Ile Pro Tyr Ala Asp
 85 90 95
 Cys Leu Thr Gln Met Tyr Phe Phe Leu Tyr Phe Ser Asp Leu Glu Ser
 100 105 110
 Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe
 115 120 125
 Pro Met His Tyr Thr Ala Ile Cys Phe Leu Leu His Tyr Thr Ala Ile
 130 135 140
 Met Ser Pro Met Leu Cys Leu Ser Val Val Ala Leu Ser Trp Val Leu
 145 150 155 160
 Thr Thr Phe His Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Cys
 165 170 175
 Phe Cys Ala Asp Asn Val Ile Pro His Phe Phe Cys Asp Met Ser Ala
 180 185 190
 Leu Leu Lys Leu Ala Cys Ser Asp Thr Arg Val Asn Glu Trp Val Ile
 195 200 205
 Phe Ile Met Gly Gly Leu Ile Leu Val Ile Pro Phe Leu Leu Ile Leu
 210 215 220
 Gly Ser Tyr Ala Arg Ile Val Ser Ser Ile Leu Lys Val Pro Ser Ser
 225 230 235 240
 Lys Gly Ile Cys Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val
 245 250 255
 Val Ser Leu Phe Tyr Gly Thr Val Ile Gly Leu Tyr Leu Cys Pro Ser
 260 265 270
 Ala Asn Ser Ser Thr Leu Lys Asp Thr Val Met Ala Met Met Tyr Thr
 275 280 285
 Val Val Thr Pro Met Leu Thr Pro Phe Ile Tyr Ser Leu Arg Asn Arg
 290 295 300
 Asp Met Lys Gly Ala Leu Glu Arg Val Ile Cys Lys Arg Lys Asn Pro
 305 310 315 320
 Phe Leu Leu

<210> 1273

<211> 311

<212> PRT

<213> Unknown (H38g190 protein)

<220>

<223> Synthetic construct

<400> 1273

```

Met Gly Arg Arg Asn Asn Thr Asn Val Pro Asp Phe Ile Leu Thr Gly
 1           5           10           15
Leu Ser Asp Ser Glu Glu Val Gln Met Ala Leu Phe Ile Leu Phe Leu
          20           25           30
Leu Ile Tyr Leu Ile Thr Met Leu Gly Asn Val Gly Met Ile Leu Ile
          35           40           45
Ile Arg Leu Asp Leu Gln Leu His Thr Pro Met Tyr Phe Phe Leu Thr
          50           55           60
His Leu Ser Phe Ile Asp Leu Ser Tyr Ser Thr Val Ile Thr Pro Lys
65           70           75           80
Thr Leu Ala Asn Leu Leu Thr Ser Asn Tyr Ile Ser Phe Met Gly Cys
          85           90           95
Phe Ala Gln Met Phe Phe Phe Val Phe Leu Gly Ala Ala Glu Cys Phe
          100          105          110
Leu Leu Ser Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Ser Pro
          115          120          125
Leu Arg Tyr Pro Val Ile Met Ser Lys Arg Leu Cys Cys Ala Leu Val
          130          135          140
Thr Gly Pro Tyr Val Ile Ser Phe Ile Asn Ser Phe Val Asn Val Val
145          150          155          160
Trp Met Ser Arg Leu His Phe Cys Asp Ser Asn Val Val Arg His Phe
          165          170          175
Phe Cys Asp Thr Ser Pro Ile Leu Ala Leu Ser Cys Met Asp Thr Tyr
          180          185          190
Asp Ile Glu Ile Met Ile His Ile Leu Ala Gly Ser Thr Leu Met Val
          195          200          205
Ser Leu Ile Thr Ile Ser Ala Ser Tyr Val Ser Ile Leu Ser Thr Ile
          210          215          220
Leu Lys Ile Asn Ser Thr Ser Gly Lys Gln Lys Ala Leu Ser Thr Cys
225          230          235          240
Ala Ser His Leu Leu Gly Val Thr Ile Phe Tyr Gly Thr Met Ile Phe
          245          250          255
Thr Tyr Leu Lys Pro Arg Lys Ser Tyr Ser Leu Gly Arg Asp Gln Val
          260          265          270
Ala Ser Val Phe Tyr Thr Ile Val Ile Pro Met Leu Asn Pro Leu Ile
          275          280          285
Tyr Ser Leu Arg Asn Lys Glu Val Lys Asn Ala Leu Ile Arg Val Met
          290          295          300
Gln Arg Arg Gln Asp Ser Arg
305          310

```

<210> 1274

<211> 305

<212> PRT

<213> Unknown (H38g191 protein)

<220>

<223> Synthetic construct

<400> 1274

```

Met Val Thr Glu Phe Ile Phe Leu Gly Leu Ser Asp Ser Gln Glu Leu
 1           5           10           15
Gln Thr Phe Leu Phe Met Leu Phe Phe Val Phe Tyr Gly Gly Ile Val
          20           25           30
Phe Gly Asn Leu Leu Ile Val Ile Thr Val Val Ser Asp Ser His Leu
          35           40           45

```

His Ser Pro Met Tyr Phe Leu Leu Ala Asn Leu Ser Leu Ile Asp Leu
 50 55 60
 Ser Leu Ser Ser Val Thr Ala Pro Lys Met Ile Thr Asp Phe Phe Ser
 65 70 75 80
 Gln Arg Lys Val Ile Ser Phe Lys Gly Cys Leu Val Gln Ile Phe Leu
 85 90 95
 Leu His Phe Phe Gly Gly Ser Glu Met Val Ile Leu Ile Ala Met Gly
 100 105 110
 Phe Asp Arg Tyr Ile Ala Ile Cys Lys Pro Leu His Tyr Thr Thr Ile
 115 120 125
 Met Cys Gly Asn Ala Cys Val Gly Ile Met Ala Val Thr Trp Gly Fle
 130 135 140
 Gly Phe Leu His Ser Val Ser Gln Leu Ala Phe Ala Val His Leu Leu
 145 150 155 160
 Phe Cys Gly Pro Asn Glu Val Asp Ser Phe Tyr Cys Asp Leu Pro Arg
 165 170 175
 Val Ile Lys Leu Ala Cys Thr Asp Thr Tyr Arg Leu Asp Ile Met Val
 180 185 190
 Ile Ala Asn Ser Gly Val Leu Thr Val Cys Ser Phe Val Leu Leu Ile
 195 200 205
 Ile Ser Tyr Thr Ile Ile Leu Met Thr Ile Gln His Arg Pro Leu Asp
 210 215 220
 Lys Ser Ser Lys Ala Leu Ser Thr Leu Thr Ala His Ile Thr Val Val
 225 230 235 240
 Leu Leu Phe Phe Gly Pro Cys Val Phe Ile Tyr Ala Trp Pro Phe Pro
 245 250 255
 Ile Lys Ser Leu Asp Lys Phe Leu Ala Val Phe Tyr Ser Val Ile Thr
 260 265 270
 Pro Leu Leu Asn Pro Ile Ile Tyr Thr Leu Arg Asn Lys Asp Met Lys
 275 280 285
 Thr Ala Ile Arg Gln Leu Arg Lys Trp Asp Ala His Ser Ser Val Lys
 290 295 300
 Phe
 305

<210> 1275

<211> 312

<212> PRT

<213> Unknown (H38g192 protein)

<220>

<223> Synthetic construct

<400> 1275

Met Glu Arg Val Asn Glu Thr Val Val Arg Glu Val Ile Phe Leu Gly
 1 5 10 15
 Phe Ser Ser Leu Ala Arg Leu Gln Gln Leu Leu Phe Val Ile Phe Leu
 20 25 30
 Leu Leu Tyr Leu Phe Thr Leu Gly Thr Asn Ala Ile Ile Ile Ser Thr
 35 40 45
 Ile Val Leu Asp Arg Ala Leu His Ile Pro Met Tyr Phe Phe Leu Ala
 50 55 60
 Ile Leu Ser Cys Ser Glu Ile Cys Tyr Thr Phe Ile Ile Val Pro Lys
 65 70 75 80
 Met Leu Val Asp Leu Leu Ser Gln Lys Lys Thr Ile Ser Phe Leu Gly
 85 90 95
 Cys Ala Ile Gln Met Phe Ser Phe Leu Phe Leu Gly Cys Ser His Ser
 100 105 110
 Phe Leu Leu Ala Val Met Gly Tyr Asp Arg Tyr Ile Ala Ile Cys Asn
 115 120 125
 Pro Leu Arg Tyr Ser Val Leu Met Gly His Gly Val Cys Met Gly Leu

130	135	140
Val Ala Ala Ala Cys	Ala Cys Gly Phe Thr	Val Ala Gln Ile Ile Thr
145	150	155
Ser Leu Val Phe His	Leu Pro Phe Tyr Ser	Ser Asn Gln Leu His His
165	170	175
Phe Phe Cys Asp Ile	Ala Pro Val Leu Lys Leu	Ala Ser His His Asn
180	185	190
His Phe Ser Gln Ile	Val Ile Phe Met Leu Cys Thr	Leu Val Leu Ala
195	200	205
Ile Pro Leu Leu Leu	Ile Leu Val Ser Tyr Val	His Ile Leu Ser Ala
210	215	220
Ile Leu Gln Phe Pro	Ser Thr Leu Gly Arg Cys	Lys Ala Phe Ser Thr
225	230	235
Cys Val Ser His Leu	Ile Ile Val Thr Val	His Tyr Gly Cys Ala Ser
245	250	255
Phe Ile Tyr Leu Arg	Pro Gln Ser Asn Tyr Ser	Ser Ser Gln Asp Ala
260	265	270
Leu Ile Ser Val Ser	Tyr Thr Ile Thr Pro	Leu Phe Asn Pro Met
275	280	285
Ile Tyr Ser Leu Arg	Asn Lys Glu Phe Lys Ser	Ala Leu Cys Lys Ile
290	295	300
Val Arg Arg Thr Ile	Ser Leu Leu	
305	310	

<210> 1276

<211> 244

<212> PRT

<213> Unknown (H38g193 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(244)

<223> Xaa = Any Amino Acid

<400> 1276

Met Met Ile Ser Ser	Asp Glu Glu Asn Asp Thr	Asn Met Met Glu Phe
1	5	10
Ile Leu Val Gly Leu	Ser Arg Gln Pro Ala Ser	Gln Leu Leu Phe Phe
20	25	30
Xaa Ala Ile Leu Phe	Ile Tyr Ser Val Thr	Leu Val Gly Asn Ile Leu
35	40	45
Ile Ile Val Ile Ile	Gln Ile Asp Ser His	Leu Gln Thr Pro Met Tyr
50	55	60
Phe Phe Leu Ile Gln	Val Ser Phe Leu Asp Ile	Cys Ser Thr Pro Thr
65	70	75
Val Leu Val Asn Cys	Xaa Lys Asp Phe Pro Ser	Val Ser Tyr Ser Gly
85	90	95
Cys Leu Phe Xaa Met	Thr Ile Phe Leu Tyr Leu	Gly Val Thr Glu Cys
100	105	110
Val Phe Phe Leu Phe	Cys Phe Glu Cys Phe Leu	Ile Ala Val Met Ala
115	120	125
Tyr Asp Arg Phe Val	Ala Ile Ser Lys Pro Leu	Cys Tyr Pro Phe Ile
130	135	140
Ile Asn Ser Asn Val	Cys Ile Trp Met Val Ala	Gly Val Trp Ala His
145	150	155
Pro Gly Arg Thr Asn	Pro Ile Leu Trp Pro Gln	Cys Ser Gln His Phe
165	170	175
Thr Cys Glu Leu Gln	Val Ile Phe Lys Leu Thr	Cys Ser Pro Val Leu
180	185	190

Val Lys Glu Ile Gln Xaa Phe Met Ile Pro Gly Cys Thr Leu Xaa Ala
 195 200 205
 Leu Tyr Gln His Xaa Val Cys Ser Tyr Ser Xaa Ala Arg Gln Gln Thr
 210 215 220
 His Pro Arg Ser Xaa Glu Ala Tyr Asn Xaa Gly Ile Arg Xaa Gly Ile
 225 230 235 240
 Ile Gly Val His

<210> 1277

<211> 306

<212> PRT

<213> Unknown (H38g194 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(306)

<223> Xaa = Any Amino Acid

<400> 1277

Thr Ala Gly Ser Asn Phe Thr Glu Val Thr Val Phe Ile Leu Ser Gly
 1 5 10 15
 Tyr Ala Asn His Pro Glu Leu Gln Val Ser Phe Phe Leu Met Phe Leu
 20 25 30
 Phe Ile Tyr Leu Phe Thr Ile Leu Gly Asn Leu Gly Leu Ile Met Leu
 35 40 45
 Ile Arg Met Asp Ser Gln Leu His Thr Pro Met Tyr Phe Phe Leu Ser
 50 55 60
 Asn Leu Ala Phe Ile Asp Ile Phe Tyr Ser Ser Val Thr Pro Lys
 65 70 75 80
 Thr Leu Ala Asn Phe Gln Ser Asn Gln Arg Ser Ile Ser Phe Val Gly
 85 90 95
 Cys Phe Val Gln Met Tyr Phe Ser Val Gly Leu Val Cys Thr Glu Cys
 100 105 110
 Phe Leu Leu Gly Ser Met Ala Tyr Asp Cys Tyr Val Ala Ile Trp Asn
 115 120 125
 Pro Tyr Ser Val Val Ile Ser Xaa Lys Ala Cys Asn Trp Leu Gly Val
 130 135 140
 Met Ser Tyr Thr Ile Gly Phe Thr Asn Ser Leu Val Ser Val Trp Val
 145 150 155 160
 Ile Ser Gly Leu Phe Cys Asp Ser Ser Ile Asn Phe Phe Phe Cys Asp
 165 170 175
 Thr Thr Ala Leu Leu Ala Leu Ser Cys Val Asp Ala Phe Ser Thr Glu
 180 185 190
 Met Val Ser Phe Ala Leu Ala Gly Phe Thr Leu Leu Gly Ser Ile Leu
 195 200 205
 Ile Ile Thr Val Thr Tyr Ile Ala Ile Thr Ser Ala Ile Leu Lys Asn
 210 215 220
 Gln Trp Ala Ala Gly Trp Gln Lys Ala Phe Ser Thr Cys Ala Phe His
 225 230 235 240
 Leu Met Ala Leu Thr Ile Phe Tyr Gly Ser Leu Ile Phe Thr Tyr Leu
 245 250 255
 Gln Leu Asp Lys Thr Ser Ser Leu Ile His Ala Gln Leu Ala Phe Val
 260 265 270
 Phe Tyr Met Thr Val Ile Pro Met Leu Asn Pro Leu Ile Xaa Ser Leu
 275 280 285
 Arg Asn Lys Asp Val Lys Asn Ala Leu Leu Arg Val Ile His Arg Lys
 290 295 300
 Leu Phe

305

<210> 1278

<211> 251

<212> PRT

<213> Unknown (H38g195 protein)

<220>

<223> Synthetic construct

<400> 1278

```

Met Ala Asn Ser Ser Ser Val Thr Glu Phe Leu Val Leu Gly Phe Ser
 1          5          10          15
Ser Leu Gly Glu Leu Gln Leu Val Leu Phe Ala Val Phe Leu Cys Leu
          20          25          30
Tyr Leu Ile Ile Leu Ser Gly Asn Ile Ile Ile Ile Ser Val Ile His
          35          40          45
Leu Asp His Ser Leu His Thr Pro Met Tyr Phe Phe Leu Gly Ile Leu
          50          55          60
Ser Ile Ser Glu Ile Phe Tyr Thr Thr Val Ile Leu Pro Lys Met Leu
          65          70          75          80
Ile Asn Leu Phe Ser Val Phe Arg Thr Leu Ser Phe Val Ser Cys Ala
          85          90          95
Thr Gln Met Phe Phe Phe Leu Gly Phe Ala Val Thr Asn Cys Leu Leu
          100          105          110
Leu Gly Val Met Gly Tyr Asp Arg Tyr Ala Ala Ile Cys Gln Pro Leu
          115          120          125
Gln Tyr Ala Val Leu Met Ser Trp Arg Val Cys Gly Gln Leu Ile Ala
          130          135          140
Thr Cys Ile Ile Ser Gly Phe Leu Ile Ser Leu Val Gly Thr Thr Phe
          145          150          155          160
Val Phe Ser Leu Pro Phe Cys Gly Ser Asn Lys Val Asn His Tyr Phe
          165          170          175
Cys Asp Ile Ser Pro Val Ile Arg Leu Ala Cys Ala Asp Ser Tyr Ile
          180          185          190
Ser Glu Leu Val Ile Phe Ile Phe Gly Val Leu Val Leu Val Val Pro
          195          200          205
Leu Ile Phe Ile Cys Ile Ser Tyr Gly Phe Ile Val Arg Thr Ile Leu
          210          215          220
Lys Ile Pro Ser Ala Glu Gly Lys Gln Lys Ala Phe Ser Thr Cys Ala
          225          230          235          240
Ser His Leu Ile Val Val Ile Val His Tyr Gly
          245          250

```

<210> 1279

<211> 315

<212> PRT

<213> Unknown (H38g196 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(315)

<223> Xaa = Any Amino Acid

<400> 1279

```

Met Gly Gly Leu Lys Arg Asp Asn Ala Ser Glu Met Thr Glu Leu Ile
 1          5          10          15
Leu Val Gly Phe Ala Gln His Pro Glu Ile Gln Thr Ala Phe Phe Leu
          20          25          30

```

Glu Leu Leu Phe Phe Tyr Xaa Ser Gln Leu Phe Glu Asn Ile Leu Ile
 35 40 45
 Val Ala Val Val Arg Xaa Asp Ser Arg Leu His Thr Pro Met Gly Phe
 50 55 60
 Phe Phe Leu Ser Thr Leu Ser Ser Leu Glu Met Cys Tyr Ser Ile Ser
 65 70 75 80
 Trp Glu Leu Xaa Val Leu Ala Gln Cys Ile Lys Asp Phe Pro Thr Ile
 85 90 95
 Ser Tyr Asn Ser Cys Ser Val Gln Met Ile Thr His Leu Phe Leu Gly
 100 105 110
 Thr Ala Gln Cys Leu Leu Leu Ala Gly Met Ala Tyr Asn Arg Phe Val
 115 120 125
 Glu Ile Ser Tyr Leu Leu His Tyr Thr Ile Ile Met Ser Asn Arg Val
 130 135 140
 Cys Ile Gln Leu Ala Leu Gly Ile Trp Thr His Ala Phe Leu Val Ala
 145 150 155 160
 Val Thr Leu Ile Ile Ala Ile Pro Ala Ser Tyr Tyr Gly His Asn Val
 165 170 175
 Ile Asn His Phe Thr Cys Glu Ile Gln Ala Leu Leu Lys Leu Val Cys
 180 185 190
 Ser Asp Thr Leu Val Ser Leu Ile Gln Gly Leu Val Ile Ser Val Phe
 195 200 205
 Thr Leu Pro Leu Pro Phe Thr Phe Ile Leu Ile Ser Xaa Phe Cys Ile
 210 215 220
 Phe Val Arg Ala Val Glu Ala Arg Arg Glu Ala Phe Ser Thr Cys Gly
 225 230 235 240
 Ser His Leu Thr Gly Val Thr Ile Phe Tyr Gly Ala Ala Ile Cys Met
 245 250 255
 Tyr Leu Lys Pro Gln Ser Lys Gly Thr Gln Glu Glu Asp Lys Val Val
 260 265 270
 Ser Lys Leu Tyr Gly Ala Val Thr Pro Met Leu Asn Pro Pro Ile Tyr
 275 280 285
 Ile Gln Arg Asn Lys Asp Ile Lys Gly Ala Leu Arg Lys Leu Ala Lys
 290 295 300
 Gly Asn Glu Lys Ser Xaa Gln Phe Ser Leu Asn
 305 310 315

<210> 1280

<211> 319

<212> PRT

<213> Unknown (H38g197 protein)

<220>

<223> Synthetic construct

<400> 1280

Met Asn His Val Val Lys His Asn His Thr Ala Val Thr Lys Val Thr
 1 5 10 15
 Glu Phe Ile Leu Met Gly Ile Thr Asp Asn Pro Gly Leu Gln Ala Pro
 20 25 30
 Leu Phe Gly Leu Phe Leu Ile Ile Tyr Leu Val Thr Val Ile Gly Asn
 35 40 45
 Leu Gly Met Val Ile Leu Thr Tyr Leu Asp Ser Lys Leu His Thr Pro
 50 55 60
 Met Tyr Phe Phe Leu Arg His Leu Ser Ile Thr Asp Leu Gly Tyr Ser
 65 70 75 80
 Thr Val Ile Ala Pro Lys Met Leu Val Asn Phe Ile Val His Lys Asn
 85 90 95
 Thr Ile Ser Tyr Asn Trp Tyr Ala Thr Gln Leu Ala Phe Phe Glu Ile
 100 105 110
 Phe Ile Ile Ser Glu Leu Phe Ile Leu Ser Ala Met Ala Tyr Asp Arg

```

      115              120              125
Tyr Val Ala Ile Cys Lys Pro Leu Leu Tyr Val Ile Ile Met Ala Glu
  130              135              140
Lys Val Leu Trp Val Leu Val Ile Val Pro Tyr Leu Tyr Ser Thr Phe
  145              150              155              160
Val Ser Leu Phe Leu Thr Ile Lys Leu Phe Lys Leu Ser Phe Cys Gly
      165              170              175
Ser Asn Ile Ile Ser Tyr Phe Tyr Cys Asp Cys Ile Pro Leu Met Ser
      180              185              190
Ile Leu Cys Ser Asp Thr Asn Glu Leu Glu Leu Ile Ile Leu Ile Phe
      195              200              205
Ser Gly Cys Asn Leu Leu Phe Ser Leu Ser Ile Val Leu Ile Ser Tyr
      210              215              220
Met Phe Ile Leu Val Ala Ile Leu Arg Met Asn Ser Arg Lys Gly Arg
      225              230              235              240
Tyr Lys Ala Phe Ser Thr Cys Ser Ser His Leu Thr Val Val Ile Met
      245              250              255
Phe Tyr Gly Thr Leu Leu Phe Ile Tyr Leu Gln Pro Lys Ser Ser His
      260              265              270
Thr Leu Ala Ile Asp Lys Met Ala Ser Val Phe Tyr Thr Leu Leu Ile
      275              280              285
Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys
      290              295              300
Asp Ala Leu Lys Arg Thr Leu Thr Asn Arg Phe Lys Ile Pro Ile
  305              310              315

```

<210> 1281

<211> 157

<212> PRT

<213> Unknown (H38g198 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(157)

<223> Xaa = Any Amino Acid

<400> 1281

```

Phe Leu Lys Met Arg Leu Lys Glu Leu Met Xaa Asp Arg Thr Ile Met
  1           5           10           15
Asp Tyr Trp Arg Glu Gly Arg His Ile Xaa Gly Met Phe Leu Ala Phe
      20           25           30
Pro Phe Gly Xaa Pro Ile Pro Lys Leu Phe Leu Trp Val Ser Ile Arg
      35           40           45
Asp Met Ala Val Thr Trp Met Asp His Arg His Glu Ser Cys Ser Pro
      50           55           60
Phe Leu Pro Lys Leu Gln Pro Phe Ser Ser Cys His Val Ser Glu Leu
      65           70           75           80
Cys Thr Cys Leu Asp Thr Phe Thr Lys Ser Tyr Ile Thr Xaa Ile Arg
      85           90           95
Gly Leu Lys Gly Phe Asn His Leu Cys Phe Leu Leu His Tyr Cys His
      100          105          110
Cys Ala Arg Ala Gln Val Ser Xaa Asn Ala Pro Trp Ser Leu Ala Gln
      115          120          125
Arg Cys Gln Pro Asn Met Leu Ile Arg Xaa Leu Phe Cys Leu Lys Leu
      130          135          140
Val Val His Asp Arg Leu Xaa His Val Leu Ser Leu Leu
  145          150          155

```

<210> 1282

<211> 317
 <212> PRT
 <213> Unknown (H38g199 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(317)
 <223> Xaa = Any Amino Acid

<400> 1282

```

Met Gly Gln Lys Asn Leu Thr Val Leu Thr Glu Leu Ile Leu Met Glu
 1      5      10      15
Ile Thr Arg Arg Leu Glu Leu Gln Leu Ser Leu Phe Trp Val Phe Leu
      20      25      30
Ile Ile Cys Thr Phe Thr Val Val Ser Lys Glu Cys Ile Ile Leu
      35      40      45
Asn Asn Val Asp Leu Gly Leu Gln Thr Phe Val Tyr Phe Leu Ile Arg
      50      55      60
Tyr Leu Asn Phe Ile Asn Leu Gly Asn Ser Met Val Ile Tyr Pro Lys
      65      70      75      80
Ile Leu Val Asn Phe Val Val Ala Gln Asn Ala Ile Pro Cys Tyr Ala
      85      90      95
Cys Thr Met Gln Met Ala Phe Phe Ile Met Phe Ile Ile Cys Glu Leu
      100     105     110
Phe Val Ser Ser Ala Met Ala Tyr Asp His Tyr Val Asp Ile His Ser
      115     120     125
Leu Leu Pro Xaa Asn Val Met Ser Gln Glu Leu Cys His Val Leu Val
      130     135     140
Ala Ile Pro Tyr Leu Tyr Ser Thr Phe Gln Ala Leu Met Val Thr Ile
      145     150     155     160
Lys Ile Phe Ile Leu Ala Phe Tyr Gly Ser Asn Val Ile Ser Tyr Phe
      165     170     175
Tyr Cys Xaa Asp Val Ser Leu Leu Ala Met Val Asp Ser Asn Ala Xaa
      180     185     190
Gly Ile Glu Met Leu Ile Thr Leu Phe Ser Val Leu Asn Leu Ile Phe
      195     200     205
Phe Leu Leu Val Val Leu Met Ser Ser Met Leu Ile Leu Leu Thr Val
      210     215     220
Cys Xaa Met His Ser Ala Gly Glu Gln Xaa Lys Thr Phe Phe Thr Tyr
      225     230     235     240
Val Ser Cys Leu Ile Val Val Val Val Phe Cys Gly Phe Leu Tyr Phe
      245     250     255
Met Tyr Leu Gln Leu Lys Phe Ser Ser Phe Phe Phe Asp Asn Asn Lys
      260     265     270
Met Thr Ser Met Phe Ser Ser Leu Val Ile Thr Met Leu Tyr His Leu
      275     280     285
Val Cys Ser Val Lys Asn Lys Gly Ser Lys Lys Asn Ala Phe Tyr Ser
      290     295     300
Phe Phe Met Lys Gln Xaa Lys Leu Cys Asn Leu Met Val
      305     310     315

```

<210> 1283
 <211> 302
 <212> PRT
 <213> Unknown (H38g200 protein)

<220>
 <223> Synthetic construct

<400> 1283

```

Met Thr Asn Leu Asn Ala Ser Gln Ala Asn His Arg Asn Phe Ile Leu
 1           5           10           15
Thr Gly Ile Pro Gly Thr Pro Asp Lys Asn Pro Trp Leu Ala Phe Pro
          20           25           30
Leu Gly Phe Leu Tyr Thr Leu Thr Leu Leu Gly Asn Gly Thr Ile Leu
          35           40           45
Ala Val Ile Lys Val Glu Pro Ser Leu His Glu Pro Thr Tyr Tyr Phe
          50           55           60
Leu Ser Ile Leu Ala Leu Thr Asp Val Ser Leu Ser Met Ser Thr Leu
65           70           75           80
Pro Ser Met Leu Ser Ile Tyr Trp Phe Asn Ala Pro Gln Ile Val Phe
          85           90           95
Asp Ala Cys Ile Met Gln Met Phe Phe Ile His Val Phe Gly Ile Val
          100          105          110
Glu Ser Gly Val Leu Val Ser Met Ala Phe Asp Arg Phe Val Ala Ile
          115          120          125
Arg Asn Pro Leu His Tyr Val Ser Ile Leu Thr His Asp Val Ile Arg
          130          135          140
Lys Thr Gly Ile Ser Val Leu Thr Arg Ala Val Cys Val Val Phe Pro
145           150           155           160
Val Pro Phe Leu Ile Lys Cys Leu Pro Phe Cys His Ser Asn Val Leu
          165          170          175
Ser His Ser Tyr Cys Leu His Gln Asn Met Met Arg Leu Ala Cys Ala
          180          185          190
Ser Thr Arg Ile Asn Ser Leu Tyr Gly Leu Ile Val Val Ile Phe Thr
          195          200          205
Leu Gly Leu Asp Val Leu Leu Thr Leu Leu Ser Tyr Val Leu Thr Leu
          210          215          220
Lys Thr Val Leu Gly Ile Val Ser Arg Gly Glu Arg Leu Lys Thr Leu
225           230           235           240
Ser Thr Cys Leu Ser His Met Ser Thr Val Leu Leu Phe Tyr Val Pro
          245          250          255
Phe Met Gly Ala Ala Ser Met Ile His Arg Phe Trp Glu His Leu Ser
          260          265          270
Pro Val Val His Met Val Met Ala Asp Ile Tyr Leu Leu Leu Pro Pro
          275          280          285
Val Leu Asn Pro Ile Val Tyr Ser Val Lys Thr Lys Gln Ile
          290          295          300

```

<210> 1284

<211> 324

<212> PRT

<213> Unknown (H38g201 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(324)

<223> Xaa = Any Amino Acid

<400> 1284

```

His Thr Glu Pro Arg Asn Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu
 1           5           10           15
Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Leu Leu Ser
          20           25           30
Leu Ser Leu Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ser
          35           40           45
Ile Pro Ala Val Ser Ser Asp Ser His Leu His Thr Pro Thr Tyr Phe
          50           55           60

```

Phe Leu Ser Ile Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Thr
 65 70 75 80
 Val Pro Lys Met Ile Val Asp Met Gln Trp Tyr Ser Arg Val Ile Ser
 85 90 95
 His Ala Gly Cys Leu Thr Gln Met Ser Phe Leu Val Leu Phe Ala Cys
 100 105 110
 Ile Glu Gly Met Leu Leu Thr Val Met Ala Tyr Asp Cys Phe Val Gly
 115 120 125
 Ile Tyr Arg Pro Leu His Tyr Pro Val Ile Val Asn Pro His Leu Cys
 130 135 140
 Val Phe Phe Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln
 145 150 155 160
 Leu His Ser Trp Ile Val Leu Gln Phe Thr Ile Ile Lys Asn Val Glu
 165 170 175
 Ile Ser Asn Phe Val Cys Asp Pro Ser Gln Leu Leu Lys Leu Ala Ser
 180 185 190
 Tyr Asp Ser Val Ile Asn Ser Ile Phe Ile Tyr Phe Asp Ser Thr Met
 195 200 205
 Phe Gly Phe Leu Pro Ile Ser Gly Ile Leu Ser Ser Tyr Tyr Lys Ile
 210 215 220
 Val Pro Ser Ile Leu Arg Met Ser Ser Ser Asp Gly Lys Tyr Lys Thr
 225 230 235 240
 Phe Ser Thr Tyr Gly Ser His Leu Ala Phe Val Cys Xaa Phe Tyr Gly
 245 250 255
 Thr Gly Ile Asp Met Tyr Leu Ala Ser Ala Met Ser Pro Thr Pro Arg
 260 265 270
 Asn Gly Val Val Val Ser Val Met Xaa Ala Val Val Thr Pro Met Leu
 275 280 285
 Asn Leu Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu
 290 295 300
 Arg Arg Leu Arg Ser Arg Thr Val Glu Ser Pro Xaa Ser Val Pro Ser
 305 310 315 320
 Phe Phe Trp Cys

<210> 1285

<211> 144

<212> PRT

<213> Unknown (H38g202 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(144)

<223> Xaa = Any Amino Acid

<400> 1285

Phe Ser Val Thr Gly Ile Ser Val Val Asp Cys Cys Phe Xaa Ser Thr
 1 5 10 15
 Val Ile Pro Glu Met Leu Phe Ser Cys Gln Val Gln His Leu Val His
 20 25 30
 Asn Pro Lys Gly Ile Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu
 35 40 45
 Leu Leu Thr Phe Phe Xaa Lys Ile Ser Phe His Arg Met His Phe Cys
 50 55 60
 Ile Arg Asp Ser Ser Ser Gly Lys Ile Thr Val Tyr Tyr Leu Xaa Phe
 65 70 75 80
 Tyr Ile Cys Gly Gln Ile Val Leu Glu Gln Val Lys His Ile Xaa Glu
 85 90 95
 Xaa Ser Leu Ser Leu Glu Phe Val Ile Phe Xaa Tyr Phe Tyr Lys Gly

	100		105		110										
Asp	Leu	Ala	Leu	Lys	Gln	Asn	Phe	Ala	Ile	Leu	Arg	Ser	Ile	Pro	Ser
	115		120		125										
Phe	Ser	Ser	Xaa	Asp	Leu	Glu	Ile	His	Asn	Val	Arg	Tyr	Gln	His	Phe
	130				135						140				

<210> 1286

<211> 314

<212> PRT

<213> Unknown (H38g203 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(314)

<223> Xaa = Any Amino Acid

<400> 1286

Thr	His	Gly	Tyr	Thr	Phe	Ser	Leu	Arg	Leu	Phe	Leu	His	Cys	Leu	Thr
1				5				10					15		
Tyr	Val	Xaa	Val	Ser	His	Cys	Leu	Leu	Ile	Trp	Leu	Ile	Thr	Phe	Ser
	20						25					30			
Pro	Phe	Asn	Leu	Leu	Phe	Lys	Xaa	Asn	Leu	Xaa	Phe	Thr	Ile	Xaa	Leu
	35					40					45				
Ile	Thr	Xaa	Ile	Glu	Ser	Arg	Tyr	Ser	Lys	His	Trp	Pro	Phe	Phe	Leu
	50				55					60					
Leu	Xaa	Cys	Phe	Cys	Asn	Val	Leu	Phe	His	Leu	Asp	Cys	Asp	Ser	Pro
65				70				75						80	
Val	Cys	Asn	Thr	Lys	Arg	Ile	Arg	Ser	Phe	Phe	Val	Leu	Glu	Arg	Xaa
		85				90						95			
Lys	Ser	Ser	Xaa	Lys	Ser	Glu	Lys	Ile	His	Phe	Xaa	Thr	Arg	Asn	Lys
		100				105						110			
Val	Ser	Cys	Phe	Xaa	Asp	Phe	Gly	Ile	Lys	Tyr	Thr	Val	Tyr	Leu	Leu
	115					120					125				
Leu	Leu	Lys	His	Phe	Leu	Leu	Ile	His	Ser	Ile	Leu	Arg	Tyr	Leu	Xaa
	130				135					140					
Val	Ala	Gly	Tyr	Gly	Thr	Ser	Xaa	Phe	Leu	Ser	Arg	Ile	Ser	Ser	Ile
145				150				155						160	
Thr	Leu	Lys	Thr	Ile	Ile	Cys	Ile	Leu	Lys	Lys	Ser	Tyr	His	Phe	Phe
		165				170							175		
Ser	Val	Gln	Tyr	Thr	Ile	Ser	Tyr	Ile	Asp	Pro	Phe	Ile	Asn	Ser	Leu
	180					185						190			
Val	Met	Phe	Val	Val	Phe	Thr	Ala	Phe	Ile	Gln	Ala	Phe	Ala	Phe	Met
	195				200						205				
Ile	Ile	Ile	Val	Ser	Tyr	Thr	Gln	Val	Leu	Phe	Ala	Leu	Leu	Lys	Lys
	210				215					220					
Asn	Ser	Glu	Lys	Gly	Arg	Ser	Lys	Ser	Phe	Leu	Met	Cys	Ser	Ala	His
225				230					235					240	
Leu	Leu	Ser	Val	Ser	Leu	Phe	Tyr	Ser	Ser	Val	Phe	Phe	Met	Tyr	Gly
		245						250					255		
Cys	Pro	Arg	Ser	Gly	Pro	Asp	Xaa	Gln	Trp	Asn	Glu	Met	Tyr	Phe	Pro
		260				265						270			
Phe	Tyr	Met	Ile	Ile	Ile	Pro	Leu	Gln	Thr	Pro	Phe	Ile	Tyr	Ser	Met
	275				280						285				
Lys	Asn	Lys	Glu	Val	Leu	Gly	Thr	Leu	Arg	Thr	Met	Ile	Lys	Lys	Tyr
	290				295					300					
Phe	Trp	Arg	Thr	Leu	Ser	Xaa	Phe	Phe	Pro						
305				310											

<210> 1287

<211> 253
 <212> PRT
 <213> Unknown (H38g204 protein)

<220>
 <223> Synthetic construct

<400> 1287

```

Met Cys Leu Phe Leu Cys His Leu Ser Phe Leu Asp Met Thr Ile Ser
 1           5           10           15
Cys Ala Ile Val Pro Lys Met Leu Ala Gly Phe Leu Leu Gly Ser Arg
          20           25           30
Ile Ile Ser Phe Gly Gly Cys Val Ile Gln Leu Phe Ser Phe His Phe
          35           40           45
Leu Gly Cys Thr Glu Cys Phe Leu Tyr Thr Leu Met Ala Tyr Asp Arg
          50           55           60
Phe Leu Ala Ile Cys Lys Pro Leu His Tyr Ala Thr Ile Met Thr His
          65           70           75           80
Arg Val Cys Asn Ser Leu Ala Leu Gly Thr Trp Leu Gly Gly Thr Ile
          85           90           95
His Ser Leu Phe Gln Thr Ser Phe Val Phe Arg Leu Pro Phe Cys Gly
          100          105          110
Pro Asn Arg Val Asp Tyr Ile Phe Cys Asp Ile Pro Ala Met Leu Arg
          115          120          125
Leu Ala Cys Ala Asp Thr Ala Ile Asn Glu Leu Val Thr Phe Ala Asp
          130          135          140
Ile Gly Phe Leu Ala Leu Thr Cys Phe Met Leu Ile Leu Thr Ser Tyr
          145          150          155          160
Gly Tyr Ile Val Ala Ala Ile Leu Arg Ile Pro Ser Ala Asp Gly Arg
          165          170          175
Arg Asn Ala Phe Ser Thr Cys Ala Ala His Leu Thr Val Val Ile Val
          180          185          190
Tyr Tyr Val Pro Cys Thr Phe Ile Tyr Leu Arg Pro Cys Ser Gln Glu
          195          200          205
Pro Leu Asp Gly Val Val Ala Val Phe Tyr Thr Val Ile Thr Pro Leu
          210          215          220
Leu Asn Ser Ile Ile Tyr Thr Leu Cys Asn Lys Glu Met Lys Ala Ala
          225          230          235          240
Leu Gln Arg Leu Gly Gly His Lys Glu Val Gln Pro His
          245          250

```

<210> 1288
 <211> 311
 <212> PRT
 <213> Unknown (H38g205 protein)

<220>
 <223> Synthetic construct

<400> 1288

```

Met Gly Ser Phe Asn Thr Ser Phe Glu Asp Gly Phe Ile Leu Val Gly
 1           5           10           15
Phe Ser Asp Trp Pro Gln Leu Glu Pro Ile Leu Phe Val Phe Ile Phe
          20           25           30
Ile Phe Tyr Ser Leu Thr Leu Phe Gly Asn Thr Ile Ile Ile Ala Leu
          35           40           45
Ser Trp Leu Asp Leu Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser
          50           55           60
His Leu Ser Leu Leu Asp Leu Cys Phe Thr Thr Ser Thr Val Pro Gln
          65           70           75           80
Leu Leu Ile Asn Leu Cys Gly Val Asp Arg Thr Ile Thr Arg Gly Gly

```

```

      85              90              95
Cys Val Ala Gln Leu Phe Ile Tyr Leu Ala Leu Gly Ser Thr Glu Cys
      100              105              110
Val Leu Leu Val Val Met Ala Phe Asp Arg Tyr Ala Ala Val Cys Arg
      115              120              125
Pro Leu His Tyr Met Ala Ile Met His Pro His Leu Cys Gln Thr Leu
      130              135              140
Ala Ile Ala Ser Trp Gly Ala Gly Phe Val Asn Ser Leu Ile Gln Thr
      145              150              155              160
Gly Leu Ala Met Ala Met Pro Leu Cys Gly His Arg Leu Asn His Phe
      165              170              175
Phe Cys Glu Met Pro Val Phe Leu Lys Leu Ala Cys Ala Asp Thr Glu
      180              185              190
Gly Thr Glu Ala Lys Met Phe Val Ala Arg Val Ile Val Val Ala Val
      195              200              205
Pro Ala Ala Leu Ile Leu Gly Ser Tyr Val His Ile Ala His Ala Val
      210              215              220
Leu Arg Val Lys Ser Thr Ala Gly Arg Arg Lys Ala Phe Gly Thr Cys
      225              230              235              240
Gly Ser His Leu Leu Val Val Phe Leu Phe Tyr Gly Ser Ala Ile Tyr
      245              250              255
Thr Tyr Leu Gln Ser Ile His Asn Tyr Ser Glu Arg Glu Gly Lys Phe
      260              265              270
Val Ala Leu Phe Tyr Thr Ile Ile Thr Pro Ile Leu Asn Pro Leu Ile
      275              280              285
Tyr Thr Leu Arg Asn Lys Asp Val Lys Gly Ala Leu Trp Lys Val Leu
      290              295              300
Trp Arg Gly Arg Asp Ser Gly
      305              310

```

<210> 1289

<211> 311

<212> PRT

<213> Unknown (H38g206 protein)

<220>

<223> Synthetic construct

<400> 1289

```

Met Lys Ile Lys Asn His Thr Pro Val Thr Glu Val Pro Leu Met Gly
  1              5              10              15
Ile Pro His Thr Lys Gly Met Glu Asn Val Leu Phe Val Leu Phe Leu
      20              25              30
Ala Phe Tyr Leu Phe Thr Leu Leu Gly Asn Leu Leu Ile Leu Leu Ala
      35              40              45
Val Leu Thr Phe Ser Asn Leu His Thr Pro Met Tyr Phe Phe Leu Gly
      50              55              60
Asn Leu Ser Val Phe Asp Ile Phe Phe Pro Ser Val Ser Ser Pro Lys
      65              70              75              80
Met Met Leu Cys Leu Val Gly Gln Ser Cys Thr Ile Ser Phe Gln Gly
      85              90              95
Cys Ala Ser Gln Leu Phe Phe His His Phe Leu Gly Cys Thr Glu Cys
      100              105              110
Phe Leu Tyr Thr Val Met Ala Tyr Asp Arg Phe Ala Ala Ile Cys His
      115              120              125
Pro Leu Pro Tyr Thr Val Ile Met Lys Arg Arg Val Cys Ala Leu Leu
      130              135              140
Thr Leu Gly Thr Trp Thr Gly Ser Cys Leu His Ala Ser Val Leu Thr
      145              150              155              160
Leu Leu Ile Phe Lys Leu Ser Tyr Cys Gly Pro Asn Glu Val Asp Asn
      165              170              175

```

Phe Phe Cys Asp Ile Pro Val Val Leu Pro Leu Ala Cys Ala Asp Thr
 180 185 190
 Ser Leu Ala Arg Thr Val Ser Phe Ile Asn Val Gly Val Val Ala Leu
 195 200 205
 Met Cys Phe Leu Leu Ile Leu Thr Ser Tyr Ala Cys Ile Val Ile Ser
 210 215 220
 Ile Leu Lys Ile Ser Ser Glu Gly Arg Arg Ala Phe Ser Thr
 225 230 235 240
 Cys Ser Ala His Leu Thr Ser Ile Leu Leu Phe Tyr Gly Pro Ile Val
 245 250 255
 Leu Ile Tyr Leu Arg Pro Ala Ser Ser Pro Trp Leu Asp Ser Val Val
 260 265 270
 Gln Val Leu Asn Asn Ile Val Ile Pro Ser Leu Asn Pro Leu Ile Tyr
 275 280 285
 Thr Leu Arg Asn Lys Gly Val Lys Leu Ala Leu Arg Lys Val Leu Ile
 290 295 300
 Gln Gly Val His Asn Cys Gly
 305 310

<210> 1290

<211> 298

<212> PRT

<213> Unknown (H38g207 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(298)

<223> Xaa = Any Amino Acid

<400> 1290

Val Arg Gly Ser Lys Gln Leu Arg Asn Gly Thr Leu Val Ser Gln Phe
 1 5 10 15
 Leu Leu Lys Gly Leu Arg Asp Ser Lys Ala Trp Arg Pro Leu Leu Phe
 20 25 30
 Thr Thr Phe Leu Leu Ile Tyr Ile Val Val Val Gly Ser His Met
 35 40 45
 Phe Thr Val Asp Tyr Arg Arg His Thr Pro Met Tyr Phe Phe Leu Gly
 50 55 60
 Gly His Ser Leu Met Asp Ala Ala Cys Ile Ser Asn Met Val Thr Gln
 65 70 75 80
 Val Leu Val His Leu Leu Ala Pro Val Gly Pro Val Leu Tyr Cys Ala
 85 90 95
 Cys Leu Ile Gln Ile Cys Phe Leu His Phe Leu Ala Pro Xaa Glu Ser
 100 105 110
 Phe Leu Leu Thr Ala Val Ala Tyr Asp Ser Met Leu Ala Ile Cys Gln
 115 120 125
 Pro Leu His Tyr Phe Val Leu Val Gly Arg Leu Thr His Thr Gly Leu
 130 135 140
 Thr Ser Ile Ser Cys Leu Leu Ala Leu Ala Asn Ala Phe Thr Tyr Ser
 145 150 155 160
 Ile Leu Thr Ala Leu Pro Lys Phe Cys Arg Pro Cys Leu Ile Thr His
 165 170 175
 Phe Phe Cys Asp Leu Pro Ser Leu Leu Arg Leu Ser Cys Phe Ser Thr
 180 185 190
 Arg Thr Asn Glu Leu Ala Leu Phe Phe Ser Phe Leu Val Ala Leu Ala
 195 200 205
 His Cys Val Leu Val Val Val Ser Tyr Gly His Val Val Ala Ala Val
 210 215 220
 Gln Ile His Ser Thr Gln Gly Xaa Arg Lys Ala Phe Ser Thr Cys Val

225											230											235											240
Ala	His	Leu	Ala	Met	Ile	Gly	Leu	Phe	Tyr	Val	Thr	Ser	Val	Pro	Cys																		
					245						250						255																
Tyr	Ile	Leu	Pro	Asn	Ser	Ala	Tyr	Ser	Gly	Leu	Gly	Asp	Trp	Val	Leu																		
					260						265						270																
Ser	Val	Leu	Cys	Val	Val	Leu	Thr	His	Met	Leu	Asn	Pro	Ile	Phe	Pro																		
					275						280						285																
Ser	Met	Leu	Gly	Xaa	Gln	Cys	Met	Ser	His																								
					290						295																						

<210> 1291
<211> 312
<212> PRT
<213> Unknown (H38g208 protein)

<220>
<223> Synthetic construct

<400> 1291

[illegible]

<210> 1292

<211> 251
 <212> PRT
 <213> Unknown (H38g209 protein)

<220>
 <223> Synthetic construct

<400> 1292

```

Met Tyr Tyr Phe Leu Ser His Leu Ala Phe Val Asp Leu Cys Tyr Ser
 1           5           10           15
Ser Ala Ile Thr Pro Lys Met Met Val Asn Phe Val Val Glu Arg Asn
           20           25           30
Thr Ile Pro Phe His Ala Cys Ala Thr Gln Leu Gly Cys Phe Leu Thr
           35           40           45
Phe Met Ile Thr Glu Cys Phe Leu Leu Ala Ser Met Ala Tyr Asp Cys
           50           55           60
Tyr Val Ala Ile Cys Ser Pro Leu His Tyr Ser Thr Leu Met Ser Arg
           65           70           75           80
Arg Val Cys Ile Gln Leu Val Ala Val Pro Tyr Ile Tyr Ser Phe Leu
           85           90           95
Val Ala Leu Phe His Thr Val Ile Thr Phe Arg Leu Thr Tyr Cys Gly
           100          105          110
Pro Asn Leu Ile Asn His Phe Tyr Cys Asp Asp Leu Pro Phe Leu Ala
           115          120          125
Leu Ser Cys Ser Asp Thr His Met Lys Glu Ile Leu Ile Phe Ala Phe
           130          135          140
Ala Gly Phe Asp Met Ile Ser Ser Ser Ser Ile Val Leu Thr Ser Tyr
           145          150          155          160
Ile Phe Ile Ile Ala Ala Ile Leu Arg Ile Arg Ser Thr Gln Gly Gln
           165          170          175
His Lys Ala Ile Ser Thr Cys Gly Ser His Met Val Thr Val Thr Ile
           180          185          190
Phe Tyr Gly Thr Leu Ile Phe Met Tyr Leu Gln Pro Lys Ser Asn His
           195          200          205
Ser Leu Asp Thr Asp Lys Met Ala Ser Val Phe Tyr Thr Val Val Ile
           210          215          220
Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys
           225          230          235          240
Asp Ala Ser Lys Lys Ala Leu Asp Lys Gly Cys
           245          250

```

<210> 1293
 <211> 311
 <212> PRT
 <213> Unknown (H38g210 protein)

<220>
 <223> Synthetic construct

<400> 1293

```

Met Ser Asn Ala Thr Leu Leu Thr Ala Phe Ile Leu Thr Gly Leu Pro
 1           5           10           15
His Ala Pro Gly Leu Asp Ala Pro Leu Phe Gly Ile Phe Leu Val Val
           20           25           30
Tyr Val Leu Thr Val Leu Gly Asn Leu Leu Ile Leu Leu Val Ile Arg
           35           40           45
Val Asp Ser His Leu His Thr Pro Met Tyr Tyr Phe Leu Thr Asn Leu
           50           55           60
Ser Phe Ile Asp Met Trp Phe Ser Thr Val Thr Val Pro Lys Met Leu
           65           70           75           80
Met Thr Leu Val Ser Pro Ser Gly Arg Thr Ile Ser Phe His Ser Cys

```

<400> 1294															
His	Ser	Ser	Leu	Leu	Phe	Ala	Val	Phe	Leu	Leu	Thr	Tyr	Ser	Val	Thr
1				5					10					15	
Leu	Val	Gly	Asn	Leu	Gly	Met	Thr	Asp	Leu	Ile	Cys	Gln	Ser	Arg	Thr
			20					25					30		
Ser	Ser	Ala	Leu	His	Thr	Pro	Met	Cys	Phe	Leu	Leu	Ser	Val	Phe	Ser
		35					40					45			
Phe	Leu	Asp	Ile	Cys	Ser	Ser	Ser	Ile	Val	His	Pro	Arg	Leu	Leu	Ile
	50					55					60				
His	Phe	Leu	Thr	Thr	Arg	Pro	Ser	Ile	Ser	Phe	Ala	Gly	Gly	Ile	Ile
65					70					75					80
Gln	Met	Ala	Leu	Met	Thr	Phe	Tyr	Gly	Thr	Gly	Glu	Cys	Leu	Leu	Leu
				85					90					95	
Ala	Ile	Val	Ala	Tyr	Asp	Xaa	Val	Val	Ala	Ile	Cys	His	Pro	Phe	Pro
			100					105					110		
Xaa	His	Ile	Ile	Met	Ser	Lys	Gly	Leu	Cys	Ala	Gln	Leu	Val	Val	Val
		115					120					125			
Thr	Ser	Ala	Val	Gly	Val	Leu	Ile	Ser	Ala	His	Arg	Gln	Asp	Ala	Phe
	130					135					140				

```

Ile Ser Pro Tyr Arg Gly Leu Asn Ile Ile Asp His Tyr Tyr Cys Ser
145          150          155          160
Val Thr Phe Pro Thr Pro Met Leu Gln Leu Ala Cys Ser Asp Ala Thr
          165          170          175
Val Ala Asn Met Ile Leu Phe Val Ser Ser Ala Leu Ile Thr Ile Pro
          180          185          190
Thr Ile Ser Val Ile Leu Val Ser Tyr Thr Tyr Ile Leu Val Asn Leu
          195          200          205
Val Arg Met Arg Ser Leu Asp Ala Gln Cys Lys Ala Phe Ser Thr Arg
          210          215          220
Ala Ser His Leu Thr Ala His Cys Leu Phe Tyr Gly Phe Val Phe Leu
225          230          235          240
Val Tyr Ile Pro Pro Asn Pro Glu Met Ala Ser Ala Tyr Asn Lys Ile
          245          250          255
Leu Phe Thr Val Val Ile Pro Met Leu Asn Leu Leu Val Xaa Gly Leu
          260          265          270
Arg Asn Lys Asp Val Lys
          275

```

<210> 1295

<211> 312

<212> PRT

<213> Unknown (H38g212 protein)

<220>

<223> Synthetic construct

<400> 1295

```

Ser Val Ala Lys Gly Asn His Ser Thr Val Tyr Glu Phe Ile Leu Leu
1      5      10      15
Gly Leu Thr Asp Asn Ala Glu Leu Gln Val Thr Leu Phe Gly Ile Phe
20     25     30
Leu Val Val Tyr Leu Ala Ser Phe Met Gly Asn Phe Gly Leu Ile Met
35     40     45
Leu Ile Gln Ile Ser Pro Gln Leu His Thr Pro Met Tyr Phe Phe Leu
50     55     60
Ser His Leu Ala Phe Val Asp Phe Ser Phe Thr Ser Ser Val Ala Pro
65     70     75     80
Asn Thr Leu Val Asn Phe Leu Cys Glu Val Lys Ser Ile Thr Phe Tyr
85     90     95
Ala Cys Ala Ile Gln Val Cys Cys Phe Ile Thr Phe Val Val Cys Glu
100    105    110
Leu Tyr Leu Leu Ser Ile Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys
115    120    125
Asn Pro Leu Leu Tyr Val Ile Leu Ile Pro Arg Lys Cys Ile Lys Leu
130    135    140
Ile Ala Ser Thr Tyr Val Tyr Gly Phe Thr Val Gly Leu Val Gln Thr
145    150    155    160
Val Ala Thr Ser Tyr Leu Ser Phe Cys Asp Ser Asn Val Ile Asn His
165    170    175
Phe Tyr His Asp Asp Val Pro Leu Val Ala Leu Ala Cys Ser Asp Thr
180    185    190
His Val Lys Glu Leu Met Leu Leu Ile Ile Ala Gly Phe Asn Thr Leu
195    200    205
Cys Ser Leu Val Ile Val Leu Ile Ser Tyr Gly Phe Ile Phe Phe Ala
210    215    220
Ile Leu Arg Ile His Ser Ala Glu Gly Arg Gln Lys Ala Phe Ser Thr
225    230    235    240
Ser Ala Ser His Leu Thr Ser Ile Thr Ile Phe Tyr Gly Thr Ile Ile
245    250    255
Phe Met Tyr Pro Gln Pro Lys Ser Ser His Ser Leu Asn Met Asp Lys

```

260 265 270
 Val Ala Ser Val Phe Asn Val Val Val Ile Pro Thr Leu Asn Pro Leu
 275 280 285
 Ile Tyr Ser Leu Arg Asn Gln Glu Val Lys Asn Ala Leu Lys Arg Ile
 290 295 300
 Ile Glu Lys Leu Cys Leu Ala Val
 305 310

<210> 1296

<211> 232

<212> PRT

<213> Unknown (H38g213 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(232)

<223> Xaa = Any Amino Acid

<400> 1296

Ser Gly Leu Val Pro Lys Ser Phe Pro Gly Cys Leu Thr Gln Leu Phe
 1 5 10 15
 Phe Leu His Tyr Ser Phe Val Leu Asp Ser Ala Ile Leu Leu Ala Met
 20 25 30
 Ala Phe Asp Arg Tyr Met Ala Ile Cys Ser Pro Leu Arg Tyr Thr Thr
 35 40 45
 Ile Leu Thr Pro Lys Thr Ile Val Lys Ile Ala Val Gly Ile Cys Phe
 50 55 60
 Arg Ser Phe Cys Val Phe Val Pro Cys Val Phe Leu Val Asn Arg Leu
 65 70 75 80
 Pro Phe Cys Arg Thr His Ile Ile Ser His Thr Tyr Cys Glu His Ile
 85 90 95
 Gly Val Ala Gln Leu Ala Cys Ala Asp Ile Ser Ile Asn Ile Trp Cys
 100 105 110
 Gly Phe Cys Val Pro Ile Met Thr Val Met Thr Asp Val Ile Leu Ile
 115 120 125
 Ala Val Ser Tyr Thr Leu Ile Leu Cys Ala Val Phe Cys Leu Pro Ser
 130 135 140
 Gln Asp Ala Arg Gln Lys Ala Leu Cys Ser Cys Gly Ser His Val Cys
 145 150 155 160
 Val Ile Leu Ile Phe Tyr Ile Pro Ala Phe Phe Ser Ile Leu Ala His
 165 170 175
 Cys Phe Gly His Asn Val Pro His Thr Phe His Ile Met Phe Ala Asn
 180 185 190
 Leu Tyr Val Ile Ile Pro Pro Ala Leu Asn Ser Ile Val Tyr Arg Ile
 195 200 205
 Lys Thr Lys Gln Ile Gln Asn Arg Ile Leu Leu Leu Phe Pro Lys Gly
 210 215 220
 Ser Gln Xaa Xaa Val Pro Glu Leu
 225 230

<210> 1297

<211> 310

<212> PRT

<213> Unknown (H38g214 protein)

<220>

<223> Synthetic construct

<400> 1297

```

Met Ser Asn Ala Ser Leu Leu Thr Ala Phe Ile Leu Met Gly Leu Pro
 1          5          10          15
His Ala Pro Ala Leu Asp Ala Pro Leu Phe Gly Val Phe Leu Val Val
          20          25          30
Tyr Val Leu Thr Val Leu Gly Asn Leu Leu Ile Leu Leu Val Ile Arg
          35          40          45
Val Asp Ser His Leu His Thr Thr Met Tyr Tyr Phe Leu Thr Asn Leu
          50          55          60
Ser Phe Ile Asp Met Trp Phe Ser Thr Val Thr Val Pro Lys Leu Leu
65          70          75          80
Met Thr Leu Val Phe Pro Ser Gly Arg Ala Ile Ser Phe His Ser Cys
          85          90          95
Met Ala Gln Leu Tyr Phe Phe His Phe Leu Gly Gly Thr Glu Cys Phe
          100          105          110
Leu Tyr Arg Val Met Ser Cys Asp Arg Tyr Leu Ala Ile Ser Tyr Pro
          115          120          125
Leu Arg Tyr Thr Ser Met Met Thr Gly Arg Ser Cys Thr Leu Leu Ala
          130          135          140
Thr Ser Thr Trp Leu Ser Gly Ser Leu His Ser Ala Val Gln Ala Ile
          145          150          155          160
Leu Thr Phe His Leu Pro Tyr Cys Gly Pro Asn Trp Ile Gln His Tyr
          165          170          175
Leu Cys Asp Ala Pro Pro Ile Leu Lys Leu Ala Cys Ala Asp Thr Ser
          180          185          190
Ala Ile Glu Thr Val Ile Phe Val Thr Val Gly Ile Val Ala Ser Gly
          195          200          205
Cys Phe Val Leu Ile Val Leu Ser Tyr Val Ser Ile Val Cys Ser Ile
          210          215          220
Leu Arg Ile Arg Thr Ser Glu Gly Lys His Arg Ala Phe Gln Thr Cys
          225          230          235          240
Ala Ser His Cys Ile Val Val Leu Cys Phe Phe Gly Pro Gly Leu Phe
          245          250          255
Ile Tyr Leu Arg Pro Gly Ser Arg Lys Ala Val Asp Gly Val Val Ala
          260          265          270
Val Phe Tyr Thr Val Leu Thr Pro Leu Leu Asn Pro Val Val Tyr Thr
          275          280          285
Leu Arg Asn Lys Glu Val Lys Lys Ala Leu Leu Lys Leu Lys Asp Lys
          290          295          300
Val Ala His Ser Gln Ser
          305          310

```

<210> 1298

<211> 311

<212> PRT

<213> Unknown (H38g215 protein)

<220>

<223> Synthetic construct

<400> 1298

```

Met Arg Arg Asn Cys Thr Leu Val Thr Glu Phe Ile Leu Leu Gly Leu
 1          5          10          15
Thr Ser Arg Arg Glu Leu Gln Ile Leu Leu Phe Thr Leu Phe Leu Ala
          20          25          30
Ile Tyr Met Val Thr Val Ala Gly Asn Leu Gly Met Ile Val Leu Ile
          35          40          45
Gln Ala Asn Ala Trp Leu His Met Pro Met Tyr Phe Phe Leu Ser His
          50          55          60
Leu Ser Phe Val Asp Leu Cys Phe Ser Ser Asn Val Thr Pro Lys Met
65          70          75          80
Leu Glu Ile Phe Leu Ser Glu Lys Lys Ser Ile Ser Tyr Pro Ala Cys

```

```

      85      90      95
Leu Val Gln Cys Tyr Leu Phe Ile Ala Leu Val His Val Glu Ile Tyr
      100      105      110
Ile Leu Ala Val Met Ala Phe Asp Arg Tyr Met Ala Ile Cys Asn Pro
      115      120      125
Leu Leu Tyr Gly Ser Arg Met Ser Lys Ser Val Cys Ser Phe Leu Ile
      130      135      140
Thr Val Pro Tyr Val Tyr Gly Ala Leu Thr Gly Leu Met Glu Thr Met
      145      150      155      160
Trp Thr Tyr Asn Leu Ala Phe Cys Gly Pro Asn Glu Ile Asn His Phe
      165      170      175
Tyr Cys Ala Asp Pro Pro Leu Ile Lys Leu Ala Cys Ser Asp Thr Tyr
      180      185      190
Asn Lys Glu Leu Ser Met Phe Ile Val Ala Gly Trp Asn Leu Ser Phe
      195      200      205
Ser Leu Phe Ile Ile Cys Ile Ser Tyr Leu Tyr Ile Phe Pro Ala Ile
      210      215      220
Leu Lys Ile Arg Ser Thr Glu Gly Arg Gln Lys Ala Phe Ser Thr Cys
      225      230      235      240
Gly Ser His Leu Thr Ala Val Thr Ile Phe Tyr Ala Thr Leu Phe Phe
      245      250      255
Met Tyr Leu Arg Pro Pro Ser Lys Glu Ser Val Glu Gln Gly Lys Met
      260      265      270
Val Ala Val Phe Tyr Thr Thr Val Ile Pro Met Leu Asn Leu Ile Ile
      275      280      285
Tyr Ser Leu Arg Asn Lys Asn Val Lys Glu Ala Leu Ile Lys Glu Leu
      290      295      300
Ser Met Lys Ile Tyr Phe Ser
      305      310

```

<210> 1299

<211> 315

<212> PRT

<213> Unknown (H38g216 protein)

<220>

<223> Synthetic construct

<400> 1299

```

Met Leu Leu Ser Asn Ile Thr Gln Phe Ser Pro Ile Phe Tyr Leu Thr
  1      5      10      15
Ser Phe Pro Gly Leu Glu Gly Ile Lys His Trp Ile Phe Ile Pro Phe
      20      25      30
Phe Phe Met Tyr Met Val Ala Ile Ser Gly Asn Cys Phe Ile Leu Ile
      35      40      45
Ile Ile Lys Thr Asn Pro Arg Leu His Thr Pro Met Tyr Tyr Leu Leu
      50      55      60
Ser Leu Leu Ala Leu Thr Asp Leu Gly Leu Cys Val Ser Thr Leu Pro
      65      70      75      80
Thr Thr Met Gly Ile Phe Trp Phe Asn Ser Gln Ser Ile Tyr Phe Gly
      85      90      95
Ala Cys Gln Ile Gln Met Phe Cys Ile His Ser Phe Ser Phe Met Glu
      100      105      110
Ser Ser Val Leu Leu Met Met Ser Phe Asp Arg Phe Val Ala Ile Cys
      115      120      125
His Pro Leu Arg Tyr Ser Val Ile Ile Thr Gly Gln Gln Val Val Arg
      130      135      140
Ala Gly Leu Ile Val Ile Phe Arg Gly Pro Val Ala Thr Ile Pro Ile
      145      150      155      160
Val Leu Leu Leu Lys Ala Phe Pro Tyr Cys Gly Ser Val Val Leu Ser
      165      170      175

```

His Ser Phe Cys Leu His Gln Glu Val Ile Gln Leu Ala Cys Thr Asp
 180 185 190
 Thr Thr Phe Asn Asn Leu Tyr Gly Leu Met Val Val Val Phe Thr Val
 195 200 205
 Met Leu Asp Leu Val Leu Ile Ala Leu Ser Tyr Gly Leu Ile Leu His
 210 215 220
 Thr Val Ala Gly Leu Ala Ser Gln Glu Glu Gln Arg Arg Ala Phe Gln
 225 230 235 240
 Thr Cys Thr Ala His Leu Cys Ala Val Leu Val Phe Phe Val Pro Met
 245 250 255
 Met Gly Leu Ser Leu Val His Arg Phe Gly Lys His Ala Pro Pro Ala
 260 265 270
 Ile His Leu Leu Met Ala Asn Val Tyr Leu Phe Val Pro Pro Met Leu
 275 280 285
 Asn Pro Ile Ile Tyr Ser Ile Lys Thr Lys Glu Ile His Arg Ala Ile
 290 295 300
 Ile Lys Leu Leu Gly Leu Lys Lys Ala Ser Lys
 305 310 315

<210> 1300

<211> 323

<212> PRT

<213> Unknown (H38g217 protein)

<220>

<223> Synthetic construct

<400> 1300

Met Asn Pro Glu Asn Trp Thr Gln Val Thr Ser Phe Val Leu Leu Gly
 1 5 10 15
 Phe Pro Ser Ser His Leu Ile Gln Phe Leu Val Phe Leu Gly Leu Met
 20 25 30
 Val Thr Tyr Ile Val Thr Ala Thr Gly Lys Leu Leu Ile Ile Val Leu
 35 40 45
 Ser Trp Ile Asp Gln Arg Leu His Ile Gln Met Tyr Phe Phe Leu Arg
 50 55 60
 Asn Phe Ser Phe Leu Glu Leu Leu Val Thr Val Val Val Pro Lys
 65 70 75 80
 Met Leu Val Val Ile Leu Thr Gly Asp His Thr Ile Ser Phe Val Ser
 85 90 95
 Cys Ile Ile Gln Ser Tyr Leu Tyr Phe Phe Leu Gly Thr Thr Asp Phe
 100 105 110
 Phe Leu Leu Ala Val Met Ser Leu Asp Arg Tyr Leu Ala Ile Cys Arg
 115 120 125
 Pro Leu Arg Tyr Glu Thr Leu Met Asn Gly His Val Cys Ser Gln Leu
 130 135 140
 Val Leu Ala Ser Trp Leu Ala Gly Phe Leu Trp Val Leu Cys Pro Thr
 145 150 155 160
 Val Leu Met Ala Ser Leu Pro Phe Cys Gly Pro Asn Gly Ile Asp His
 165 170 175
 Phe Phe Arg Asp Ser Trp Pro Leu Leu Arg Leu Ser Cys Gly Asp Thr
 180 185 190
 His Leu Leu Lys Leu Val Ala Phe Met Leu Ser Thr Leu Val Leu Leu
 195 200 205
 Gly Ser Leu Ala Leu Thr Ser Val Ser Tyr Ala Cys Ile Leu Ala Thr
 210 215 220
 Val Leu Arg Ala Pro Thr Ala Ala Glu Arg Arg Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Ala Ser His Leu Thr Val Val Val Ile Ile Tyr Gly Ser Ser Ile
 245 250 255
 Phe Leu Tyr Ile Arg Met Ser Glu Ala Gln Ser Lys Leu Leu Asn Lys

			260			265						270					
Gly	Ala	Ser	Val	Leu	Ser	Cys	Ile	Ile	Thr	Pro	Leu	Leu	Asn	Pro	Phe		
			275			280						285					
Ile	Phe	Thr	Leu	Arg	Asn	Asp	Lys	Val	Gln	Gln	Ala	Leu	Arg	Glu	Ala		
			290			295						300					
Leu	Gly	Trp	Pro	Arg	Leu	Thr	Ala	Val	Met	Lys	Leu	Arg	Val	Thr	Ser		
			305			310						315			320		
Gln	Arg	Lys															

<210> 1301
<211> 338
<212> PRT
<213> Unknown (H38g218 protein)

<220>
<223> Synthetic construct

```
<221> VARIANT
<222> (1)...(338)
<223> Xaa = Any Amino Acid
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<400>	1301														
Met	Met	Gly	Glu	Ala	Arg	Asn	Arg	Thr	Val	Val	Gln	Glu	Phe	Ile	Leu
1				5					10					15	
Glu	Gly	Phe	Pro	Ala	Val	Gln	His	Leu	Gly	Asn	Val	Leu	Phe	Leu	Val
			20					25					30		
His	Leu	Leu	Ala	Tyr	Leu	Ala	Ser	Ile	Met	Ala	Asn	Met	Leu	Ile	Ile
		35					40					45			
Thr	Ile	Thr	Trp	Ala	Asp	His	His	Leu	Gln	Thr	Pro	Met	Tyr	Phe	Phe
	50				55						60				
Leu	Asn	Ser	Phe	Ser	Phe	Cys	Glu	Cys	Cys	Phe	Ile	Thr	Thr	Val	Ile
65				70					75					80	
Pro	Lys	Leu	Leu	Val	Ile	Phe	Leu	Ser	Gly	Arg	Gln	Ile	Ile	Pro	Phe
				85					90					95	
Thr	Thr	Cys	Leu	Met	Gln	Ser	Phe	Ser	Phe	Leu	Phe	Leu	Gly	Ser	Thr
		100						105					110		
Val	Phe	Phe	Leu	Met	Ala	Val	Met	Ser	Leu	Asp	Xaa	Tyr	Leu	Ala	Ile
		115					120					125			
Cys	Lys	Pro	Leu	His	Tyr	Ser	Thr	Ile	Met	Ser	Leu	Arg	Thr	Ser	Phe
	130					135					140				
His	Leu	Val	Thr	Val	Cys	Phe	Val	Val	Gly	Phe	Thr	Leu	Ile	Thr	Gly
145				150					155						160
Leu	Met	Val	Lys	Val	Ser	Gln	Leu	Ser	Phe	Cys	Gly	Pro	His	Val	Ile
			165						170					175	
Pro	His	Phe	Phe	Arg	Asp	Leu	Gly	Pro	Leu	Ile	Gln	Leu	Ser	Cys	Ser
			180					185					190		
Asp	Thr	Arg	Ser	Thr	Glu	Thr	Leu	Ala	Phe	Val	Leu	Val	Ser	Phe	Val
		195					200					205			
Leu	Phe	Thr	Ser	Leu	Ile	Ile	Thr	Ile	Ile	Ala	Tyr	Gly	Asn	Ile	Val
	210				215						220				
Val	Thr	Ile	Val	Arg	Leu	Pro	Ser	Ala	Lys	Glu	Arg	Gln	Lys	Ala	Phe
225				230						235					240
Ser	Thr	Cys	Ser	Ser	His	Leu	Ile	Val	Leu	Ser	Leu	Val	Tyr	Gly	Ser
				245					250					255	
Cys	Val	Phe	Ile	Tyr	Val	Lys	Pro	Lys	Gln	Met	Asp	Arg	Leu	Asp	Ser
		260						265					270		
Asn	Arg	Met	Ala	Ala	Leu	Val	Asn	Thr	Val	Val	Thr	Pro	Leu	Leu	Asn
		275					280					285			
Pro	Ile	Ile	Tyr	Thr	Leu	Arg	Asn	Lys	Gln	Val	His	Gln	Ala	Leu	Arg
	290					295					300				

Asp Ala Gln Ser Arg Met Lys Leu Xaa Lys Gln Asn His Asn Leu Gln
 305 310 315 320
 Xaa Arg Asn Ala Pro Phe Leu Asp Leu Ile Gln Ser Phe Ser Cys Phe
 325 330 335
 Trp Asn

<210> 1302

<211> 309

<212> PRT

<213> Unknown (H38g219 protein)

<220>

<223> Synthetic construct

<400> 1302

Met Ala Ser Thr Ser Asn Val Thr Glu Leu Ile Phe Thr Gly Leu Phe
 1 5 10 15
 Gln Asp Pro Ala Val Gln Ser Val Cys Phe Val Val Phe Leu Pro Val
 20 25 30
 Tyr Leu Ala Thr Val Val Gly Asn Gly Leu Ile Val Leu Thr Val Ser
 35 40 45
 Ile Ser Lys Ser Leu Asp Ser Pro Met Tyr Phe Phe Leu Ser Cys Leu
 50 55 60
 Ser Leu Val Glu Ile Ser Tyr Ser Ser Thr Ile Ala Pro Lys Phe Ile
 65 70 75 80
 Ile Asp Leu Leu Ala Lys Ile Lys Thr Ile Ser Leu Glu Gly Cys Leu
 85 90 95
 Thr Gln Ile Phe Phe Phe His Phe Phe Gly Val Ala Glu Ile Leu Leu
 100 105 110
 Ile Val Val Met Ala Tyr Asp Cys Tyr Val Ala Ile Cys Lys Pro Leu
 115 120 125
 His Tyr Met Asn Ile Ile Ser Arg Gln Leu Cys His Leu Leu Val Ala
 130 135 140
 Gly Ser Trp Leu Gly Gly Phe Cys His Ser Ile Ile Gln Ile Leu Val
 145 150 155 160
 Ile Ile Gln Leu Pro Phe Cys Gly Pro Asn Val Ile Asp His Tyr Phe
 165 170 175
 Cys Asp Leu Gln Pro Leu Phe Lys Leu Ala Cys Thr Asp Thr Phe Met
 180 185 190
 Glu Gly Val Ile Val Leu Ala Asn Ser Gly Leu Phe Ser Val Phe Ser
 195 200 205
 Phe Leu Ile Leu Val Ser Ser Tyr Ile Val Ile Leu Val Asn Leu Arg
 210 215 220
 Asn His Ser Ala Glu Gly Arg His Lys Ala Leu Ser Thr Cys Ala Ser
 225 230 235 240
 His Ile Thr Val Val Ile Leu Phe Phe Gly Pro Ala Ile Phe Leu Tyr
 245 250 255
 Met Arg Pro Ser Ser Thr Phe Thr Glu Asp Lys Leu Val Ala Val Phe
 260 265 270
 Tyr Thr Val Ile Thr Pro Met Leu Asn Pro Ile Ile Tyr Thr Leu Arg
 275 280 285
 Asn Ala Glu Val Lys Ile Ala Ile Arg Arg Leu Trp Ser Lys Lys Glu
 290 295 300
 Asn Pro Gly Arg Glu
 305

<210> 1303

<211> 322

<212> PRT

<213> Unknown (H38g220 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(322)

<223> Xaa = Any Amino Acid

<400> 1303

```

Met Ala Lys Gly Asn His Ser Ser Val Thr Glu Phe Ile Leu Leu Gly
 1          5          10          15
Leu Thr Asp Asn Gln Glu Leu Gln Val Ile Leu Phe Gly Val Phe Leu
 20          25          30
Leu Ile Tyr Leu Val Thr Val Leu Gly Asn Leu Gly Leu Ile Val Leu
 35          40          45
Ile His Ile Ser Pro Gln Leu His Thr Pro Met Tyr Phe Phe Leu Ser
 50          55          60
His Leu Ala Phe Val Asp Phe Tyr Gly Thr Ser Ala Ile Thr Pro Asn
 65          70          75          80
Thr Leu Val Asn Ser Leu His Glu Ile Lys Ser Met Ser Phe Tyr Ala
 85          90          95
Cys Ala Thr Gln Val Cys Cys Phe Ile Thr Leu Ser Val Trp Glu Val
 100          105          110
Ile Val Ala Leu Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro
 115          120          125
Leu Leu Tyr Val Val Leu Met Pro Arg Arg Leu Cys Ile Gln Met Val
 130          135          140
Thr Gly Leu Tyr Ile Tyr Gly Phe Thr Met Gly Leu Ile Gln Ala Val
 145          150          155          160
Ala Thr Phe His Met Ser Phe Cys Asp Ser Asn Val Val Asn Gln Phe
 165          170          175
Tyr Cys Asp Asp Val Pro Leu Ile Ala Leu Ala Cys Ser Asp Thr Gln
 180          185          190
Val Lys Glu Leu Met Leu Phe Ile Ile Ala Ala Phe Asn Val Phe Cys
 195          200          205
Ser Leu Ile Ile Val Leu Ile Ser Tyr Val Phe Ile Val Phe Ala Ile
 210          215          220
Leu Arg Ile His Ser Ala Val Gly Arg Gln Lys Ala Phe Ser Thr Cys
 225          230          235          240
Ala Ser His Met Phe Ser Ile Ser Ile Tyr Tyr Gly Thr Leu Ser Phe
 245          250          255
Met Tyr Leu Gln Pro Lys Ser Ser His Ser Leu Asp Lys Asp Lys Phe
 260          265          270
Ala Ser Val Phe Tyr Ala Val Val Ile Pro Met Leu Asn Pro Leu Ile
 275          280          285
Tyr Ser Leu Arg Asn Gln Glu Val Lys Asn Ala Met Lys Lys Ile Ile
 290          295          300
Glu Lys Met Cys Ser Ser Asn Gln Gln Xaa Asn Leu Leu Val Leu Lys
 305          310          315          320
Glu Ile

```

<210> 1304

<211> 317

<212> PRT

<213> Unknown (H38g221 protein)

<220>

<223> Synthetic construct

<400> 1304

```

Met Ser Gln Val Thr Asn Thr Thr Gln Glu Gly Ile Tyr Phe Ile Leu
 1           5           10           15
Thr Asp Ile Pro Gly Phe Glu Ala Ser His Ile Trp Ile Ser Ile Pro
          20           25           30
Val Cys Cys Leu Tyr Thr Ile Ser Ile Met Gly Asn Thr Thr Ile Leu
          35           40           45
Thr Val Ile Arg Thr Glu Pro Ser Val His Gln Arg Met Tyr Leu Phe
          50           55           60
Leu Ser Met Leu Ala Leu Thr Asp Leu Gly Leu Thr Leu Thr Thr Leu
65           70           75           80
Pro Thr Val Met Gln Leu Leu Trp Phe Asn Val Arg Arg Ile Ser Ser
          85           90           95
Glu Ala Cys Phe Ala Gln Phe Phe Phe Leu His Gly Phe Ser Phe Met
          100          105          110
Glu Ser Ser Val Leu Leu Ala Met Ser Val Asp Cys Tyr Val Ala Ile
          115          120          125
Cys Cys Pro Leu His Tyr Ala Ser Ile Leu Thr Asn Glu Val Ile Gly
          130          135          140
Arg Thr Gly Leu Ala Ile Ile Cys Cys Cys Val Leu Ala Val Leu Pro
145           150           155           160
Ser Leu Phe Leu Leu Lys Arg Leu Pro Phe Cys His Ser His Leu Leu
          165          170          175
Ser Arg Ser Tyr Cys Leu His Gln Asp Met Ile Arg Leu Val Cys Ala
          180          185          190
Asp Ile Arg Leu Asn Ser Trp Tyr Gly Phe Ala Leu Ala Leu Ile
          195          200          205
Ile Ile Val Asp Pro Leu Leu Ile Val Ile Ser Tyr Thr Leu Ile Leu
          210          215          220
Lys Asn Ile Leu Gly Thr Ala Thr Trp Ala Glu Arg Leu Arg Ala Leu
225           230           235           240
Asn Asn Cys Leu Ser His Ile Leu Ala Val Leu Val Leu Tyr Ile Pro
          245          250          255
Met Val Gly Val Ser Met Thr His Arg Phe Ala Lys His Ala Ser Pro
          260          265          270
Leu Val His Val Ile Met Ala Asn Ile Tyr Leu Leu Ala Pro Pro Val
          275          280          285
Met Asn Pro Ile Ile Tyr Ser Val Lys Asn Lys Gln Ile Gln Trp Gly
          290          295          300
Met Leu Asn Phe Leu Ser Leu Lys Asn Met His Ser Arg
305           310           315

```

<210> 1305

<211> 315

<212> PRT

<213> Unknown (H38g222 protein)

<220>

<223> Synthetic construct

<400> 1305

```

Met Asn Pro Ala Asn His Ser Gln Val Ala Gly Phe Val Leu Leu Gly
 1           5           10           15
Leu Ser Gln Val Trp Glu Leu Arg Phe Val Phe Phe Thr Val Phe Ser
          20           25           30
Ala Val Tyr Phe Met Thr Val Val Gly Asn Leu Leu Ile Val Val Ile
          35           40           45
Val Thr Ser Asp Pro His Leu His Thr Thr Met Tyr Phe Leu Leu Gly
          50           55           60
Asn Leu Ser Phe Leu Asp Phe Cys Tyr Ser Ser Ile Thr Ala Pro Arg
65           70           75           80
Met Leu Val Asp Leu Leu Ser Gly Asn Pro Thr Ile Ser Phe Gly Gly

```

```
<210> 1306
<211> 320
<212> PRT
<213> Unknown (H38q223 protein)
```

<220>
<223> Synthetic construct

622

Pro His Thr Tyr Cys Asp His Met Ser Val Ala Lys Ile Ser Cys Gly
 180 185 190
 Asn Val Arg Val Asn Ala Ile Tyr Gly Leu Ile Val Ala Leu Leu Ile
 195 200 205
 Gly Gly Phe Asp Ile Leu Cys Ile Thr Ile Ser Tyr Thr Met Ile Leu
 210 215 220
 Gln Ala Val Val Ser Leu Ser Ser Ala Asp Ala Arg Gln Lys Ala Phe
 225 230 235 240
 Ser Thr Cys Thr Ala His Phe Cys Ala Ile Val Leu Thr Tyr Val Pro
 245 250 255
 Ala Phe Phe Thr Phe Phe Thr His His Phe Gly Gly His Thr Ile Pro
 260 265 270
 Leu His Ile His Ile Ile Met Ala Asn Leu Tyr Leu Leu Met Pro Pro
 275 280 285
 Thr Met Asn Pro Ile Val Tyr Gly Val Lys Thr Arg Gln Val Arg Glu
 290 295 300
 Ser Val Ile Arg Phe Phe Leu Lys Gly Lys Asp Asn Ser His Asn Phe
 305 310 315 320

<210> 1307

<211> 305

<212> PRT

<213> Unknown (H38g224 protein)

<220>

<223> Synthetic construct

<400> 1307

Met Val Ala Thr Asn Asn Val Thr Glu Ile Ile Phe Val Gly Phe Ser
 1 5 10 15
 Gln Asn Trp Ser Glu Gln Arg Val Ile Ser Val Met Phe Leu Leu Met
 20 25 30
 Tyr Thr Ala Val Val Leu Gly Asn Gly Leu Ile Val Val Thr Ile Leu
 35 40 45
 Ala Ser Lys Val Leu Thr Ser Pro Met Tyr Phe Phe Leu Ser Tyr Leu
 50 55 60
 Ser Phe Val Glu Ile Cys Tyr Cys Ser Val Met Ala Pro Lys Leu Ile
 65 70 75 80
 Phe Asp Ser Phe Ile Lys Arg Lys Val Ile Ser Leu Lys Gly Cys Leu
 85 90 95
 Thr Gln Met Phe Ser Leu His Phe Phe Gly Gly Thr Glu Ala Phe Leu
 100 105 110
 Leu Met Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu
 115 120 125
 His Tyr Met Ala Ile Met Asn Gln Arg Met Cys Gly Leu Leu Val Arg
 130 135 140
 Ile Ala Trp Gly Gly Gly Leu Leu His Ser Val Gly Gln Thr Phe Leu
 145 150 155 160
 Ile Phe Gln Leu Pro Phe Cys Gly Pro Asn Ile Met Asp His Tyr Phe
 165 170 175
 Cys Asp Val His Pro Val Leu Glu Leu Ala Cys Ala Asp Thr Phe Phe
 180 185 190
 Ile Ser Leu Leu Ile Ile Thr Asn Gly Gly Ser Ile Ser Val Val Ser
 195 200 205
 Phe Phe Val Leu Met Ala Ser Tyr Leu Ile Ile Leu His Phe Leu Arg
 210 215 220
 Ser His Asn Leu Glu Gly Gln His Lys Ala Leu Ser Thr Cys Ala Ser
 225 230 235 240
 His Val Thr Val Val Asp Leu Phe Phe Ile Pro Cys Ser Leu Val Tyr
 245 250 255
 Ile Arg Pro Cys Val Thr Leu Pro Ala Asp Lys Ile Val Ala Val Phe

260 265 270
 Tyr Thr Val Val Thr Pro Leu Leu Asn Pro Val Ile Tyr Ser Phe Arg
 275 280 285
 Asn Ala Glu Val Lys Asn Ala Met Arg Arg Phe Ile Gly Gly Lys Val
 290 295 300
 Ile
 305

<210> 1308
 <211> 313
 <212> PRT
 <213> Unknown (H38g225 protein)

<220>
 <223> Synthetic construct

<400> 1308
 Met Ala Pro Glu Asn Phe Thr Arg Val Thr Glu Phe Ile Leu Thr Gly
 1 5 10 15
 Val Ser Ser Cys Pro Glu Leu Gln Ile Pro Leu Phe Leu Val Phe Leu
 20 25 30
 Val Leu Tyr Gly Leu Thr Met Ala Gly Asn Leu Gly Ile Ile Thr Leu
 35 40 45
 Thr Ser Val Asp Ser Arg Leu Gln Thr Pro Met Tyr Phe Phe Leu Gln
 50 55 60
 His Leu Ala Leu Ile Asn Leu Gly Asn Ser Thr Val Ile Ala Pro Lys
 65 70 75 80
 Met Leu Ile Asn Phe Leu Val Lys Lys Lys Thr Thr Ser Phe Tyr Glu
 85 90 95
 Cys Ala Thr Gln Leu Gly Gly Phe Leu Phe Phe Ile Val Ser Glu Val
 100 105 110
 Ile Met Leu Ala Leu Met Ala Cys Asp Arg Tyr Val Ala Ile Cys Asn
 115 120 125
 Pro Leu Leu Tyr Met Val Val Val Ser Arg Arg Leu Cys Leu Leu Leu
 130 135 140
 Val Ser Leu Thr Tyr Leu Tyr Gly Phe Ser Thr Ala Ile Val Val Ser
 145 150 155 160
 Ser Tyr Val Phe Ser Val Ser Tyr Cys Ser Ser Asn Ile Ile Asn His
 165 170 175
 Phe Tyr Cys Asp Asn Val Pro Leu Leu Ala Leu Ser Cys Ser Asp Thr
 180 185 190
 Tyr Leu Pro Glu Thr Val Val Phe Ile Ser Ala Ala Thr Asn Val Val
 195 200 205
 Gly Ser Leu Ile Ile Val Leu Val Ser Tyr Phe Asn Ile Val Leu Ser
 210 215 220
 Ile Leu Lys Ile Cys Ser Ser Glu Gly Arg Lys Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Ala Ser His Met Met Ala Val Thr Ile Phe Tyr Gly Thr Leu Leu
 245 250 255
 Phe Met Tyr Val Gln Pro Arg Ser Asn His Ser Leu Asp Thr Asp Asp
 260 265 270
 Lys Met Ala Ser Val Phe Tyr Thr Leu Val Ile Pro Met Leu Asn Pro
 275 280 285
 Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Thr Ala Leu Gln Arg
 290 295 300
 Phe Met Thr Asn Leu Cys Tyr Ser Phe
 305 310

<210> 1309
 <211> 326
 <212> PRT

<213> Unknown (H38g226 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(326)

<223> Xaa = Any Amino Acid

<400> 1309

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Met Lys Ile Ser Asn Asn Ser Leu Gly Phe Leu Pro Thr Thr Phe Ile
 1           5           10          15
Leu Val Gly Ile Pro Gly Leu Glu Ser Glu His Leu Trp Ile Ser Val
          20          25          30
Pro Phe Ser Leu Ile Tyr Ile Ile Phe Leu Gly Asn Gly Ile Ile
 35          40          45
Leu His Val Ile Arg Thr Asp Ile Ala Leu His Gln Pro Met Tyr Leu
 50          55          60
Phe Leu Ala Met Leu Ala Leu Ala Glu Val Arg Val Ser Ala Ser Thr
 65          70          75          80
Leu Pro Thr Val Leu Gly Ile Phe Leu Phe Gly Asn Thr Glu Ile Ser
          85          90          95
Leu Glu Ala Phe Phe Phe Gln Met Phe Ser Ile His Ser Leu Ser Met
          100         105         110
Met Glu Ser Ala Val Leu Leu Ala Met Ser Leu Asp Arg Phe Ile Ala
          115         120         125
Ile Tyr Ser Pro Leu Ser Tyr Thr Ala Ile Leu Thr Leu Pro Arg Val
          130         135         140
Phe Gly Thr Gly Ala Ile Ile Val Leu Lys Ser Ile Met Leu Met Ala
          145         150         155         160
Pro Leu Pro Ile Leu Leu Trp Arg Leu Pro Phe Cys Gly His Asn Ala
          165         170         175
Leu Ser His Ser Tyr Cys Leu His Pro Asn Leu Ile Tyr Leu Ser Cys
          180         185         190
Gly Asn Ile Ser Val Asn Asn Ile Tyr Gly Ile Phe Ile Val Thr Ser
          195         200         205
Thr Phe Gly Leu Asp Ser Leu Leu Ile Val Ile Ser Tyr Gly Leu Ile
          210         215         220
Leu His Thr Val Leu Gly Ile Ala Thr Gly Glu Gly Arg Lys Lys Ala
          225         230         235         240
Leu Asn Thr Cys Gly Ser His Val Cys Ala Val Leu Ala Tyr Tyr Val
          245         250         255
Pro Met Ile Gly Leu Ser Ile Val His Arg Leu Gly His Arg Val Ser
          260         265         270
Pro Leu Leu Gln Ala Met Met Ala Asn Ala Tyr Leu Phe Phe Pro Pro
          275         280         285
Val Val Asn Pro Ile Val Tyr Ser Ile Lys Thr Lys Glu Ile His Gly
          290         295         300
Ala Ile Val Arg Met Leu Leu Glu Lys Arg Arg Arg Val Xaa Pro Lys
          305         310         315         320
Thr Ile Val Gly Arg Asn
          325

```

<210> 1310

<211> 311

<212> PRT

<213> Unknown (H38g227 protein)

<220>

<223> Synthetic construct

<400> 1310

```

Met Ser Lys Thr Ser Leu Val Thr Ala Phe Ile Leu Thr Gly Leu Pro
 1           5           10           15
His Ala Pro Gly Leu Asp Ala Pro Leu Phe Gly Ile Phe Leu Val Val
          20           25           30
Tyr Val Leu Thr Val Leu Gly Asn Leu Leu Ile Leu Leu Val Ile Arg
          35           40           45
Val Asp Ser His Leu His Thr Pro Met Tyr Tyr Phe Leu Thr Asn Leu
          50           55           60
Ser Phe Ile Asp Met Trp Phe Ser Thr Val Thr Val Pro Lys Met Leu
65           70           75           80
Met Thr Leu Val Ser Pro Ser Gly Arg Ala Ile Ser Phe His Ser Cys
          85           90           95
Val Ala Gln Leu Tyr Phe Phe His Phe Leu Gly Ser Thr Glu Cys Phe
          100          105          110
Leu Tyr Thr Val Met Ser Tyr Asp Arg Tyr Leu Ala Ile Ser Tyr Pro
          115          120          125
Leu Arg Tyr Thr Ser Met Met Ser Gly Ser Arg Cys Ala Leu Leu Ala
          130          135          140
Thr Ser Thr Trp Leu Ser Gly Ser Leu His Ser Ala Val Gln Thr Ile
145          150          155          160
Leu Thr Phe His Leu Pro Tyr Cys Gly Pro Asn Gln Ile Gln His Tyr
          165          170          175
Leu Cys Asp Ala Pro Pro Ile Leu Lys Leu Ala Cys Ala Asp Thr Ser
          180          185          190
Ala Asn Glu Met Val Ile Phe Val Asp Ile Gly Leu Val Ala Ser Gly
          195          200          205
Cys Phe Leu Leu Ile Val Leu Ser Tyr Val Ser Ile Val Cys Ser Ile
          210          215          220
Leu Arg Ile His Thr Ser Glu Gly Arg His Arg Ala Phe Gln Thr Cys
225          230          235          240
Ala Ser His Cys Ile Val Val Leu Cys Phe Phe Val Pro Cys Val Phe
          245          250          255
Ile Tyr Leu Arg Pro Gly Ser Arg Asp Val Val Asp Gly Val Val Ala
          260          265          270
Ile Phe Tyr Thr Val Leu Thr Pro Leu Leu Asn Pro Val Val Tyr Thr
          275          280          285
Leu Arg Asn Lys Glu Val Lys Lys Ala Val Leu Lys Leu Arg Asp Lys
          290          295          300
Val Ala His Ser Gln Gly Glu
305          310

```

<210> 1311

<211> 312

<212> PRT

<213> Unknown (H38g228 protein)

<220>

<223> Synthetic construct

<400> 1311

```

Met Pro Ser Ile Asn Asp Thr His Phe Tyr Pro Pro Phe Phe Leu Leu
 1           5           10           15
Leu Gly Ile Pro Gly Leu Asp Thr Leu His Ile Trp Ile Ser Phe Pro
          20           25           30
Phe Cys Ile Val Tyr Leu Ile Ala Ile Val Gly Asn Met Thr Ile Leu
          35           40           45
Phe Val Ile Lys Thr Glu His Ser Leu His Gln Pro Met Phe Tyr Phe
          50           55           60
Leu Ala Met Leu Ser Met Ile Asp Leu Gly Leu Ser Thr Ser Thr Ile
65           70           75           80

```

Pro Lys Met Leu Gly Ile Phe Trp Phe Asn Leu Gln Glu Ile Ser Phe
 85 90 95
 Gly Gly Cys Leu Leu Gln Met Phe Phe Ile His Met Phe Thr Gly Met
 100 105 110
 Glu Thr Val Leu Leu Val Val Met Ala Tyr Asp Arg Phe Val Ala Ile
 115 120 125
 Cys Asn Pro Leu Gln Tyr Thr Met Ile Leu Thr Asn Lys Thr Ile Ser
 130 135 140
 Ile Leu Ala Ser Val Val Val Gly Arg Asn Leu Val Leu Val Thr Pro
 145 150 155 160
 Phe Val Phe Leu Ile Leu Arg Leu Pro Phe Cys Gly His Asn Ile Val
 165 170 175
 Pro His Thr Tyr Cys Glu His Arg Gly Leu Ala Gly Leu Ala Cys Ala
 180 185 190
 Pro Ile Lys Ile Asn Ile Ile Tyr Gly Leu Met Val Ile Ser Tyr Ile
 195 200 205
 Ile Val Asp Val Ile Leu Ile Ala Ser Ser Tyr Val Leu Ile Leu Arg
 210 215 220
 Ala Val Phe Arg Leu Pro Ser Gln Asp Val Arg Leu Lys Ala Phe Asn
 225 230 235 240
 Thr Cys Gly Ser His Val Cys Val Met Leu Cys Phe Tyr Thr Pro Ala
 245 250 255
 Phe Phe Ser Phe Met Thr His Arg Phe Gly Gln Asn Ile Pro His Tyr
 260 265 270
 Ile His Ile Leu Leu Ala Asn Leu Tyr Val Val Val Pro Pro Ala Leu
 275 280 285
 Asn Pro Val Ile Tyr Gly Val Arg Thr Lys Gln Ile Arg Glu Gln Ile
 290 295 300
 Val Lys Ile Phe Val Gln Lys Glu
 305 310

<210> 1312

<211> 303

<212> PRT

<213> Unknown (H38g229 protein)

<220>

<223> Synthetic construct

<400> 1312

Met Thr Glu Phe Ile Phe Leu Val Leu Ser Pro Asn Gln Glu Val Gln
 1 5 10 15
 Arg Val Cys Phe Val Ile Phe Leu Phe Leu Tyr Thr Ala Ile Val Leu
 20 25 30
 Gly Asn Phe Leu Ile Val Leu Thr Val Met Thr Ser Arg Ser Leu Gly
 35 40 45
 Ser Pro Met Tyr Phe Phe Leu Ser Tyr Leu Ser Phe Met Glu Ile Cys
 50 55 60
 Tyr Ser Ser Ala Thr Ala Pro Lys Leu Ile Ser Asp Leu Leu Ala Glu
 65 70 75 80
 Arg Lys Val Ile Ser Trp Trp Gly Cys Met Ala Gln Leu Phe Phe Leu
 85 90 95
 His Phe Phe Gly Gly Thr Glu Ile Phe Leu Leu Thr Val Met Ala Tyr
 100 105 110
 Asp His Tyr Val Ala Ile Cys Lys Pro Leu Ser Tyr Thr Thr Ile Met
 115 120 125
 Asn Trp Gln Val Cys Thr Val Leu Val Gly Ile Ala Trp Val Gly Gly
 130 135 140
 Phe Met His Ser Phe Ala Gln Ile Leu Leu Ile Phe His Leu Leu Phe
 145 150 155 160
 Cys Gly Pro Asn Val Ile Asn His Tyr Phe Cys Asp Leu Val Pro Leu

```

      165      170      175
Leu Lys Leu Ala Cys Ser Asp Thr Phe Leu Ile Gly Leu Leu Ile Val
      180      185      190
Ala Asn Gly Gly Thr Leu Ser Val Ile Ser Phe Gly Val Leu Leu Ala
      195      200      205
Ser Tyr Met Val Ile Leu Leu His Leu Arg Thr Trp Ser Ser Glu Gly
      210      215      220
Trp Cys Lys Ala Leu Ser Thr Cys Gly Ser His Phe Ala Val Val Ile
      225      230      235      240
Leu Phe Phe Gly Pro Cys Val Phe Asn Ser Leu Arg Pro Ser Thr Thr
      245      250      255
Leu Pro Ile Asp Lys Met Val Ala Val Phe Tyr Thr Val Ile Thr Ala
      260      265      270
Ile Leu Asn Pro Val Ile Tyr Ser Leu Arg Asn Ala Glu Met Arg Lys
      275      280      285
Ala Met Lys Arg Leu Trp Ile Arg Thr Leu Arg Leu Asn Glu Lys
      290      295      300

```

<210> 1313

<211> 316

<212> PRT

<213> Unknown (H38g230 protein)

<220>

<223> Synthetic construct

<400> 1313

```

Leu Ile Ala Thr Gly Asn Trp Thr Arg Ile Ser Glu Phe Ile Leu Met
 1      5      10      15
Ser Phe Ser Ser Leu Pro Thr Glu Ile Gln Ser Leu Leu Phe Leu Thr
      20      25      30
Phe Leu Thr Ile Tyr Leu Val Thr Leu Met Gly Asn Cys Leu Ile Ile
      35      40      45
Leu Val Thr Leu Ala Asp Pro Met Leu His Ser Pro Met Tyr Phe Phe
      50      55      60
Leu Arg Asn Leu Ser Phe Leu Glu Ile Gly Phe Asn Leu Val Ile Val
      65      70      75      80
Pro Lys Met Leu Gly Thr Leu Leu Ala Gln Asp Thr Thr Ile Ser Phe
      85      90      95
Leu Gly Cys Ala Thr Gln Met Tyr Phe Phe Phe Phe Gly Val Ala
      100      105      110
Glu Cys Phe Leu Gln Ala Thr Met Ala Tyr Asp Arg Tyr Val Ala Ile
      115      120      125
Cys Ser Pro Leu His Tyr Pro Val Ile Met Asn Gln Arg Thr Arg Ala
      130      135      140
Lys Leu Ala Ala Ala Ser Trp Phe Pro Gly Phe Pro Val Ala Thr Val
      145      150      155      160
Gln Thr Thr Trp Leu Phe Ser Phe Pro Phe Cys Gly Thr Asn Lys Val
      165      170      175
Asn His Phe Phe Cys Asp Ser Pro Pro Val Leu Arg Leu Val Cys Ala
      180      185      190
Asp Thr Ala Leu Phe Glu Ile Tyr Ala Ile Val Gly Thr Ile Leu Val
      195      200      205
Val Met Ile Pro Cys Leu Leu Ile Leu Cys Ser Tyr Thr Arg Ile Ala
      210      215      220
Ala Ala Ile Leu Lys Ile Pro Ser Ala Lys Gly Lys Asn Lys Ala Phe
      225      230      235      240
Ser Thr Cys Ser Ser His Leu Leu Val Val Ser Leu Phe Tyr Ile Ser
      245      250      255
Leu Ser Leu Thr Tyr Phe Arg Pro Lys Ser Asn Asn Ser Pro Glu Gly
      260      265      270

```

Thr Lys Leu Leu Ser Leu Ser Tyr Thr Val Met Thr Pro Met Leu Asn
 275 280 285
 Pro Ile Ile Tyr Ser Leu Arg Asn Asn Glu Val Lys Asn Ala Leu Ser
 290 295 300
 Arg Thr Val Ser Lys Ala Leu Gly Pro Gln Lys Leu
 305 310 315

<210> 1314

<211> 309

<212> PRT

<213> Unknown (H38g231 protein)

<220>

<223> Synthetic construct

<400> 1314

Met Pro Asn Phe Thr Asp Val Thr Glu Phe Thr Leu Leu Gly Leu Thr
 1 5 10 15
 Cys Arg Gln Glu Leu Gln Val Leu Phe Phe Val Val Phe Leu Ala Val
 20 25 30
 Tyr Met Ile Thr Leu Leu Gly Asn Ile Gly Met Ile Ile Leu Ile Ser
 35 40 45
 Ile Ser Pro Gln Leu Gln Ser Pro Met Tyr Phe Phe Leu Ser His Leu
 50 55 60
 Ser Phe Ala Asp Val Cys Phe Ser Ser Asn Val Thr Pro Lys Met Leu
 65 70 75 80
 Glu Asn Leu Leu Ser Glu Thr Lys Thr Ile Ser Tyr Val Gly Cys Leu
 85 90 95
 Val Gln Cys Tyr Phe Phe Ile Ala Val Val His Val Glu Val Tyr Ile
 100 105 110
 Leu Ala Val Met Ala Phe Asp Arg Tyr Met Ala Gly Cys Asn Pro Leu
 115 120 125
 Leu Tyr Gly Ser Lys Met Ser Arg Thr Val Cys Val Arg Leu Ile Ser
 130 135 140
 Val Pro Tyr Val Tyr Gly Phe Ser Val Ser Leu Ile Cys Thr Leu Trp
 145 150 155 160
 Thr Tyr Gly Leu Tyr Phe Cys Gly Asn Phe Glu Ile Asn His Phe Tyr
 165 170 175
 Cys Ala Asp Pro Pro Leu Ile Gln Ile Ala Cys Gly Arg Val His Ile
 180 185 190
 Lys Glu Ile Thr Met Ile Val Ile Ala Gly Ile Asn Phe Thr Tyr Ser
 195 200 205
 Leu Ser Val Val Leu Ile Ser Tyr Thr Leu Ile Val Val Ala Val Leu
 210 215 220
 Arg Met Arg Ser Ala Asp Gly Arg Arg Lys Ala Phe Ser Thr Cys Gly
 225 230 235 240
 Ser His Leu Thr Ala Val Ser Met Phe Tyr Gly Thr Pro Ile Phe Met
 245 250 255
 Tyr Leu Arg Arg Pro Thr Glu Glu Ser Val Glu Gln Gly Lys Met Val
 260 265 270
 Ala Val Phe Tyr Thr Thr Val Ile Pro Met Leu Asn Pro Met Ile Tyr
 275 280 285
 Ser Leu Arg Asn Lys Asp Val Lys Glu Ala Val Asn Lys Ala Ile Thr
 290 295 300
 Lys Thr Tyr Val Arg
 305

<210> 1315

<211> 320

<212> PRT

<213> Unknown (H38g232 protein)

<220>

<223> Synthetic construct

<400> 1315

```

Met Leu His Thr Asn Asn Thr Gln Phe His Pro Ser Thr Phe Leu Val
 1           5           10           15
Val Gly Val Pro Gly Leu Glu Asp Val His Val Trp Ile Gly Phe Pro
          20           25           30
Phe Phe Ala Val Tyr Leu Thr Ala Leu Leu Gly Asn Ile Ile Ile Leu
          35           40           45
Phe Val Ile Gln Thr Glu Gln Ser Leu His Gln Pro Met Phe Tyr Phe
          50           55           60
Leu Ala Met Leu Ala Gly Thr Asp Leu Gly Leu Ser Thr Ala Thr Ile
65           70           75           80
Pro Lys Met Leu Gly Ile Phe Trp Phe Asn Leu Gly Glu Ile Ala Phe
          85           90           95
Gly Ala Cys Ile Thr Gln Met Tyr Thr Ile His Ile Cys Thr Gly Leu
          100          105          110
Glu Ser Val Val Leu Thr Val Thr Gly Ile Asp Arg Tyr Ile Ala Ile
          115          120          125
Cys Asn Pro Leu Arg Tyr Ser Met Ile Leu Thr Asn Lys Val Ile Ala
          130          135          140
Ile Leu Gly Ile Val Ile Ile Val Arg Thr Leu Val Phe Val Thr Pro
145          150          155          160
Phe Thr Phe Leu Thr Leu Arg Leu Pro Phe Cys Gly Val Arg Ile Ile
          165          170          175
Pro His Thr Tyr Cys Glu His Met Gly Leu Ala Lys Leu Ala Cys Ala
          180          185          190
Ser Ile Asn Val Ile Tyr Gly Leu Ile Ala Phe Ser Val Gly Tyr Ile
          195          200          205
Asp Ile Ser Val Ile Gly Phe Ser Tyr Val Gln Ile Leu Arg Ala Val
          210          215          220
Phe His Leu Pro Ala Trp Asp Ala Arg Leu Lys Ala Leu Ser Thr Cys
225          230          235          240
Gly Ser His Val Cys Val Met Leu Ala Phe Tyr Leu Pro Ala Leu Phe
          245          250          255
Ser Phe Met Thr His Arg Phe Gly His Asn Ile Pro His Tyr Ile His
          260          265          270
Ile Leu Leu Ala Asn Leu Tyr Val Val Phe Pro Pro Ala Leu Asn Ser
          275          280          285
Val Ile Tyr Gly Val Lys Thr Lys Gln Ile Arg Glu Gln Val Leu Arg
          290          295          300
Ile Leu Asn Pro Lys Ser Phe Trp His Phe Asp Pro Lys Arg Ile Phe
305          310          315          320

```

<210> 1316

<211> 312

<212> PRT

<213> Unknown (H38g233 protein)

<220>

<223> Synthetic construct

<400> 1316

```

Met Glu Gln His Asn Leu Thr Thr Val Asn Glu Phe Ile Leu Thr Gly
 1           5           10           15
Ile Thr Asp Ile Ala Glu Leu Gln Ala Pro Leu Phe Ala Leu Phe Leu
          20           25           30
Met Ile Tyr Val Ile Ser Val Met Gly Asn Leu Gly Met Ile Val Leu
          35           40           45

```

Thr Lys Leu Asp Ser Arg Leu Gln Thr Pro Met Tyr Phe Phe Leu Arg
 50 55 60
 His Leu Ala Phe Met Asp Leu Gly Tyr Ser Thr Thr Val Gly Pro Lys
 65 70 75 80
 Met Leu Val Asn Phe Val Val Asp Lys Asn Ile Ile Ser Tyr Tyr Phe
 85 90 95
 Cys Ala Thr Gln Leu Ala Phe Phe Leu Val Phe Ile Gly Ser Glu Leu
 100 105 110
 Phe Ile Leu Ser Ala Met Ser Tyr Asp Leu Tyr Val Ala Ile Cys Asn
 115 120 125
 Pro Leu Leu Tyr Thr Val Ile Met Ser Arg Arg Val Cys Gln Val Leu
 130 135 140
 Val Ala Ile Pro Tyr Leu Tyr Cys Thr Phe Ile Ser Leu Leu Val Thr
 145 150 155 160
 Ile Lys Ile Phe Thr Leu Ser Phe Cys Gly Tyr Asn Val Ile Ser His
 165 170 175
 Phe Tyr Cys Asp Ser Leu Pro Leu Leu Pro Leu Leu Cys Ser Asn Thr
 180 185 190
 His Glu Ile Glu Leu Ile Ile Leu Ile Phe Ala Ala Ile Asp Leu Ile
 195 200 205
 Ser Ser Leu Leu Ile Val Leu Leu Ser Tyr Leu Leu Ile Leu Val Ala
 210 215 220
 Ile Leu Arg Met Asn Ser Ala Gly Arg Gln Lys Ala Phe Ser Thr Cys
 225 230 235 240
 Gly Ala His Leu Thr Val Val Ile Val Phe Tyr Gly Thr Leu Leu Phe
 245 250 255
 Met Tyr Val Gln Pro Lys Ser Ser His Ser Phe Asp Thr Asp Lys Val
 260 265 270
 Ala Ser Ile Phe Tyr Thr Leu Val Ile Pro Met Leu Asn Pro Leu Ile
 275 280 285
 Tyr Ser Leu Arg Asn Lys Asp Val Lys Tyr Ala Leu Arg Arg Thr Trp
 290 295 300
 Asn Asn Leu Cys Asn Ile Phe Val
 305 310

<210> 1317

<211> 315

<212> PRT

<213> Unknown (H38g234 protein)

<220>

<223> Synthetic construct

<400> 1317

Met Met Trp Glu Asn Trp Thr Ile Val Ser Glu Phe Val Leu Val Ser
 1 5 10 15
 Phe Ser Ala Leu Ser Thr Glu Leu Gln Ala Leu Leu Phe Leu Leu Phe
 20 25 30
 Leu Thr Ile Tyr Leu Val Thr Leu Met Gly Asn Val Leu Ile Ile Leu
 35 40 45
 Val Thr Ile Ala Asp Ser Ala Leu Gln Ser Pro Met Tyr Phe Phe Leu
 50 55 60
 Arg Asn Leu Ser Phe Leu Glu Ile Gly Phe Asn Leu Val Ile Val Pro
 65 70 75 80
 Lys Met Leu Gly Thr Leu Ile Ile Gln Asp Thr Thr Ile Ser Phe Leu
 85 90 95
 Gly Cys Ala Thr Gln Met Tyr Phe Phe Phe Phe Gly Ala Ala Glu
 100 105 110
 Cys Cys Leu Ala Thr Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys
 115 120 125
 Asp Pro Leu His Tyr Pro Val Ile Met Gly His Ile Ser Cys Ala Gln

```

      130              135              140
Leu Ala Ala Ala Ser Trp Phe Ser Gly Phe Ser Val Ala Thr Val Gln
145              150              155              160
Thr Thr Trp Ile Phe Ser Phe Pro Phe Cys Gly Pro Asn Arg Val Asn
      165              170              175
His Phe Phe Cys Asp Ser Pro Pro Val Ile Ala Leu Val Cys Ala Asp
      180              185              190
Thr Ser Val Phe Glu Leu Glu Ala Leu Thr Ala Thr Val Pro Phe Ile
      195              200              205
Leu Phe Pro Phe Leu Leu Ile Leu Gly Ser Tyr Val Arg Ile Leu Ser
210              215              220
Thr Ile Phe Arg Met Pro Ser Ala Glu Gly Lys His Gln Ala Phe Ser
225              230              235              240
Thr Cys Ser Ala His Leu Leu Val Val Ser Leu Phe Tyr Ser Thr Ala
      245              250              255
Ile Leu Thr Tyr Phe Arg Pro Gln Ser Ser Ala Ser Ser Glu Ser Lys
260              265              270
Lys Leu Leu Ser Leu Ser Ser Thr Val Val Thr Pro Met Leu Asn Pro
275              280              285
Ile Ile Tyr Ser Ser Arg Asn Lys Glu Val Lys Ala Ala Leu Lys Arg
290              295              300
Leu Ile His Arg Thr Leu Gly Ser Gln Lys Leu
305              310              315

```

<210> 1318

<211> 310

<212> PRT

<213> Unknown (H38g235 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(310)

<223> Xaa = Any Amino Acid

<400> 1318

```

Met Ala Lys Thr Asn Asn Ser Glu Val Thr Glu Phe Ile Leu Leu Gly
 1              5              10              15
Leu Thr Asp Asn Pro Glu Leu Gln Ala Leu Phe Trp Gly Ile Phe Leu
      20              25              30
Val Ile Asn Leu Ser Ser Val Met Gly Ser Leu Gly Leu Ile Met Leu
      35              40              45
Ile His Ile Ser Pro Gln Leu His Thr Ala Met Tyr Phe Phe Leu Ser
      50              55              60
His Val Ala Phe Val Tyr Phe Cys Tyr Thr Ser Ser Ile Thr Pro Asn
65              70              75              80
Ser Leu Val Asn Leu Leu Gln Glu Thr Lys Arg Ile Ser Leu Pro Thr
      85              90              95
Cys Ala Ser Gln Leu His Cys Phe Ile Met Phe Val Val Cys Asp Met
      100              105              110
Tyr Val Leu Ser Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn
      115              120              125
Pro Leu Leu Tyr Ser Ile Ile Met Asn Arg Arg Val Cys Ile Gln Met
      130              135              140
Val Val Ser Thr Tyr Leu Tyr Gly Phe Ser Val Arg Leu Leu Gln Ala
145              150              155              160
Ile Leu Thr Phe His Leu Ser Phe Xaa Asp Ser Asn Ile Ile Asn Asn
      165              170              175
Ser Tyr Cys Asp Asp Val Pro Leu Ala Cys Leu Pro Tyr His Lys Asn
      180              185              190

```

His Tyr Lys Asp Val Lys Glu Leu Ile Leu Phe Thr Leu Ala Gly Phe
 195 200 205
 Asn Thr Leu Phe Ser Leu Leu Ile Ile Leu Ile Ser Tyr Ile Ser Val
 210 215 220
 Leu Ser Ala Ile Leu Arg Ile Asn Ser Ala Glu Ser Arg Gln Lys Ala
 225 230 235 240
 Phe Ser Thr Cys Asp Ser His Leu Thr Ser Ile Ile Ile Phe Tyr Gly
 245 250 255
 Ile Ile Thr Phe Met Tyr Met Gln Xaa Lys Thr Asn Asn Ser Leu Asp
 260 265 270
 Thr Asp Lys Ile Ala Ser Val Phe Cys Ile Val Lys Ile Pro Ser Ile
 275 280 285
 Tyr Ser Leu Arg Asn His Glu Val Lys Asp Ala Leu Lys Met Ile Met
 290 295 300
 Glu Asn Leu Cys Leu Thr
 305 310

<210> 1319

<211> 184

<212> PRT

<213> Unknown (H38g236 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(184)

<223> Xaa = Any Amino Acid

<400> 1319

Leu Val Lys Val Lys Lys Asn Xaa Asn Ile Phe Leu Ser Thr Ala Tyr
 1 5 10 15
 His Phe Phe Pro Thr Leu Ser Val Asn Asn Asn Lys Phe Leu Xaa Ile
 20 25 30
 Ile Asn Asn Asn Phe Xaa Val Xaa Phe Asn Leu His Ser Glu Thr Ser
 35 40 45
 His Ser Xaa Val Tyr Ser Leu Val Leu Ser Ser Lys Val Cys Ile Leu
 50 55 60
 Leu Ala Ala Gly Val Val Gly Gly Ile Leu Ser Arg Arg Ile Val Cys
 65 70 75 80
 Gly Pro Thr Val Ser Leu Ser Ser Ser Arg Ser Asn Ala Ile Asn His
 85 90 95
 Phe Phe Cys Asn Lys Ser Leu Gly Leu Gly Leu Ser Cys Tyr Asn Ile
 100 105 110
 Tyr Ile Ser Thr Ala Val Pro Ala Phe Val Gly Val Xaa Val Leu His
 115 120 125
 Ser Leu Pro Tyr Leu Val Ile Met Phe Ser Trp Thr Tyr Ile Leu Val
 130 135 140
 Ala Ile Lys Arg Met Ser Ser Val Gly Arg Lys Glu Leu Ser Ile Cys
 145 150 155 160
 Val Ser His Leu Lys Thr Ser Thr Ile Phe His Thr Ala Leu Phe Tyr
 165 170 175
 Val Tyr Leu Gln Pro Asp Phe Phe
 180

<210> 1320

<211> 321

<212> PRT

<213> Unknown (H38g237 protein)

<220>

<223> Synthetic construct

<400> 1320

```

Met Ser Gly Asp Asn Ser Ser Ser Leu Thr Pro Gly Phe Phe Ile Leu
 1           5           10           15
Asn Gly Val Pro Gly Leu Glu Ala Thr His Ile Trp Ile Ser Leu Pro
          20           25           30
Phe Cys Phe Met Tyr Ile Ile Ala Val Val Gly Asn Cys Gly Leu Ile
          35           40           45
Cys Leu Ile Ser His Glu Glu Ala Leu His Arg Pro Met Tyr Tyr Phe
          50           55           60
Leu Ala Leu Leu Ser Phe Thr Asp Val Thr Leu Cys Thr Thr Met Val
65           70           75           80
Pro Asn Met Leu Cys Ile Phe Trp Phe Asn Leu Lys Glu Ile Asp Phe
          85           90           95
Asn Ala Cys Leu Ala Gln Met Phe Phe Val His Met Leu Thr Gly Met
          100          105          110
Glu Ser Gly Val Leu Met Leu Met Ala Leu Asp Arg Tyr Val Ala Ile
          115          120          125
Cys Tyr Pro Leu Arg Tyr Ala Thr Ile Leu Thr Asn Pro Val Ile Ala
          130          135          140
Lys Ala Gly Leu Ala Thr Phe Leu Arg Asn Val Met Leu Ile Ile Pro
145          150          155          160
Phe Thr Leu Leu Thr Lys Arg Leu Pro Tyr Cys Arg Gly Asn Phe Ile
          165          170          175
Pro His Thr Tyr Cys Asp His Met Ser Val Ala Lys Val Ser Cys Gly
          180          185          190
Asn Phe Lys Val Asn Ala Ile Tyr Gly Leu Met Val Ala Leu Leu Ile
          195          200          205
Gly Val Phe Asp Ile Cys Cys Ile Ser Val Ser Tyr Thr Met Ile Leu
          210          215          220
Gln Ala Val Met Ser Leu Ser Ser Ala Asp Ala Arg His Lys Ala Phe
225          230          235          240
Ser Thr Cys Thr Ser His Met Cys Ser Ile Val Ile Thr Tyr Val Ala
          245          250          255
Ala Phe Phe Thr Phe Phe Thr His Arg Phe Val Gly His Asn Ile Pro
          260          265          270
Asn His Ile His Ile Ile Val Ala Asn Leu Tyr Leu Leu Leu Pro Pro
          275          280          285
Thr Met Asn Pro Ile Val Tyr Gly Val Lys Thr Lys Gln Ile Gln Glu
          290          295          300
Gly Val Ile Lys Phe Leu Leu Gly Asp Lys Val Ser Phe Thr Tyr Asp
305          310          315          320
Lys

```

<210> 1321

<211> 134

<212> PRT

<213> Unknown (H38g238 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(134)

<223> Xaa = Any Amino Acid

<400> 1321

```

Cys Phe Cys Gly Phe Ala Val Leu Thr Ser Cys Leu Phe Cys Leu Thr
 1           5           10           15

```

Pro Glu Arg Xaa His Asn Thr Leu Arg Met Ala Leu Gly Ser His Arg
 20 25 30
 Phe Pro Ser Xaa Pro Ile Lys Lys Asn Tyr Lys Trp Pro His Tyr Gln
 35 40 45
 Pro Glu Leu Leu Pro His Trp Ser Ser Lys Thr Glu Arg Ile Cys Ser
 50 55 60
 Pro Ala Pro Ser Gly Leu Glu Met Leu Arg Asn Ala Lys Pro Leu Gly
 65 70 75 80
 Phe Gln Leu Tyr Leu Ile Xaa Asn Glu Gln Ser Arg Leu Ala Pro Gln
 85 90 95
 Gly Val Pro Gln Lys Thr Xaa Ser Leu Cys Ser Ser Ala Leu Ser Ser
 100 105 110
 Tyr Cys Leu Lys Asp Thr Gly Gly Gly Gly Lys Xaa Ser Gly Glu Arg
 115 120 125
 Ser Ser Phe Pro Arg Glu
 130

<210> 1322

<211> 318

<212> PRT

<213> Unknown (H38g239 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(318)

<223> Xaa = Any Amino Acid

<400> 1322

Met Lys Pro Thr Ile Gln Met Ala Ser Gly Asn Leu Thr Trp Val Thr
 1 5 10 15
 Glu Phe Ile Leu Val Gly Val Ser Asp Asp Pro Glu Leu Gln Ile Pro
 20 25 30
 Leu Phe Leu Val Phe Leu Val Leu Tyr Leu Leu Thr Val Ala Gly Asn
 35 40 45
 Leu Gly Ile Ile Thr Leu Thr Ser Val Asp Pro Gln Leu Gln Thr Pro
 50 55 60
 Met Tyr Phe Phe Leu Xaa His Leu Ala Ile Ile Asn Leu Cys Asn Ser
 65 70 75 80
 Thr Val Val Ala Pro Lys Met Leu Val Asn Phe Leu Val Thr Lys Lys
 85 90 95
 Thr Ile Ser Tyr Tyr Gly Cys Ala Ala Gln Leu Gly Gly Phe Leu Val
 100 105 110
 Phe Ile Val Ala Glu Ile Phe Thr Leu Ala Ala Met Ala Tyr Asp Arg
 115 120 125
 Tyr Val Ala Ile Trp Ser Pro Leu Leu Tyr Ala Val Val Val Ser Pro
 130 135 140
 Lys Val Cys Arg Leu Leu Val Ser Leu Thr Tyr Leu Gln Ser Leu Ile
 145 150 155 160
 Thr Ala Leu Thr Val Ser Ser Cys Val Phe Ser Val Ser Tyr Cys Ser
 165 170 175
 Ser Asn Ile Ile Asn His Phe Tyr Cys Asp Asp Val Pro Leu Leu Ala
 180 185 190
 Leu Ser Cys Ser Asp Thr Tyr Ile Pro Glu Thr Ala Val Phe Ile Phe
 195 200 205
 Ser Gly Thr Asn Leu Leu Phe Ser Met Ile Val Val Leu Ile Ser Tyr
 210 215 220
 Phe Asn Ile Val Ile Thr Ile Leu Arg Ile Arg Ser Ser Glu Gly Arg
 225 230 235 240
 Gln Lys Ala Phe Ser Thr Cys Ala Ser His Met Ile Ala Val Val Val

				245					250					255			
Phe	Tyr	Gly	Thr	Leu	Leu	Phe	Met	Tyr	Leu	Gln	Pro	Arg	Ser	Asn	His		
			260						265					270			
Ser	Leu	Asp	Thr	Asp	Lys	Met	Ala	Ser	Val	Phe	Tyr	Thr	Leu	Val	Ile		
		275					280						285				
Pro	Val	Leu	Asn	Pro	Leu	Ile	Tyr	Ser	Leu	Arg	Asn	Lys	Asn	Val	Lys		
	290					295					300						
Asp	Ala	Leu	Lys	Arg	Phe	Leu	Asp	Asn	Pro	Cys	Arg	Ser	Leu				
305					310					315							

<210> 1323

<211> 315

<212> PRT

<213> Unknown (H38g240 protein)

<220>

<223> Synthetic construct

<400> 1323

Met	Leu	Ser	Pro	Asn	His	Thr	Ile	Val	Thr	Glu	Phe	Ile	Leu	Leu	Gly		
1				5					10					15			
Leu	Thr	Asp	Asp	Pro	Val	Leu	Glu	Lys	Ile	Leu	Phe	Gly	Val	Phe	Leu		
		20						25					30				
Ala	Ile	Tyr	Leu	Ile	Thr	Leu	Ala	Gly	Asn	Leu	Cys	Met	Ile	Leu	Leu		
	35						40					45					
Ile	Arg	Thr	Asn	Ser	Gln	Leu	Gln	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Gly		
	50					55					60						
His	Leu	Ser	Phe	Val	Asp	Ile	Cys	Tyr	Ser	Ser	Asn	Val	Thr	Pro	Asn		
65				70					75					80			
Met	Leu	His	Asn	Phe	Leu	Ser	Glu	Gln	Lys	Thr	Ile	Ser	Tyr	Ala	Gly		
			85						90					95			
Cys	Phe	Thr	Gln	Cys	Leu	Leu	Phe	Ile	Ala	Leu	Val	Ile	Thr	Glu	Phe		
		100						105					110				
Tyr	Phe	Leu	Ala	Ser	Met	Ala	Leu	Asp	Arg	Tyr	Val	Ala	Ile	Cys	Ser		
	115					120						125					
Pro	Leu	His	Tyr	Ser	Ser	Arg	Met	Ser	Lys	Asn	Ile	Cys	Ile	Ser	Leu		
	130					135					140						
Val	Thr	Val	Pro	Tyr	Met	Tyr	Gly	Phe	Leu	Asn	Gly	Leu	Ser	Gln	Thr		
145				150						155				160			
Leu	Leu	Thr	Phe	His	Leu	Ser	Phe	Cys	Gly	Ser	Leu	Glu	Ile	Asn	His		
			165						170					175			
Phe	Tyr	Cys	Ala	Asp	Pro	Pro	Leu	Ile	Met	Leu	Ala	Cys	Ser	Asp	Thr		
		180						185					190				
Arg	Val	Lys	Lys	Met	Ala	Met	Phe	Val	Val	Ala	Gly	Phe	Thr	Leu	Ser		
	195					200						205					
Ser	Ser	Leu	Phe	Ile	Ile	Leu	Ser	Tyr	Leu	Phe	Ile	Phe	Ala	Ala			
	210					215				220							
Ile	Phe	Arg	Ile	Arg	Ser	Ala	Glu	Gly	Arg	His	Lys	Ala	Phe	Ser	Thr		
225				230					235					240			
Cys	Ala	Ser	His	Leu	Thr	Ile	Val	Thr	Leu	Phe	Tyr	Gly	Thr	Leu	Phe		
			245						250					255			
Cys	Met	Tyr	Val	Arg	Pro	Pro	Ser	Glu	Lys	Ser	Val	Glu	Glu	Ser	Lys		
		260						265					270				
Ile	Ile	Ala	Val	Phe	Tyr	Thr	Phe	Leu	Ser	Pro	Met	Leu	Asn	Pro	Leu		
	275						280					285					
Ile	Tyr	Ser	Leu	Arg	Asn	Arg	Asp	Val	Ile	Leu	Ala	Ile	Gln	Gln	Met		
	290					295					300						
Ile	Arg	Gly	Lys	Ser	Phe	Cys	Lys	Ile	Ala	Val							
305					310					315							

<210> 1324

<211> 313

<212> PRT

<213> Unknown (H38g241 protein)

<220>

<223> Synthetic construct

<400> 1324

```

Met Pro Ile Ala Asn Asp Thr Gln Phe His Thr Ser Ser Phe Leu Leu
 1           5           10           15
Leu Gly Ile Pro Gly Leu Glu Asp Val His Ile Trp Ile Gly Phe Pro
          20           25           30
Phe Phe Ser Val Tyr Leu Ile Ala Leu Leu Gly Asn Ala Ala Ile Phe
          35           40           45
Phe Val Ile Gln Thr Glu Gln Ser Leu His Glu Pro Met Tyr Tyr Cys
          50           55           60
Leu Ala Met Leu Asp Ser Ile Asp Leu Ser Leu Ser Thr Ala Thr Ile
65           70           75           80
Pro Lys Met Leu Gly Ile Phe Trp Phe Asn Ile Lys Glu Ile Ser Phe
          85           90           95
Gly Gly Tyr Leu Ser Gln Met Phe Phe Ile His Phe Phe Thr Val Met
          100          105          110
Glu Ser Ile Val Leu Val Ala Met Ala Phe Asp Arg Tyr Ile Ala Ile
          115          120          125
Cys Lys Pro Leu Trp Tyr Thr Met Ile Leu Thr Ser Lys Ile Ile Ser
          130          135          140
Leu Ile Ala Gly Ile Ala Val Leu Arg Ser Leu Tyr Met Val Ile Pro
145          150          155          160
Leu Val Phe Leu Leu Arg Leu Pro Phe Cys Gly His Arg Ile Ile
          165          170          175
Pro His Thr Tyr Cys Glu His Met Gly Ile Ala Arg Leu Ala Cys Ala
          180          185          190
Ser Ile Lys Val Asn Ile Met Phe Gly Leu Gly Ser Ile Ser Leu Leu
          195          200          205
Leu Leu Asp Val Leu Leu Ile Ile Leu Ser His Ile Arg Ile Leu Tyr
210          215          220
Ala Val Phe Cys Leu Pro Ser Trp Glu Ala Arg Leu Lys Ala Leu Asn
225          230          235          240
Thr Cys Gly Ser His Ile Gly Val Ile Leu Ala Phe Ser Thr Pro Ala
          245          250          255
Phe Phe Ser Phe Phe Thr His Cys Phe Gly His Asp Ile Pro Gln Tyr
          260          265          270
Ile His Ile Phe Leu Ala Asn Leu Tyr Val Val Val Pro Pro Thr Leu
          275          280          285
Asn Pro Val Ile Tyr Gly Val Arg Thr Lys His Ile Arg Glu Thr Val
          290          295          300
Leu Arg Ile Phe Phe Lys Thr Asp His
305           310

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<210> 1325

<211> 328

<212> PRT

<213> Unknown (H38g242 protein)

<220>

<223> Synthetic construct

<400> 1325

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Met His Ile Phe Lys Phe Val Leu Asp Phe Asn Met Lys Asn Val Thr
 1           5           10           15
Glu Val Thr Leu Phe Val Leu Lys Gly Phe Thr Asp Asn Leu Glu Leu

```

```

      20      25      30
Gln Thr Ile Phe Phe Phe Leu Phe Leu Ala Ile Tyr Leu Phe Thr Leu
      35      40      45
Met Gly Asn Leu Gly Leu Ile Leu Val Val Ile Arg Asp Ser Gln Leu
      50      55      60
His Lys Pro Met Tyr Tyr Phe Leu Ser Met Leu Ser Ser Val Asp Ala
      65      70      75      80
Cys Tyr Ser Ser Val Ile Thr Pro Asn Met Leu Val Asp Phe Thr Thr
      85      90      95
Lys Asn Lys Val Ile Ser Phe Leu Gly Cys Val Ala Gln Val Phe Leu
      100      105      110
Ala Cys Ser Phe Gly Thr Thr Glu Cys Phe Leu Leu Ala Ala Met Ala
      115      120      125
Tyr Asp Arg Tyr Val Ala Ile Tyr Asn Pro Leu Leu Tyr Ser Val Ser
      130      135      140
Met Ser Pro Arg Val Tyr Met Pro Leu Ile Asn Ala Ser Tyr Val Ala
      145      150      155      160
Gly Ile Leu His Ala Thr Ile His Thr Val Ala Thr Phe Ser Leu Ser
      165      170      175
Phe Cys Gly Ala Asn Glu Ile Arg Arg Val Phe Cys Asp Ile Pro Pro
      180      185      190
Leu Leu Ala Ile Ser Tyr Ser Asp Thr His Thr Asn Gln Leu Leu Leu
      195      200      205
Phe Tyr Phe Val Gly Ser Ile Glu Leu Val Thr Ile Leu Ile Val Leu
      210      215      220
Ile Ser Tyr Gly Leu Ile Leu Leu Ala Ile Leu Lys Met Tyr Ser Ala
      225      230      235      240
Glu Gly Arg Arg Lys Val Phe Ser Thr Cys Gly Ala His Leu Thr Gly
      245      250      255
Val Ser Ile Tyr Tyr Gly Thr Ile Leu Phe Met Tyr Val Arg Pro Ser
      260      265      270
Ser Ser Tyr Ala Ser Asp His Asp Met Ile Val Ser Ile Phe Tyr Thr
      275      280      285
Ile Val Ile Pro Leu Leu Asn Pro Val Ile Tyr Ser Leu Arg Asn Lys
      290      295      300
Asp Val Lys Asp Ser Met Lys Lys Met Phe Gly Lys Asn Gln Val Ile
      305      310      315      320
Asn Lys Val Tyr Phe His Thr Lys
      325

```

<210> 1326

<211> 329

<212> PRT

<213> Unknown (H38g243 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(329)

<223> Xaa = Any Amino Acid

<400> 1326

```

Met Asn Gly Ala Asn Ser Ser Ser Leu Thr Pro Arg Tyr Phe Ile Leu
  1          5          10          15
Ser Gly Val Pro Gly Leu Glu Ala Ala His Ile Trp Ile Ser Leu Pro
      20      25      30
Phe Cys Phe Met Tyr Ile Ile Val Val Leu Gly Asn Cys Gly Leu Ile
      35      40      45
Tyr Leu Ile Ser His Glu Glu Ala Leu His Gln Pro Thr Tyr Tyr Phe
      50      55      60

```

Leu Asp Leu Leu Ser Leu Thr Asp Val Thr Gly Cys Thr Ser Phe Val
 65 70 75 80
 Pro Asn Met Leu Cys Ile Phe Trp Phe Gly Leu Lys Glu Ile Asp Phe
 85 90 95
 Asn Ala Cys Leu Val Gln Met Phe Phe Ile His Met Leu Thr Gly Met
 100 105 110
 Glu Ser Gly Ala Leu Met Leu Met Ala Leu Asp Arg Tyr Val Ala Ile
 115 120 125
 Cys Tyr Pro Leu His Tyr Ser Thr Ile Phe Thr Asn Thr Val Ile Thr
 130 135 140
 Lys Val Gly Leu Val Thr Phe Ile Gln Ser Val Leu Leu Met Ile Pro
 145 150 155 160
 Phe Ala Phe Leu Ile Lys Cys Leu Pro Tyr Cys Arg Gly Asn Leu Ile
 165 170 175
 His His Thr Tyr Cys Xaa His Met Ser Val Ala Lys Leu Ser Cys Gly
 180 185 190
 Asn Val Gln Ile Asn Ala Ile Tyr Gly Leu Ile Ala Ala Ile Leu Ile
 195 200 205
 Gly Gly Phe Asp Met Phe Cys Ile Ser Met Ser Tyr Thr Met Ile Ile
 210 215 220
 Arg Ala Val Val Asn Leu Ser Ser Ala Asp Ala Arg His Lys Ala Phe
 225 230 235 240
 Ser Thr Cys Thr Ala His Ile Cys Ala Ile Phe Ile Thr Tyr Val Pro
 245 250 255
 Ala Phe Phe Asn Phe Phe Thr His Arg Phe Gly Gly His Thr Ile Pro
 260 265 270
 His His Val His Ile Phe Ile Ala Asn Leu Tyr Leu Met Leu Pro Pro
 275 280 285
 Thr Leu Asn Pro Ile Val Tyr Gly Val Lys Thr Lys Gln Ile Arg Glu
 290 295 300
 Gly Val Ile Lys Leu Phe Phe Arg Glu Lys Val Tyr Phe Lys Tyr Asp
 305 310 315 320
 Ile Asn Leu Xaa Tyr Arg Ser Leu Asn
 325

<210> 1327

<211> 301

<212> PRT

<213> Unknown (H38g244 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(301)

<223> Xaa = Any Amino Acid

<400> 1327

Met Ala Ser Thr Asn Asn Val Thr Glu Ser Met Ile Thr Ser Leu Phe
 1 5 10 15
 Gln Asp Pro Ala Val Gln Arg Val Cys Phe Val Val Phe Leu Pro Val
 20 25 30
 Tyr Leu Ala Met Glu Val Gly Asn Gly Leu Ile Val Leu Thr Val Ser
 35 40 45
 Ile Ser Lys Ser Leu His Ser Pro Val Tyr Phe Phe Leu Ser Tyr Leu
 50 55 60
 Ser Leu Met Glu Ile Ser Tyr Phe Thr Val Val Pro Lys Phe Ile Thr
 65 70 75 80
 Asp Leu Leu Ala Lys Ile Lys Ala Ile Ser Leu Glu Gly Tyr Leu Ala
 85 90 95
 Gln Ile Phe Leu His Phe Phe Gly Ile Pro Trp Ile Phe Leu Leu Pro

100	105	110
Leu Met Thr Asn Asp Gln Tyr	Met Ala Asn Cys Lys	Leu Tyr Tyr Tyr
115	120	125
Thr Thr Ile Met Ser Cys Arg	Val Cys His Leu Leu	Val Ala Gly Phe
130	135	140
Trp Leu Arg Gly Ile Ile His	Ser Met Val Gln Ile	Leu Val Ser Val
145	150	155
Gln Leu Phe Phe Cys Gly Pro	Asn Met Ile Asp His	Ser Phe Cys Asp
165	170	175
Leu Gln Val Leu Phe Lys Leu	Ala Cys Thr Asp Thr	Phe Val Glu Gly
180	185	190
Val Ile Val Leu Ala Asn Ser	Glu Leu Val Ser Val	Phe Phe Leu Ile
195	200	205
Leu Val Ser Ser Tyr Ile Ile	Ile Leu Val Asn Leu	Arg Asn His Ser
210	215	220
Ala Glu Gly Arg Cys Lys Ala	Leu Ser Thr Cys Ala	Ser Tyr Leu Val
225	230	235
Phe Xaa Thr Cys Ile Phe Leu	Tyr Val Xaa Leu	Ser Ser Thr Phe Thr
245	250	255
Lys Asp Lys Leu Val Ala Val	Phe Tyr Val Val Ile	Thr Pro Met Leu
260	265	270
Asn Pro Phe Ile Tyr Thr Leu	Gly Asn Ala Glu Met	Lys Ile Thr Met
275	280	285
Arg Arg Leu Leu Gly Arg Thr	Val Asn Ser Gly Met	Glu
290	295	300

<210> 1328

<211> 324

<212> PRT

<213> Unknown (H38g245 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(324)

<223> Xaa = Any Amino Acid

<400> 1328

Gly Ser Xaa Lys Gln Xaa Lys Ser Xaa Pro Pro Ile Phe Phe Leu Thr	1	5	10	15
Gly Ile Pro Gly Leu Glu Ala Gln His Gly Trp Leu Ser Ile Pro Phe	20	25	30	
Phe Thr Met Tyr Ile Val Ala Ile Val Gly Asn Ile Leu Ile Met Ala	35	40	45	
Ala Val Gln Glu Asp Ser Ala Leu His Glu Pro Met Tyr Leu Phe Leu	50	55	60	
Ser Met Leu Ala Val Thr Glu Val Gly Val Ser Val Ser Thr Leu Pro	65	70	75	80
Thr Val Thr Gly Ile Leu Trp Phe Asp Ala His Arg Val Asp Phe Asp	85	90	95	
Gly Cys Leu Ala Gln Met Phe Phe Ile His Thr Phe Ser Cys Met Glu	100	105	110	
Ser Gly Val Leu Leu Ala Met Ser Tyr Asp Arg Phe Val Ala Ile Tyr	115	120	125	
Asn Leu Leu Arg Tyr Thr Ala Ile Leu Thr Leu Pro Arg Ile Ile Cys	130	135	140	
Met Gly Leu Gly Ile Thr Leu Lys Ser Val Ala Leu Met Ala Pro Leu	145	150	155	160
Pro Ile Leu Leu Arg Gln Leu Pro Tyr Cys His Thr Asn Val Leu Ser	165	170	175	

His Ser Tyr Cys Leu His Ser Asp Leu Ile Gln Leu Pro Cys Ala Asp
 180 185 190
 Thr Lys Leu Asn Ser Ile Leu Gly Leu Ala Ile Val Leu Ala Asn Phe
 195 200 205
 Gly Leu Asp Ser Leu Leu Ile Val Val Ser Tyr Val Leu Ile Leu Tyr
 210 215 220
 Thr Val Met Gly Ile Ala Ser Gly Glu Gly Arg Trp Lys Ala Leu Asn
 225 230 235 240
 Thr Cys Val Ser His Ile Cys Ala Val Leu Ile Tyr Tyr Val Pro Met
 245 250 255
 Ile Gly Val Ser Val Met His Arg Ala Ala Lys His Ala Ser Pro Ile
 260 265 270
 Val His Thr Leu Met Ser Ser Ile Cys Leu Leu Val Pro Pro Val Leu
 275 280 285
 Asn Pro Ile Ile Tyr Ser Val Lys Thr Gln Thr Ile Arg Gln Gly Ile
 290 295 300
 Leu Thr Leu Phe Ser Cys Lys Arg Glu Leu Leu Xaa Ile Thr Ala Arg
 305 310 315 320
 Ser Gln Glu Leu

<210> 1329

<211> 292

<212> PRT

<213> Unknown (H38g246 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(292)

<223> Xaa = Any Amino Acid

<400> 1329

Thr Leu Phe Ile Ile Ser Lys Phe Gln Gly Cys Xaa Lys Val Gly Leu
 1 5 10 15
 Tyr Thr Gln Ser Leu Tyr Leu Leu Ala Glu Tyr Phe His Arg Gly Gln
 20 25 30
 Leu Met Lys Met Leu Thr Ser Thr Asn Leu Ser Leu Ser Val Val Thr
 35 40 45
 Ile Gly Ile Phe Gln Phe Asn Val Arg Glu Ile Val Phe Gly Ala Phe
 50 55 60
 Leu Val Tyr Ile Gln Met Phe Met Thr Tyr Leu Cys Thr Gly Leu Glu
 65 70 75 80
 Ser Gly Val Leu Ile Ile Leu Ala Ile Asp His Tyr Val Val Ile Arg
 85 90 95
 Asn Pro Leu Arg Tyr Thr Met Ile Leu Met Asn Asn Val Val Ala Ile
 100 105 110
 Leu Gly Val Met Ile Ile Arg Ser Leu Ile Phe Ile Ile Pro Phe Glu
 115 120 125
 Phe Leu Ile Leu Leu Leu Ser Phe Cys Ala Ala His Ile Ile Pro His
 130 135 140
 Thr Lys Cys Glu His Met Gly Ile Ala His Leu Ser Cys Ala Ser Val
 145 150 155 160
 Arg Ala Asn Asn Met Phe Gly Met Val Ala Phe Ser Val Gly Phe Ile
 165 170 175
 Asp Leu Ile Ala Ile Gly Phe Ser Tyr Val Lys Lys Leu Arg Ala Leu
 180 185 190
 Phe His Leu Pro Pro Trp Asn Gly Gln Phe Glu Ala Leu Asn Thr Cys
 195 200 205
 Gly Ser His Val Cys Met Leu Ile Phe Tyr Ile Pro Val Phe Phe Phe

210	215	220
Xaa Tyr Thr Ala Trp	Xaa Lys His Pro Cys Tyr	Ile Arg Ile Phe Leu
225	230	235
Ala Asn Val Tyr Thr	Val Val Leu Pro Val Phe Asn Pro Val	Ile Tyr
245	250	255
Gly Ile Arg Lys Lys Gln Ile Pro Asp Xaa Gly Ile Asp	Leu Lys Thr	
260	265	270
Phe Asp Asp Gln Ser Leu Leu Val Met Met Ile Tyr Ile	Leu Gly Tyr	
275	280	285
Ile Cys Lys Tyr		
290		

<210> 1330

<211> 312

<212> PRT

<213> Unknown (H38g247 protein)

<220>

<223> Synthetic construct

<400> 1330

Met Asp Glu Ala Asn His Ser Val Val Ser Glu Phe Val Phe Leu Gly	
1	5
Leu Ser Asp Ser Arg Lys Ile Gln Leu Leu Phe Leu Phe Ser	10
20	25
Val Phe Tyr Val Ser Ser Leu Met Gly Asn Leu Leu Ile Val Leu Thr	30
35	40
Val Thr Ser Asp Pro Arg Leu Gln Ser Pro Met Tyr Phe Leu Leu Ala	45
50	55
Asn Leu Ser Ile Ile Asn Leu Val Phe Cys Ser Ser Thr Ala Pro Lys	60
65	70
Met Ile Tyr Asp Leu Phe Arg Lys His Lys Thr Ile Ser Phe Gly Gly	75
85	90
Cys Val Val Gln Ile Phe Phe Ile His Ala Val Gly Gly Thr Glu Met	95
100	105
Val Leu Leu Ile Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Lys	110
115	120
Pro Leu His Tyr Leu Thr Ile Met Asn Pro Gln Arg Cys Ile Leu Phe	125
130	135
Leu Val Ile Ser Trp Ile Ile Gly Ile Ile His Ser Val Ile Gln Leu	140
145	150
Ala Phe Val Val Asp Leu Leu Phe Cys Gly Pro Asn Glu Leu Asp Ser	155
165	170
Phe Phe Cys Asp Leu Pro Arg Phe Ile Lys Leu Ala Cys Ile Glu Thr	175
180	185
Tyr Thr Leu Gly Phe Met Val Thr Ala Asn Ser Gly Phe Ile Ser Leu	190
195	200
Ala Ser Phe Leu Ile Leu Ile Ile Ser Tyr Ile Phe Ile Leu Val Thr	205
210	215
Val Gln Lys Lys Ser Ser Gly Gly Ile Phe Lys Ala Phe Ser Met Leu	220
225	230
Ser Ala His Val Ile Val Val Val Leu Val Phe Gly Pro Leu Ile Phe	235
245	250
Phe Tyr Ile Phe Pro Phe Pro Thr Ser His Leu Asp Lys Phe Leu Ala	255
260	265
Ile Phe Asp Ala Val Ile Thr Pro Val Leu Asn Pro Val Ile Tyr Thr	270
275	280
Phe Arg Asn Lys Glu Met Met Val Ala Met Arg Arg Arg Cys Ser Gln	285
290	295
Phe Val Asn Tyr Ser Lys Ile Phe	300
305	310

<210> 1331
 <211> 168
 <212> PRT
 <213> Unknown (H38g248 protein)

<220>
 <223> Synthetic construct

<400> 1331
 Lys Gln Ser Ser Gly Asp Ser Gly Asn Gln Thr Thr Trp Leu Ile Leu
 1 5 10 15
 Val Gly Phe Gly Glu Leu Gln Tyr Leu Gly Phe Leu Pro Phe Thr Leu
 20 25 30
 Phe Leu Ala Ile Tyr Val Val Thr Val Val Gly Asn Ala Leu Ile Met
 35 40 45
 Leu Ala Val Ala Ser Ser Arg Thr Leu His Pro Pro Met Tyr Phe Phe
 50 55 60
 Leu Cys His Phe Ser Leu Leu Glu Ile Gly Tyr Thr Ser Asn Val Ile
 65 70 75 80
 Leu Trp Leu Leu Gln Ser Phe Leu Glu Gly Lys Glu Val Ile Ser Leu
 85 90 95
 Val Ser Cys Leu Ala Gln Phe Tyr Val Phe Ser Ser Leu Ala Ala Ala
 100 105 110
 Glu Cys Leu Leu Leu Ser Ala Val Ser Tyr Asp Cys Tyr Leu Ala Ile
 115 120 125
 Cys Cys Pro Leu His Tyr Pro Ala Leu Met Ser Thr Trp Phe Cys His
 130 135 140
 Cys Leu Ala Ala Gly Ala Trp Phe Ser Gly Phe Phe Ser Ser Ala Phe
 145 150 155 160
 Thr Met Ala Leu Ala Ala Pro Leu
 165

<210> 1332
 <211> 321
 <212> PRT
 <213> Unknown (H38g249 protein)

<220>
 <223> Synthetic construct

<400> 1332
 Met Leu Thr Leu Asn Lys Thr Asp Leu Ile Pro Ala Ser Phe Ile Leu
 1 5 10 15
 Asn Gly Val Pro Gly Leu Glu Asp Thr Gln Leu Trp Ile Ser Phe Pro
 20 25 30
 Phe Cys Ser Met Tyr Val Val Ala Met Val Gly Asn Cys Gly Leu Leu
 35 40 45
 Tyr Leu Ile His Tyr Glu Asp Ala Leu His Lys Pro Met Tyr Tyr Phe
 50 55 60
 Leu Ala Met Leu Ser Phe Thr Asp Leu Val Met Cys Ser Ser Thr Ile
 65 70 75 80
 Pro Lys Ala Leu Cys Ile Phe Trp Phe His Leu Lys Asp Ile Gly Phe
 85 90 95
 Asp Glu Cys Leu Val Gln Met Phe Phe Ile His Thr Phe Thr Gly Met
 100 105 110
 Glu Ser Gly Val Leu Met Leu Met Ala Leu Asp Arg Tyr Val Ala Ile
 115 120 125
 Cys Tyr Pro Leu Arg Tyr Ser Thr Ile Leu Thr Asn Pro Val Ile Ala
 130 135 140
 Lys Val Gly Thr Ala Thr Phe Leu Arg Gly Val Leu Leu Ile Ile Pro

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145          150          155          160
Phe Thr Phe Leu Thr Lys Arg Leu Pro Tyr Cys Arg Gly Asn Ile Leu
165          170          175
Pro His Thr Tyr Cys Asp His Met Ser Val Ala Lys Leu Ser Cys Gly
180          185          190
Asn Val Lys Val Asn Ala Ile Tyr Gly Leu Met Val Ala Leu Leu Ile
195          200          205
Gly Gly Phe Asp Ile Leu Cys Ile Thr Ile Ser Tyr Thr Met Ile Leu
210          215          220
Arg Ala Val Val Ser Leu Ser Ser Ala Asp Ala Arg Gln Lys Ala Phe
225          230          235          240
Asn Thr Cys Thr Ala His Ile Cys Ala Ile Val Phe Ser Tyr Thr Pro
245          250          255
Ala Phe Phe Ser Phe Phe Ser His Arg Phe Gly Glu His Ile Ile Pro
260          265          270
Pro Ser Cys His Ile Ile Val Ala Asn Ile Tyr Leu Leu Leu Pro Pro
275          280          285
Thr Met Asn Pro Ile Val Tyr Gly Val Lys Thr Lys Gln Ile Arg Asp
290          295          300
Cys Val Ile Arg Ile Leu Ser Gly Ser Lys Asp Thr Lys Ser Tyr Ser
305          310          315          320
Met

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<210> 1333

<211> 315

<212> PRT

<213> Unknown (H38g250 protein)

<220>

<223> Synthetic construct

<400> 1333

```

Met Thr Thr His Arg Asn Asp Thr Leu Ser Thr Glu Ala Ser Asp Phe
1      5      10      15
Leu Leu Asn Cys Phe Val Arg Ser Pro Ser Trp Gln His Trp Leu Ser
20      25      30
Leu Pro Leu Ser Leu Leu Phe Leu Leu Ala Val Gly Ala Asn Thr Thr
35      40      45
Leu Leu Met Thr Ile Trp Leu Glu Ala Ser Leu His Gln Pro Leu Tyr
50      55      60
Tyr Leu Leu Ser Leu Leu Ser Leu Leu Asp Ile Val Leu Cys Leu Thr
65      70      75      80
Val Ile Pro Lys Val Leu Thr Ile Phe Trp Phe Asp Leu Arg Pro Ile
85      90      95
Ser Phe Pro Ala Cys Phe Leu Gln Met Tyr Ile Met Asn Cys Phe Leu
100     105     110
Ala Met Glu Ser Cys Thr Phe Met Val Met Ala Tyr Asp Arg Tyr Val
115     120     125
Ala Ile Cys His Pro Leu Arg Tyr Pro Ser Ile Ile Thr Asp His Phe
130     135     140
Val Val Lys Ala Ala Met Phe Ile Leu Thr Arg Asn Val Leu Met Thr
145     150     155     160
Leu Pro Ile Pro Ile Leu Ser Ala Gln Leu Arg Tyr Cys Gly Arg Asn
165     170     175
Val Ile Glu Asn Cys Ile Cys Ala Asn Met Ser Val Ser Arg Leu Ser
180     185     190
Cys Asp Asp Val Thr Ile Asn His Leu Tyr Gln Phe Ala Gly Gly Trp
195     200     205
Thr Leu Leu Gly Ser Asp Leu Ile Leu Ile Phe Leu Ser Tyr Thr Phe
210     215     220

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Ile Leu Arg Ala Val Leu Arg Leu Lys Ala Glu Gly Ala Val Ala Lys
225          230          235          240
Ala Leu Ser Thr Cys Gly Ser His Phe Met Leu Ile Leu Phe Phe Ser
          245          250          255
Thr Ile Leu Leu Val Phe Val Leu Thr His Val Ala Lys Lys Lys Val
          260          265          270
Ser Pro Asp Val Pro Val Leu Leu Asn Val Leu His His Val Ile Pro
          275          280          285
Ala Ala Leu Asn Pro Ile Ile Tyr Gly Val Arg Thr Gln Glu Ile Lys
          290          295          300
Gln Gly Met Gln Arg Leu Leu Lys Lys Gly Cys
305          310          315

```

<210> 1334

<211> 302

<212> PRT

<213> Unknown (H38g251 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(302)

<223> Xaa = Any Amino Acid

<400> 1334

```

Leu Ser Ser Met Cys Leu Thr Ile Val Met His Cys Glu Phe Phe Leu
1          5          10          15
Met Asp Leu Thr Asp Asp Pro Gln Leu His Pro Thr Phe Ser Ala Leu
          20          25          30
Phe Leu Pro Ile Tyr Val Val Met Val Met Ala Asn Leu Gly Leu Leu
          35          40          45
Ala Phe Ile Val Val Ser Pro Gln Phe Leu Thr Pro Met Tyr Phe Phe
          50          55          60
Leu Ser Asn Trp Ser Ser Val Asp Phe Cys Tyr Ser Ser Val Thr Val
65          70          75          80
Pro Lys Ile Ser Met Gly Phe Phe Ser Asp Cys Gln Val Phe Ser Phe
          85          90          95
Ser Gly Cys Met Ala Gln Leu Ser Cys Phe Xaa Ile Phe Ala Asp Thr
          100          105          110
Glu Phe Phe Leu Leu Ala Ser Met Val Tyr Tyr Arg Xaa Glu Ala Val
          115          120          125
Cys Asn Pro Leu Leu Tyr His Ile Thr Met Ser Pro Lys Leu Cys Leu
          130          135          140
Gln Leu Val Ala Thr Ser Met Asn Met Val Leu Pro Ser Ser Thr Ile
145          150          155          160
Phe His Leu Ile Phe Cys Lys Ser Arg Ala Ile Ile His Xaa Phe Cys
          165          170          175
Tyr Phe Ser Pro Pro Pro Arg Leu Xaa Lys Leu Ser Cys Ser Asp Met
          180          185          190
Gln Gly Leu Gln Leu Leu Thr Phe Ala Ser Ser Ser Phe Asn Val Ser
          195          200          205
Val Ser Arg Thr Ile Phe Leu Val Ser Tyr Leu Ile Met Arg Met Pro
          210          215          220
Ser Val Xaa Gly Lys His Cys Ala Ser His Leu Thr Ala Val Ser Leu
225          230          235          240
Cys Tyr Gly Thr Thr Val Phe Leu His Leu His Leu Ser Leu Lys Cys
          245          250          255
Ser Pro Asp Arg Asp Met Leu Val Ser Val Leu His Ser Ala Ile Leu
          260          265          270
Met Leu Asn Pro Met Val Gln Ser Leu Arg Asn Lys Asp Val Lys Lys

```

275 280 285
 Thr Phe Gly Thr Ser Ser Xaa Arg Phe Thr Ile Pro Leu Leu
 290 295 300

<210> 1335
 <211> 324
 <212> PRT
 <213> Unknown (H38g252 protein)

<220>
 <223> Synthetic construct

<400> 1335
 Met Pro Leu Phe Asn Ser Leu Cys Trp Phe Pro Thr Ile His Val Thr
 1 5 10 15
 Pro Pro Ser Phe Ile Leu Asn Gly Ile Pro Gly Leu Glu Arg Val His
 20 25 30
 Val Trp Ile Ser Leu Pro Leu Cys Thr Met Tyr Ile Ile Phe Leu Val
 35 40 45
 Gly Asn Leu Gly Leu Val Tyr Leu Ile Tyr Tyr Glu Glu Ser Leu His
 50 55 60
 His Pro Met Tyr Phe Phe Phe Gly His Ala Leu Ser Leu Ile Asp Leu
 65 70 75 80
 Leu Thr Cys Thr Thr Thr Leu Pro Asn Ala Leu Cys Ile Phe Trp Phe
 85 90 95
 Ser Leu Lys Glu Ile Asn Phe Asn Ala Cys Leu Ala Gln Met Phe Phe
 100 105 110
 Val His Gly Phe Thr Gly Val Glu Ser Gly Val Leu Met Leu Met Ala
 115 120 125
 Leu Asp Arg Tyr Val Ala Ile Cys Tyr Pro Leu Arg Tyr Ala Thr Thr
 130 135 140
 Leu Thr Asn Pro Ile Ile Ala Lys Ala Glu Leu Ala Thr Phe Leu Arg
 145 150 155 160
 Gly Val Leu Leu Met Ile Pro Phe Pro Phe Leu Val Lys Arg Leu Pro
 165 170 175
 Phe Cys Gln Ser Asn Ile Ile Ser His Thr Tyr Cys Asp His Met Ser
 180 185 190
 Val Val Lys Leu Ser Cys Ala Ser Ile Lys Val Asn Val Ile Tyr Gly
 195 200 205
 Leu Met Val Ala Leu Leu Ile Gly Val Phe Asp Ile Cys Cys Ile Ser
 210 215 220
 Leu Ser Tyr Thr Leu Ile Leu Lys Ala Ala Ile Ser Leu Ser Ser Ser
 225 230 235 240
 Asp Ala Arg Gln Lys Ala Phe Ser Thr Cys Thr Ala His Ile Ser Ala
 245 250 255
 Ile Ile Ile Thr Tyr Val Pro Ala Phe Phe Thr Phe Phe Ala His Arg
 260 265 270
 Phe Gly Gly His Thr Ile Pro Pro Ser Leu His Ile Ile Val Ala Asn
 275 280 285
 Leu Tyr Leu Leu Leu Pro Pro Thr Leu Asn Pro Ile Val Tyr Gly Val
 290 295 300
 Lys Thr Lys Gln Ile Arg Lys Ser Val Ile Lys Phe Phe Gln Gly Asp
 305 310 315 320
 Lys Gly Ala Gly

<210> 1336
 <211> 274
 <212> PRT
 <213> Unknown (H38g253 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(274)

<223> Xaa = Any Amino Acid

<400> 1336

Glu Arg Asn Pro Ser Val Ala Glu Lys Cys Leu Gln Gly Met Thr Asp
 1 5 10 15
 Ser Ser His His Tyr Leu Xaa Leu Arg Leu Pro Leu Phe Arg Leu Leu
 20 25 30
 Ile Leu Leu Tyr Thr Ile Ile Thr Ile Gly Asn Leu Gly Thr Val Ile
 35 40 45
 Leu Ile Gly Ile Ser Leu Gly Leu Tyr Val Cys Pro Pro Arg Phe Leu
 50 55 60
 Leu Phe Thr Phe Ser Met Leu Arg Val Leu Val Lys Cys Phe Xaa Ser
 65 70 75 80
 Thr Val Leu Pro Phe Ser Phe Trp Ser Leu Glu Ala Gln Ile Asn Phe
 85 90 95
 Phe Ser Ile Leu Cys Ile Thr Glu Phe Phe Pro Leu Ala Thr Met Ala
 100 105 110
 Tyr Asp Asp Asn Val Ala Thr Cys Glu Pro Leu Phe His Pro Phe Thr
 115 120 125
 Ser Leu Arg Leu Asn Ser Ala Phe Val Xaa Glu Lys Leu Tyr Leu Arg
 130 135 140
 Ala Phe Thr Ser Ala Leu Pro Ser Thr Leu Pro Phe His Leu Pro Phe
 145 150 155 160
 Phe Asn Ser His Leu Cys Ser Leu Gln Xaa His Tyr Phe Leu Gly Gln
 165 170 175
 Val Val Leu Xaa Asn Met Thr Pro Asn Phe Lys Leu Pro Asp Phe Ser
 180 185 190
 Asn Ser Asn Val Asn Leu Val Ser Leu Cys Cys Pro Thr Ile Cys Cys
 195 200 205
 Tyr Pro Ile Ile Leu Arg Ser Leu Ser Ser His Asn Xaa Ser Glu Asn
 210 215 220
 Lys Leu Leu Ile Ile Ile Phe Phe Gln Asn Ser Thr Xaa Leu Leu Phe
 225 230 235 240
 Ile Phe Cys Ser Asp Glu Asn Val Tyr Xaa Thr Ile Xaa Gly Ile Thr
 245 250 255
 Asp Xaa Phe Ile Lys Ser Lys His Cys Val His Ile Pro Leu Met Gln
 260 265 270
 Ile Leu

<210> 1337

<211> 315

<212> PRT

<213> Unknown (H38g254 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(315)

<223> Xaa = Any Amino Acid

<400> 1337

Met Ser Ser Leu Asn Val Thr Glu Pro His Leu Ser Ser Phe Leu Leu
 1 5 10 15
 Leu Gly Ile Pro Gly Leu Glu Ala Ala Gln Arg Trp Leu Gly Phe Pro

```
<210> 1338
<211> 323
<212> PRT
<213> Unknown (H38q255 protein)
```

```
<220>
<223> Synthetic construct
<221> VARIANT
<222> (1)...(323)
<223> Xaa = Any Amino Acid
```

<400> 1338															
Val	Glu	Asn	Ser	Pro	Met	Val	Thr	Asp	Phe	Ile	Phe	Leu	Gly	Met	Thr
1				5					10					15	
Asp	Asn	Ser	Gln	Leu	Glu	Val	Leu	Leu	Phe	Gly	Val	Phe	Leu	Ile	Ala
			20					25					30		
Tyr	Ile	Ile	Thr	Val	Leu	Glu	Asn	Leu	Gly	Leu	Val	Val	Leu	Ile	Arg
		35					40					45			
Val	Ser	Ser	Arg	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Ser	Asn	Gln
	50					55					60				
Ser	Phe	Leu	Asp	Val	Cys	Phe	Ser	Ser	Ile	Thr	Ile	Pro	Gln	Asn	Leu
65					70					75					80

Ala His Leu Phe Ser Lys Leu Gln Tyr Val Ser Phe Leu Phe Pro Tyr
 85 90 95
 Thr Xaa Met Ser Leu Phe Val Ile Phe Ala Ser Ala Glu Cys Asn Phe
 100 105 110
 Leu Asn Leu Met Ala Tyr Asp Arg Phe Thr Ala Ile Cys His Pro Leu
 115 120 125
 Phe Tyr His Ile Thr Met Ser Arg Gly His Tyr Leu Phe Leu Val Ala
 130 135 140
 Gly Cys Tyr Leu Gly Gly Leu Val Lys Met Val Thr Val Thr Thr Ser
 145 150 155 160
 Ile Thr Gln Leu Ser Leu Cys Gln Pro Cys Val Leu Pro Ala Phe Phe
 165 170 175
 Cys Asp Ile Pro Ser Leu Leu Val Leu Val Cys Ser Asp Pro Trp Ile
 180 185 190
 Thr Ser Ser Ile Leu Val Val Gly Cys Gly Gly Phe Thr Leu Val Thr
 195 200 205
 Ser Val Val Val Ile Leu Val Ser Tyr Met Ser Ser Leu Met Thr Ile
 210 215 220
 Leu Gly Ile Pro Leu Ala Ser Gly Lys Gln Arg Ala Phe Ser Thr Cys
 225 230 235 240
 Ala Ser His Leu Thr Ala Val Ser Leu Tyr Tyr Glu Thr Thr Met Tyr
 245 250 255
 Thr Tyr Leu Pro Ala Ser Arg His Gly Ser Gly Ala Gly Asn Gln Ile
 260 265 270
 Val Ser Val Phe Tyr Thr Met Val Ile Pro Met Leu Asn Pro Leu Ile
 275 280 285
 Tyr Ser Leu Arg Asn Glu Glu Val Lys Val Ala Leu Xaa Lys Thr Leu
 290 295 300
 Arg His Ser Pro Xaa Ser Ser Leu Ser Val Ser Lys Met Gln Asn Ile
 305 310 315 320
 Leu Xaa Arg

<210> 1339

<211> 311

<212> PRT

<213> Unknown (H38g256 protein)

<220>

<223> Synthetic construct

<400> 1339

Trp Leu Asp Glu Lys Lys Gln Asp Ser Asn Val Thr Glu Leu Val Leu
 1 5 10 15
 Leu Gly Leu Ser Ser Trp Glu Leu Gln Leu Phe Leu Leu Leu
 20 25 30
 Phe Leu Phe Phe Tyr Ile Ala Ile Val Leu Gly Asn Leu Leu Ile Val
 35 40 45
 Val Thr Val Gln Ala His Ala His Leu Leu Gln Ser Pro Met Tyr Tyr
 50 55 60
 Phe Leu Gly His Leu Ser Phe Ile Asp Leu Cys Leu Ser Cys Val Thr
 65 70 75 80
 Leu Pro Lys Met Leu Gly Asp Phe Leu Gln Gln Gly Lys Ser Ile Ser
 85 90 95
 Phe Ser Gly Cys Leu Ala Gln Ile Tyr Phe Leu His Phe Leu Gly Ala
 100 105 110
 Ser Glu Met Phe Leu Leu Thr Val Met Ala Tyr Asp Arg Tyr Val Ala
 115 120 125
 Ile Cys Asn Pro Leu Arg Tyr Leu Ile Ile Met Asn Pro Gln Leu Cys
 130 135 140
 Leu Trp Leu Val Leu Ala Cys Trp Cys Gly Gly Phe Ile His Ser Ile

```

145          150          155          160
Met Gln Val Ile Leu Val Ile Gln Leu Pro Phe Cys Gly Pro Asn Glu
165          170          175
Leu Asp Asn Phe Tyr Cys Asp Val Pro Gln Val Ile Lys Leu Ala Cys
180          185          190
Met Asp Thr Tyr Val Val Glu Val Leu Met Ile Ala Asn Ser Gly Leu
195          200          205
Leu Ser Leu Val Cys Phe Leu Val Leu Leu Phe Ser Tyr Ala Val Ile
210          215          220
Leu Ile Thr Leu Arg Thr His Phe Gly Gln Gly Gln Asn Lys Phe Leu
225          230          235          240
Ser Thr Cys Ala Ser His Leu Thr Val Val Ser Leu Ile Phe Met Pro
245          250          255
Cys Ile Phe Ile Tyr Leu Arg Pro Phe Cys Ser Phe Ser Val Asp Lys
260          265          270
Ile Phe Ser Met Phe Tyr Thr Val Met Thr Pro Met Leu Ser Pro Leu
275          280          285
Ile Tyr Thr Leu Arg Asn Ala Asp Met Lys Thr Ala Met Lys Lys Leu
290          295          300
Arg Ile Lys Pro Cys Asp Ile
305          310

```

<210> 1340

<211> 318

<212> PRT

<213> Unknown (H38g257 protein)

<220>

<223> Synthetic construct

<400> 1340

```

Met Met Val Asp Pro Asn Gly Asn Glu Ser Ser Ala Thr Tyr Phe Ile
1      5      10      15
Leu Ile Gly Leu Pro Gly Leu Glu Glu Ala Gln Phe Trp Leu Ala Phe
20     25     30
Pro Leu Cys Ser Leu Tyr Leu Ile Ala Val Leu Gly Asn Leu Thr Ile
35     40     45
Ile Tyr Ile Val Arg Thr Glu His Ser Leu His Glu Pro Met Tyr Ile
50     55     60
Phe Leu Cys Met Leu Ser Gly Ile Asp Ile Leu Ile Ser Thr Ser Ser
65     70     75     80
Met Pro Lys Met Leu Ala Ile Phe Trp Phe Asn Ser Thr Thr Ile Gln
85     90     95
Phe Asp Ala Cys Leu Leu Gln Met Phe Ala Ile His Ser Leu Ser Gly
100    105    110
Met Glu Ser Thr Val Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala
115    120    125
Ile Cys His Pro Leu Arg His Ala Thr Val Leu Thr Leu Pro Arg Val
130    135    140
Thr Lys Ile Gly Val Ala Ala Val Val Arg Gly Ala Ala Leu Met Ala
145    150    155    160
Pro Leu Pro Val Phe Ile Lys Gln Leu Pro Phe Cys Arg Ser Asn Ile
165    170    175
Leu Ser His Ser Tyr Cys Leu His Gln Asp Val Met Lys Leu Ala Cys
180    185    190
Asp Asp Ile Arg Val Asn Val Val Tyr Gly Leu Ile Val Ile Ile Ser
195    200    205
Ala Ile Gly Leu Asp Ser Leu Leu Ile Ser Phe Ser Tyr Leu Leu Ile
210    215    220
Leu Lys Thr Val Leu Gly Leu Thr Arg Glu Ala Gln Ala Lys Ala Phe
225    230    235    240

```

Gly Thr Cys Val Ser His Val Cys Ala Val Phe Ile Phe Tyr Val Pro
 245 250 255
 Phe Ile Gly Leu Ser Met Val His Arg Phe Ser Lys Arg Arg Asp Ser
 260 265 270
 Pro Leu Pro Val Ile Leu Ala Asn Ile Tyr Leu Leu Val Pro Pro Val
 275 280 285
 Leu Asn Pro Ile Val Tyr Gly Val Lys Thr Lys Glu Ile Arg Gln Arg
 290 295 300
 Ile Leu Arg Leu Phe His Val Ala Thr His Ala Ser Glu Pro
 305 310 315

<210> 1341

<211> 320

<212> PRT

<213> Unknown (H38g258 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(320)

<223> Xaa = Any Amino Acid

<400> 1341

Met Ser Ser Arg Leu Met Asn Val Phe Ser Met Glu Thr Ile Asn Phe
 1 5 10 15
 Val Ser Cys Leu Ile Leu Met Gly Phe Pro Ser Ser Pro Glu Met Gln
 20 25 30
 Leu Leu Tyr Phe Gly Leu Phe Ser Val Ala Tyr Thr Leu Thr Pro Met
 35 40 45
 Gly Asn Ala Ala Ile Val Cys Ala Val Trp Xaa Asp Gln His Leu His
 50 55 60
 Thr Pro Met Tyr Thr Leu Leu Gly Asn Phe Ser Leu Leu Glu Ile Trp
 65 70 75 80
 Tyr Val Thr Ala Thr Lys Leu Leu Ala Asn Phe Leu Ser Thr Ser Lys
 85 90 95
 Ser Ile Ser Phe Met Ser Cys Phe Ala Gln Phe Tyr Phe Phe Ser Leu
 100 105 110
 Gly Tyr Asp Glu Gly Phe Phe Leu Cys Ile Thr Ala Phe Asp Arg Tyr
 115 120 125
 Leu Ala Ile Cys Arg Pro Leu Arg Tyr Pro Cys Ile Met Thr Lys Gln
 130 135 140
 Val Cys Thr Gly Leu Ile Ile Phe Ala Trp Ser Cys Val Phe Val Ile
 145 150 155 160
 Phe Leu Thr Leu Val Ile Leu Ile Ser Gln Leu Ser Tyr Cys Gly Pro
 165 170 175
 Asn Ile Ile Asn His Phe Ile Cys Asp Pro Val Pro Leu Lys Met Leu
 180 185 190
 Ser Cys Ser Glu Asp Ile Ile Ile Thr Gln Leu Ile Tyr Ser Thr Phe
 195 200 205
 Asn Ser Val Phe Ile Ile Gly Thr Phe Leu Phe Ile Leu Cys Ser Tyr
 210 215 220
 Ala Leu Val Ile Leu Ala Ile Ile Arg Met Pro Ser Glu Ala Gly Lys
 225 230 235 240
 Arg Lys Ala Phe Ser Thr Cys Ala Ser His Leu Ala Val Val Thr Leu
 245 250 255
 Phe Tyr Gly Ser Ile Met Val Met Tyr Val Ser Pro Gly Ser Ala His
 260 265 270
 Pro Ala Lys Asn Glu Lys Ile Ile Thr Leu Phe Phe Ser Val Ile Thr
 275 280 285
 Pro Leu Cys Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Glu Met Lys

290 295 300
 Asp Tyr Leu Arg Lys Ile Phe Arg Thr Gly Lys Asp Val Asn Lys Ile
 305 310 315 320

<210> 1342
 <211> 309
 <212> PRT
 <213> Unknown (H38g259 protein)

<220>
 <223> Synthetic construct

<400> 1342
 Met Leu Asn Thr Thr Ser Val Thr Glu Phe Leu Leu Leu Gly Val Thr
 1 5 10 15
 Asp Ile Gln Glu Leu Gln Pro Phe Leu Phe Val Val Phe Leu Thr Ile
 20 25 30
 Tyr Phe Ile Ser Val Ala Gly Asn Gly Ala Ile Leu Met Ile Val Ile
 35 40 45
 Ser Asp Pro Arg Leu His Ser Pro Met Tyr Phe Phe Leu Gly Asn Leu
 50 55 60
 Ser Cys Leu Asp Ile Cys Tyr Ser Ser Val Thr Leu Pro Lys Met Leu
 65 70 75 80
 Gln Asn Phe Leu Ser Ala His Lys Ala Ile Ser Phe Leu Gly Cys Ile
 85 90 95
 Ser Gln Leu His Phe Phe His Phe Leu Gly Ser Thr Glu Ala Met Leu
 100 105 110
 Leu Ala Val Met Ala Phe Asp Arg Phe Val Ala Ile Cys Lys Pro Leu
 115 120 125
 Arg Tyr Thr Val Ile Met Asn Pro Gln Leu Cys Thr Gln Met Ala Ile
 130 135 140
 Thr Ile Trp Met Ile Gly Phe Phe His Ala Leu Leu His Ser Leu Met
 145 150 155 160
 Thr Ser Arg Leu Asn Phe Cys Gly Ser Asn Arg Ile Tyr His Phe Phe
 165 170 175
 Cys Asp Val Lys Pro Leu Leu Lys Leu Ser Leu Ile Ser Gly Trp Leu
 180 185 190
 Ser Thr Val Thr Gly Thr Ile Ala Met Gly Pro Phe Phe Leu Thr Leu
 195 200 205
 Leu Ser Tyr Phe Tyr Ile Ile Thr His Leu Phe Phe Lys Thr His Ser
 210 215 220
 Phe Ser Met Leu Arg Lys Ala Leu Ser Thr Cys Ala Ser His Phe Met
 225 230 235 240
 Val Val Ile Leu Leu Tyr Ala Pro Val Leu Phe Thr Tyr Ile His His
 245 250 255
 Ala Ser Gly Thr Ser Met Asp Gln Asp Arg Ile Thr Ala Ile Met Tyr
 260 265 270
 Thr Val Val Thr Pro Val Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn
 275 280 285
 Lys Glu Val Lys Gly Ala Phe Asn Arg Ala Met Lys Arg Trp Leu Trp
 290 295 300
 Pro Lys Glu Ile Leu
 305

<210> 1343
 <211> 331
 <212> PRT
 <213> Unknown (H38g260 protein)

<220>
 <223> Synthetic construct

<221> VARIANT

<222> (1)...(331)

<223> Xaa = Any Amino Acid

<400> 1343

```

Met Glu Ser Glu Asn Arg Thr Val Ile Arg Glu Phe Ile Leu Leu Arg
 1           5           10           15
Leu Thr Gln Phe Arg Asp Ile Xaa Leu Leu Val Phe Val Leu Val Leu
           20           25           30
Ile Phe Tyr Phe Phe Ile Leu Pro Gly Asn Phe Leu Ile Ile Phe Thr
           35           40           45
Ile Arg Ser Asp Pro Gly Leu Thr Ala Pro Leu Tyr Leu Phe Leu Gly
           50           55           60
Asn Leu Ala Phe Leu Asp Ala Ser Tyr Ser Phe Ile Val Ala Pro Arg
65           70           75           80
Met Leu Val Asp Phe Leu Ser Glu Lys Lys Val Ile Ser Tyr Arg Gly
           85           90           95
Cys Ile Thr Gln Leu Phe Phe Leu His Phe Leu Gly Gly Gly Glu Gly
           100          105          110
Leu Leu Leu Val Val Met Ala Phe Asp Arg Tyr Ile Thr Ile Cys Leu
           115          120          125
Pro Leu Gln Tyr Ser Thr Val Met Asn Ser Arg Ala Cys Tyr Ala Met
           130          135          140
Met Leu Ala Leu Trp Leu Gly Gly Phe Val His Ser Ile Ile Gln Val
145          150          155          160
Val Leu Ile Ile Arg Leu Pro Phe Cys Gly Pro Asn Gln Leu Asp Asn
           165          170          175
Phe Phe Cys Asp Val Arg Gln Val Ile Lys Leu Ala Cys Thr Asp Met
           180          185          190
Phe Val Val Glu Leu Leu Met Val Phe Asn Ser Gly Leu Met Thr Leu
           195          200          205
Met Cys Phe Leu Gly Leu Leu Ala Ser Tyr Ala Val Ile Leu Cys Arg
           210          215          220
Ile Arg Ala Ser Ser Ser Glu Ala Lys Asn Lys Ala Met Ser Thr Cys
225          230          235          240
Thr Thr His Ile Ile Val Ile Phe Phe Met Phe Gly Pro Gly Ile Phe
           245          250          255
Ile Tyr Thr Cys Pro Phe Arg Ala Phe Pro Ala Asp Lys Val Val Ser
           260          265          270
Leu Phe His Thr Val Ile Leu Pro Leu Leu Asn Pro Val Ile Tyr Thr
           275          280          285
Leu His Asn Gln Glu Val Lys Ala Ser Met Lys Lys Val Phe Asn Lys
           290          295          300
His Ile Ala Xaa Lys Arg Ala Lys Lys Lys Arg Arg Lys Ile Asp Cys
305          310          315          320
Lys Phe Tyr Leu Lys Leu Ile Cys Leu Phe Pro
           325          330

```

<210> 1344

<211> 315

<212> PRT

<213> Unknown (H38g261 protein)

<220>

<223> Synthetic construct

<400> 1344

```

Met Glu Ile Val Ser Thr Gly Asn Glu Thr Ile Thr Glu Phe Val Leu
 1           5           10           15
Leu Gly Phe Tyr Asp Ile Pro Glu Leu His Phe Leu Phe Phe Ile Val

```

```
<210> 1345
<211> 312
<212> PRT
<213> Unknown (H38g262 protein)
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<220>
<223> Synthetic construct.

Met 1	Ser	Ala	Asn	Thr 5	Ser	Met	Val	Thr	Glu 10	Phe	Leu	Leu	Leu	Gly 15	Phe
Ser	His	Leu	Ala 20	Asp	Leu	Gln	Gly	Leu 25	Leu	Phe	Ser	Val	Phe	Leu 30	Thr
Ile	Tyr	Leu 35	Leu	Thr	Val	Ala	Gly 40	Asn	Phe	Leu	Ile	Val 45	Val	Leu	Val
Ser	Thr 50	Asp	Ala	Ala	Leu	Gln 55	Ser	Pro	Met	Tyr	Phe 60	Phe	Leu	Arg	Thr
Leu 65	Ser	Ala	Leu	Glu 70	Ile	Gly	Tyr	Thr	Ser	Val 75	Thr	Val	Pro	Leu 80	Leu
Leu	His	His	Leu 85	Leu	Thr	Gly	Arg	Arg	His 90	Ile	Ser	Arg	Ser	Gly 95	Cys
Ala	Leu	Gln	Met 100	Phe	Phe	Phe	Leu	Phe 105	Phe	Gly	Ala	Thr	Glu 110	Cys	Cys

Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Ala Ala Ile Cys Glu Pro
 115 120 125
 Leu Arg Tyr Pro Leu Leu Leu Ser His Arg Val Cys Leu Gln Leu Ala
 130 135 140
 Gly Ser Ala Trp Ala Cys Gly Val Leu Val Gly Leu Gly His Thr Pro
 145 150 155 160
 Phe Ile Phe Ser Leu Pro Phe Cys Gly Pro Asn Thr Ile Pro Gln Phe
 165 170 175
 Phe Cys Glu Ile Gln Pro Val Leu Gln Leu Val Cys Gly Asp Thr Ser
 180 185 190
 Leu Asn Glu Leu Gln Ile Ile Leu Ala Thr Ala Leu Leu Ile Leu Cys
 195 200 205
 Pro Phe Gly Leu Ile Leu Gly Ser Tyr Gly Arg Ile Leu Val Thr Ile
 210 215 220
 Phe Arg Ile Pro Ser Val Ala Gly Arg Arg Lys Ala Phe Ser Thr Cys
 225 230 235 240
 Ser Ser His Leu Ile Val Val Ser Leu Phe Tyr Gly Thr Ala Leu Phe
 245 250 255
 Ile Tyr Ile Arg Pro Lys Ala Ser Tyr Asp Pro Ala Thr Asp Pro Leu
 260 265 270
 Val Ser Leu Phe Tyr Ala Val Val Thr Pro Ile Leu Asn Pro Ile Ile
 275 280 285
 Tyr Ser Leu Arg Asn Thr Glu Val Lys Ala Ala Leu Lys Arg Thr Ile
 290 295 300
 Gln Lys Thr Val Pro Met Glu Ile
 305 310

<210> 1346

<211> 316

<212> PRT

<213> Unknown (H38g263 protein)

<220>

<223> Synthetic construct

<400> 1346

Met Val Asn Gln Ser Ser Pro Met Gly Phe Leu Leu Leu Gly Phe Ser
 1 5 10 15
 Glu His Pro Ala Leu Glu Arg Thr Leu Phe Val Val Val Phe Thr Ser
 20 25 30
 Tyr Leu Leu Thr Leu Val Gly Asn Thr Leu Ile Ile Leu Leu Ser Val
 35 40 45
 Leu Tyr Pro Arg Leu His Ser Pro Met Tyr Phe Phe Leu Ser Asp Leu
 50 55 60
 Ser Phe Leu Asp Leu Cys Phe Thr Thr Ser Cys Val Pro Gln Met Leu
 65 70 75 80
 Val Asn Leu Trp Gly Pro Lys Lys Thr Ile Ser Phe Leu Gly Cys Ser
 85 90 95
 Val Gln Leu Phe Ile Phe Leu Ser Leu Gly Thr Thr Glu Cys Ile Leu
 100 105 110
 Leu Thr Val Met Ala Phe Asp Arg Tyr Val Ala Val Cys Gln Pro Leu
 115 120 125
 His Tyr Ala Thr Ile Ile His Pro Arg Leu Cys Trp Gln Leu Ala Ser
 130 135 140
 Val Ala Trp Val Met Ser Leu Val Gln Ser Ile Val Gln Thr Pro Ser
 145 150 155 160
 Thr Leu His Leu Pro Phe Cys Pro His Gln Gln Ile Asp Asp Phe Leu
 165 170 175
 Cys Glu Val Pro Ser Leu Ile Arg Leu Ser Cys Gly Asp Thr Ser Tyr
 180 185 190
 Asn Glu Ile Gln Leu Ala Val Ser Ser Val Ile Phe Val Val Val Pro

```

      195              200              205
Leu Ser Leu Ile Leu Ala Ser Tyr Gly Ala Thr Ala Gln Ala Val Leu
  210              215              220
Arg Ile Asn Ser Ala Thr Ala Trp Arg Lys Ala Phe Gly Thr Cys Ser
  225              230              235              240
Ser His Leu Thr Val Val Thr Leu Phe Tyr Ser Ser Val Ile Ala Val
      245              250              255
Tyr Leu Gln Pro Lys Asn Pro Tyr Ala Gln Gly Arg Gly Lys Phe Phe
      260              265              270
Gly Leu Phe Tyr Ala Val Gly Thr Pro Ser Leu Asn Pro Leu Val Tyr
      275              280              285
Thr Leu Arg Asn Lys Glu Ile Lys Arg Ala Leu Arg Arg Leu Leu Gly
      290              295              300
Lys Glu Arg Asp Ser Arg Glu Ser Trp Arg Ala Ala
  305              310              315

```

<210> 1347

<211> 318

<212> PRT

<213> Unknown (H38g264 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(318)

<223> Xaa = Any Amino Acid

<400> 1347

```

Met Lys Ser Glu Leu Asn Arg Asn Tyr Ser Glu Val Thr Glu Phe Ile
  1          5          10          15
Leu Leu Gly Phe Arg Thr Ser Pro Glu Ala Gln Ile Leu Leu Phe Phe
      20          25          30
Leu Phe Leu Leu Ile Tyr Met Val Ile Val Leu Arg Asn Leu Ser Met
      35          40          45
Leu Val Val Ile Glu Ile Asp Ser Arg Leu His Thr Pro Val Tyr Phe
      50          55          60
Phe Leu Arg Asn Leu Ser Tyr Leu Asp Leu Arg Tyr Ser Thr Val Ile
      65          70          75          80
Ala Pro Lys Leu Thr Thr Leu Phe Ser Lys Glu Lys Lys Ile Ser Tyr
      85          90          95
Asn Gly Xaa Ala Thr Gln Leu Phe Phe Phe Ala Leu Phe Val Gly Thr
      100          105          110
Glu Gly Phe Phe Leu Asp Met Met Ala Tyr Asp Arg Phe Ser Ala Ile
      115          120          125
Cys Ser Pro Phe Phe Tyr Thr Val Cys Met Ser Gln Gln Ala Cys Val
      130          135          140
Cys Leu Val Val Gly Ser Ser Ile Cys Gly Cys Ile Asn Ser Met Ile
      145          150          155          160
Gln Thr Gly Phe Thr Phe Ser Leu His Phe Cys Gly Glu Asn Arg Leu
      165          170          175
Glu His Phe Phe Cys Asp Val Ser Val Met Ile Lys Ile Ser Cys Ile
      180          185          190
Asp Ile Leu Val Asn Glu Val Val Leu Phe Ile Leu Ser Ala Leu Ile
      195          200          205
Thr Thr Thr Thr Thr Val Ile Leu Ala Ser Tyr Val His Ile Leu Ser
      210          215          220
Thr Val Leu Lys Ile Leu Ser Thr His Gly Arg Arg Lys Thr Phe Ser
      225          230          235          240
Thr Cys Ser Ser His Ile Thr Val Val Ser Leu Phe Tyr Gly Thr Val
      245          250          255

```

Phe Phe Met Tyr Ala Gln Pro Gly Ala Ile Pro Lys Ser Lys Val Ile
 260 265 270
 Val Val Phe Xaa Thr Leu Val Ile Pro Met Leu Asn Thr Leu Ile Tyr
 275 280 285
 Ser Leu Arg Asn Lys Val Gln Asn Ala Leu Lys Arg Tyr Ile Asp Lys
 290 295 300
 Lys Asn Ile Phe His Trp Pro Leu Ala Ile Tyr Lys Thr Ile
 305 310 315

<210> 1348

<211> 177

<212> PRT

<213> Unknown (H38g265 protein)

<220>

<223> Synthetic construct

<400> 1348

Met Ser Pro Arg Met Cys Leu Ser Phe Leu Ala Val Ala Trp Thr Leu
 1 5 10 15
 Gly Val Ser His Ser Leu Phe Gln Leu Ala Phe Leu Val Asn Leu Pro
 20 25 30
 Phe Cys Gly Pro Asn Val Leu Asp Ser Phe Tyr Cys Asp Leu Pro Arg
 35 40 45
 Leu Leu Arg Leu Ala Cys Thr Asp Thr Tyr Arg Leu Gln Phe Met Val
 50 55 60
 Thr Val Asn Ser Gly Phe Ile Cys Val Gly Thr Phe Phe Ile Leu Leu
 65 70 75 80
 Ile Ser Tyr Ile Phe Ile Leu Phe Thr Val Trp Lys His Ser Ser Gly
 85 90 95
 Gly Ser Ser Lys Ala Leu Ser Thr Leu Ser Ala His Ser Thr Ala Val
 100 105 110
 Leu Leu Phe Phe Gly Pro Pro Met Phe Val Tyr Thr Trp Pro His Pro
 115 120 125
 Asn Ser Gln Met Asp Lys Phe Leu Ala Ile Phe Asp Ala Val Leu Thr
 130 135 140
 Pro Phe Leu Asn Pro Val Val Tyr Thr Phe Arg Asn Lys Glu Met Lys
 145 150 155 160
 Ala Ala Ile Lys Arg Val Cys Lys Gln Leu Val Ile Tyr Lys Lys Ile
 165 170 175
 Ser

<210> 1349

<211> 322

<212> PRT

<213> Unknown (H38g266 protein)

<220>

<223> Synthetic construct

<400> 1349

Met Glu Ala Glu Asn Leu Thr Glu Leu Ser Lys Phe Leu Leu Leu Gly
 1 5 10 15
 Leu Ser Met Ile Leu Asn Cys Ser Pro Phe Leu Phe Gly Leu Phe Leu
 20 25 30
 Ser Met Tyr Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu Ala
 35 40 45
 Val Ser Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ser
 50 55 60
 Asn Leu Ser Phe Val Asp Ile Cys Phe Ile Ser Thr Thr Val Pro Lys

```

65          70          75          80
Met Leu Val Ser Ile Gln Ala Arg Ser Lys Asp Ile Ser Tyr Met Gly
      85          90          95
Cys Leu Thr Gln Val Tyr Phe Leu Met Met Phe Ala Gly Met Asp Thr
      100         105         110
Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His
      115         120         125
Pro Leu His Tyr Thr Val Ile Met Asn Pro Cys Leu Cys Gly Leu Leu
      130         135         140
Val Leu Ala Ser Trp Phe Ile Ile Phe Trp Phe Ser Leu Val His Ile
145         150         155         160
Leu Leu Met Lys Arg Leu Thr Phe Ser Thr Gly Thr Glu Ile Pro His
      165         170         175
Phe Phe Cys Glu Pro Ala Gln Val Leu Lys Val Ala Cys Ser Asn Thr
      180         185         190
Leu Leu Asn Asn Ile Val Leu Tyr Val Ala Thr Ala Leu Leu Gly Val
      195         200         205
Phe Pro Val Ala Gly Ile Leu Phe Ser Tyr Ser Gln Ile Val Ser Ser
      210         215         220
Leu Met Gly Met Ser Ser Thr Lys Gly Lys Tyr Lys Ala Phe Ser Thr
225         230         235         240
Cys Gly Ser His Leu Cys Val Val Ser Leu Phe Tyr Gly Thr Gly Leu
      245         250         255
Gly Val Tyr Leu Ser Ser Ala Val Thr His Ser Ser Gln Ser Ser Ser
      260         265         270
Thr Ala Ser Val Met Tyr Ala Met Val Thr Pro Met Leu Asn Pro Phe
      275         280         285
Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Gly Ala Leu Glu Arg Leu
      290         295         300
Leu Ser Arg Ala Asp Ser Cys Pro Leu Thr Asn Gln Gly Leu Arg Thr
305         310         315         320
Lys Arg

```

<210> 1350

<211> 322

<212> PRT

<213> Unknown (H38g267 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(322)

<223> Xaa = Any Amino Acid

<400> 1350

```

Tyr Thr Glu Pro Glu Asn Leu Thr Gly Val Leu Glu Phe Leu Leu Leu
1      5      10      15
Gly Leu Pro Asp Asp Pro Glu Leu Gln Pro Val Leu Phe Gly Leu Phe
      20      25      30
Leu Ser Met Tyr Leu Val Met Val Leu Gly Asn Leu Leu Ile Ile Leu
      35      40      45
Ala Val Ser Ser Asp Ser His Leu His Ser Pro Met Tyr Phe Phe Leu
      50      55      60
Ser Asn Leu Ser Leu Ala Asp Ile Gly Phe Ala Ser Thr Thr Val Pro
65      70      75      80
Lys Met Ile Val Asp Ile Gln Ala His Ser Arg Leu Ile Ser Tyr Val
      85      90      95
Gly Cys Leu Thr Gln Met Ser Phe Leu Ile Phe Phe Ala Cys Met Glu
      100     105     110

```

Ser Leu Leu Leu Ile Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys
 115 120 125
 His Pro Leu His Tyr Gln Val Ile Met Ser Pro Arg Leu Cys Gly Phe
 130 135 140
 Leu Val Leu Val Ser Phe Leu Ser Leu Leu Asp Ser Gln Leu His
 145 150 155 160
 Asn Leu Ile Val Leu Gln Leu Thr Cys Phe Asn Asp Val Glu Ile Ser
 165 170 175
 Asn Phe Phe Cys Asp Pro Ser Xaa Leu Leu Lys Leu Ala Cys Ser Asp
 180 185 190
 Thr Ser Ile Asn Asn Met Val Val Tyr Phe Ile Gly Ala Ile Phe Gly
 195 200 205
 Phe Leu Pro Leu Leu Gly Ile Leu Phe Ser Tyr Tyr Lys Ile Val Ser
 210 215 220
 Ser Ile Leu Arg Val Leu Ser Ser Gly Gly Lys Tyr Lys Ala Phe Ser
 225 230 235 240
 Thr Cys Ser Ser His Leu Ser Val Val Cys Leu Leu Tyr Gly Thr Ala
 245 250 255
 Leu Gly Gly Tyr Leu Ser Ser Ala Val Ser Leu Ser Ser Arg Lys Gly
 260 265 270
 Ala Val Ala Ser Val Met Tyr Met Val Val Thr Pro Met Leu Asn Pro
 275 280 285
 Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu Gln Arg
 290 295 300
 Leu His Gly Arg Ile Met Xaa Ser Pro Tyr Leu Leu His Leu Phe Cys
 305 310 315 320
 Ser Ile

<210> 1351

<211> 308

<212> PRT

<213> Unknown (H38g268 protein)

<220>

<223> Synthetic construct

<400> 1351

Met Arg Gln Ile Asn Gln Thr Gln Val Thr Glu Phe Leu Leu Leu Gly
 1 5 10 15
 Leu Ser Asp Gly Pro His Thr Glu Gln Leu Leu Phe Ile Val Leu Leu
 20 25 30
 Gly Val Tyr Leu Val Thr Val Leu Gly Asn Leu Leu Leu Ile Ser Leu
 35 40 45
 Val His Val Asp Ser Gln Leu His Thr Pro Met Tyr Phe Phe Leu Cys
 50 55 60
 Asn Leu Ser Leu Ala Asp Leu Cys Phe Ser Thr Asn Ile Val Pro Gln
 65 70 75 80
 Ala Leu Val His Leu Leu Ser Arg Lys Lys Val Ile Ala Phe Thr Leu
 85 90 95
 Cys Ala Ala Arg Leu Leu Phe Phe Leu Ile Phe Gly Cys Thr Gln Cys
 100 105 110
 Ala Leu Leu Ala Val Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys Asn
 115 120 125
 Pro Leu Arg Tyr Pro Asp Ile Met Thr Trp Lys Val Cys Val Gln Leu
 130 135 140
 Ala Thr Gly Ser Trp Thr Ser Gly Ile Leu Val Ser Val Val Asp Thr
 145 150 155 160
 Thr Phe Thr Leu Arg Leu Pro Tyr Arg Gly Ser Asn Ser Ile Ala His
 165 170 175
 Phe Phe Cys Glu Ala Pro Ala Leu Leu Ile Leu Ala Ser Thr Asp Thr

```
<210> 1352
<211> 321
<212> PRT
<213> Unknown (H38g269 protein)
```

<400> 1352

660

Pro Glu Ser Lys Lys Leu Leu Ser Leu Ser Tyr Thr Val Val Thr Pro
 275 280 285
 Met Leu Asn Pro Ile Ile Tyr Ser Leu Arg Asn Ser Glu Val Lys Asn
 290 295 300
 Ala Leu Ser Arg Thr Phe His Lys Val Leu Ala Leu Arg Asn Cys Ile
 305 310 315 320
 Pro

<210> 1353

<211> 260

<212> PRT

<213> Unknown (H38g270 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(260)

<223> Xaa = Any Amino Acid

<400> 1353

Ala His Leu Ser Phe Leu Asp Leu Ser Phe Thr Thr Ser Ser Ile Pro
 1 5 10 15
 Gln Leu Leu Tyr Asn Leu Asn Gly Cys Asp Lys Thr Ile Ser Tyr Met
 20 25 30
 Gly Cys Ala Ile Gln Leu Phe Leu Phe Leu Gly Leu Gly Gly Val Glu
 35 40 45
 Cys Leu Leu Leu Ala Val Met Ala Tyr Asp Arg Cys Val Ala Ile Cys
 50 55 60
 Lys Pro Leu His Tyr Met Val Ile Met Asn Pro Arg Leu Cys Arg Gly
 65 70 75 80
 Leu Val Ser Val Thr Trp Ser Cys Trp Gly Gly Gln Leu Leu Gly His
 85 90 95
 Val Ser Trp Thr Leu Arg Leu Pro Arg Cys Gly His His Glu Val Asp
 100 105 110
 His Phe Leu Arg Glu Met Pro Ala Leu Ile Arg Met Ala Cys Val Ser
 115 120 125
 Thr Val Ala Ile Glu Gly Thr Val Phe Val Leu Ala Val Gly Val Val
 130 135 140
 Leu Ser Pro Leu Val Phe Ile Leu Leu Ser Tyr Ser Tyr Ile Val Arg
 145 150 155 160
 Ala Val Leu Gln Ile Arg Ser Ala Ser Gly Arg Gln Lys Ala Phe Gly
 165 170 175
 Thr Cys Gly Ser His Leu Thr Val Val Ser Leu Phe Tyr Gly Asn Ile
 180 185 190
 Ile Tyr Met Tyr Met Gln Pro Gly Ala Ser Ser Ser Gln Asp Gln Gly
 195 200 205
 Met Phe Leu Met Leu Phe Tyr Asn Ile Val Thr Pro Leu Leu Asn Pro
 210 215 220
 Leu Ile Tyr Thr Leu Arg Asn Arg Glu Val Lys Gly Ala Leu Gly Arg
 225 230 235 240
 Leu Leu Leu Gly Lys Arg Glu Leu Gly Lys Glu Xaa Arg His Leu His
 245 250 255
 Leu Thr Ser Leu
 260

<210> 1354

<211> 329

<212> PRT

<213> Unknown (H38g271 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(329)

<223> Xaa = Any Amino Acid

<400> 1354

Glu	Glu	Ile	Leu	Xaa	Ile	Ile	Ser	Gln	His	Val	His	Thr	Gly	Cys	Val
1				5					10					15	
Gln	Asn	Xaa	Glu	Leu	Gln	Pro	Ile	Leu	Phe	Gly	Leu	Phe	Leu	Ser	Met
		20						25					30		
Cys	Leu	Val	Met	Val	Leu	Gly	Asn	Leu	Leu	Ile	Ile	Leu	Ala	Val	Ser
		35					40					45			
Ser	Asp	Ser	His	Leu	His	Thr	Pro	Thr	Tyr	Phe	Phe	Leu	Ser	Asn	Leu
	50					55					60				
Ser	Leu	Ala	Asp	Ile	Gly	Phe	Pro	Ser	Thr	Thr	Val	Pro	Lys	Met	Ile
65				70						75					80
Val	Asp	Ile	Gln	Ser	His	Ser	Arg	Val	Ile	Ser	Tyr	Ala	Gly	Cys	Leu
			85					90					95		
Thr	Gln	Ile	Ser	Leu	Phe	Ala	Val	Phe	Gly	Cys	Met	Glu	Asp	Met	Leu
		100						105					110		
Leu	Ser	Val	Met	Ala	Tyr	Asp	Arg	Phe	Val	Ala	Ile	Cys	His	Pro	Leu
		115				120						125			
Asp	Tyr	Pro	Val	Ile	Met	Asn	Pro	Cys	Phe	Cys	Gly	Phe	Leu	Val	Leu
	130					135					140				
Leu	Ser	Phe	Phe	Leu	Ser	Leu	Leu	Asp	Phe	Gln	Leu	His	Asn	Trp	Ile
145				150						155					160
Ala	Leu	Gln	Ile	Thr	Cys	Phe	Lys	Asp	Val	Glu	Ile	Pro	Ser	Phe	Phe
			165					170					175		
Cys	Asp	Pro	Ser	Gln	Leu	Pro	His	Leu	Ala	Cys	Cys	Asp	Thr	Phe	Thr
		180					185					190			
Asn	Asn	Ile	Val	Met	Tyr	Phe	Leu	Ala	Ala	Ile	Leu	Gly	Phe	Leu	Pro
		195					200					205			
Ile	Ser	Gly	Ile	Phe	Tyr	Ser	Tyr	Tyr	Lys	Ile	Val	Ser	Ser	Ile	Leu
	210					215					220				
Lys	Val	Ser	Ser	Ser	Gly	Lys	Tyr	Lys	Ala	Phe	Ser	Thr	Cys	Gly	
225				230					235					240	
Ser	His	Leu	Ser	Val	Val	Cys	Leu	Phe	Tyr	Gly	Thr	Ala	Leu	Gly	Gly
			245					250					255		
Tyr	Leu	Ser	Ser	Asp	Met	Ser	Ser	Tyr	Pro	Arg	Lys	Gly	Ala	Val	Ala
		260					265					270			
Ser	Val	Met	Tyr	Thr	Val	Val	Ala	Pro	Met	Leu	Asn	Pro	Phe	Ile	Tyr
		275					280					285			
Ser	Leu	Arg	Lys	Arg	Asp	Ile	Lys	Ser	Ala	Leu	Gln	Gln	Leu	His	Gly
	290					295					300				
Arg	Ile	Val	Xaa	Ser	His	Asp	Leu	Ile	Ile	Gly	Ser	Ile	Leu	Xaa	Pro
305					310					315					320
Trp	Val	Gly	Lys	Gly	Ser	Lys	Val	Lys							
				325											

<210> 1355

<211> 321

<212> PRT

<213> Unknown (H38g272 protein)

<220>

<223> Synthetic construct

<400> 1355

```

Met Glu Ser Pro Asn His Thr Asp Val Asp Pro Ser Val Phe Phe Leu
 1      5      10      15
Leu Gly Ile Pro Gly Leu Glu Gln Phe His Leu Trp Leu Ser Leu Pro
 20      25      30
Val Cys Gly Leu Gly Thr Ala Thr Ile Val Gly Asn Ile Thr Ile Leu
 35      40      45
Val Val Val Ala Thr Glu Pro Val Leu His Lys Pro Val Tyr Leu Phe
 50      55      60
Leu Cys Met Leu Ser Thr Ile Asp Leu Ala Ala Ser Val Ser Thr Val
 65      70      75      80
Pro Lys Leu Leu Ala Ile Phe Trp Cys Gly Ala Gly His Ile Ser Ala
 85      90      95
Ser Ala Cys Leu Ala Gln Met Phe Phe Ile His Ala Phe Cys Met Met
 100     105     110
Glu Ser Thr Val Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile
 115     120     125
Cys His Pro Leu Arg Tyr Ala Thr Ile Leu Thr Asp Thr Ile Ile Ala
 130     135     140
His Ile Gly Val Ala Ala Val Val Arg Gly Ser Leu Leu Met Leu Pro
 145     150     155     160
Cys Pro Phe Leu Ile Gly Arg Leu Asn Phe Cys Gln Ser His Val Ile
 165     170     175
Leu His Thr Tyr Cys Glu His Met Ala Val Val Lys Leu Ala Cys Gly
 180     185     190
Asp Thr Arg Pro Asn Arg Val Tyr Gly Leu Thr Ala Ala Leu Leu Val
 195     200     205
Ile Gly Val Asp Leu Phe Cys Ile Gly Leu Ser Tyr Ala Leu Ser Ala
 210     215     220
Gln Ala Val Leu Arg Leu Ser Ser His Glu Ala Arg Ser Lys Ala Leu
 225     230     235     240
Gly Thr Cys Gly Ser His Val Cys Val Ile Leu Ile Ser Tyr Thr Pro
 245     250     255
Ala Leu Phe Ser Phe Phe Thr His Arg Phe Gly His His Val Pro Val
 260     265     270
His Ile His Ile Leu Leu Ala Asn Val Tyr Leu Leu Leu Pro Pro Ala
 275     280     285
Leu Asn Pro Val Val Tyr Gly Val Lys Thr Lys Gln Ile Arg Lys Arg
 290     295     300
Val Val Arg Val Phe Gln Ser Gly Gln Gly Met Gly Ile Lys Ala Ser
 305     310     315     320
Glu

```

<210> 1356

<211> 327

<212> PRT

<213> Unknown (H38g273 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(327)

<223> Xaa = Any Amino Acid

<400> 1356

```

Met Thr Trp Ser Gly Gly Thr Ile Val Gly Glu Xaa Gly Glu Phe Val
 1      5      10      15
Leu Leu Gly Phe Pro Ala Pro Ala Pro Leu Gln Val Leu Phe Ala
 20      25      30
Leu Leu Leu Leu Ala Tyr Val Leu Val Leu Thr Glu Asn Thr Leu Ile

```

```

      35      40      45
Ile Met Ala Ile Arg Asn His Ser Thr Leu His Lys Pro Met Tyr Phe
  50      55      60
Phe Leu Ala Asn Met Ser Phe Leu Glu Ile Trp Tyr Val Thr Val Thr
  65      70      75      80
Ile Pro Lys Met Leu Ala Gly Phe Val Gly Ser Lys Gln Asp His Gly
      85      90      95
Gln Leu Ile Ser Phe Glu Gly Cys Met Thr Gln Leu Tyr Phe Phe Leu
      100      105      110
Gly Leu Gly Cys Thr Glu Cys Val Leu Leu Ala Val Met Ala Tyr Asp
      115      120      125
Arg Tyr Met Ala Ile Cys Tyr Pro Leu His Tyr Pro Val Ile Val Ser
      130      135      140
Gly Arg Leu Cys Val Gln Met Ala Ala Gly Ser Trp Ala Gly Gly Phe
      145      150      155      160
Gly Ile Ser Met Val Lys Val Phe Leu Ile Ser Gly Leu Ser Tyr Cys
      165      170      175
Gly Pro Asn Ile Ile Asn His Phe Phe Cys Asp Val Ser Pro Leu Leu
      180      185      190
Asn Leu Ser Cys Thr Asp Met Ser Thr Ala Glu Leu Thr Asp Phe Ile
      195      200      205
Leu Ala Ile Phe Ile Leu Leu Gly Pro Leu Ser Val Thr Gly Ala Ser
      210      215      220
Tyr Val Ala Ile Thr Gly Ala Val Met His Ile Pro Ser Ala Ala Gly
      225      230      235      240
Arg Tyr Lys Ala Phe Ser Thr Cys Ala Ser His Leu Thr Val Val Ile
      245      250      255
Ile Phe Tyr Ala Ala Ser Ile Phe Ile Tyr Ala Arg Pro Lys Ala Leu
      260      265      270
Ser Ala Phe Asp Thr Asn Lys Leu Val Ser Val Leu Tyr Ala Val Ile
      275      280      285
Val Pro Leu Leu Asn Pro Ile Ile Tyr Cys Leu Arg Asn Gln Glu Val
      290      295      300
Lys Arg Ala Leu Cys Cys Thr Leu His Leu Tyr Gln His Gln Asp Pro
      305      310      315      320
Asp Pro Lys Lys Ala Ser Arg
      325

```

<210> 1357

<211> 312

<212> PRT

<213> Unknown (H38g274 protein)

<220>

<223> Synthetic construct

<400> 1357

```

Met Glu Ala Gly Asn Gln Thr Gly Phe Leu Glu Phe Ile Leu Leu Gly
  1      5      10      15
Leu Ser Glu Asp Pro Glu Leu Gln Pro Phe Ile Phe Gly Leu Phe Leu
      20      25      30
Ser Met Tyr Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu Ala
      35      40      45
Ile Ser Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ser
      50      55      60
Asn Leu Ser Trp Val Asp Ile Cys Phe Ser Thr Cys Ile Val Pro Lys
      65      70      75      80
Met Leu Val Asn Ile Gln Thr Glu Asn Lys Ala Ile Ser Tyr Met Asp
      85      90      95
Cys Leu Thr Gln Val Tyr Phe Ser Met Phe Phe Pro Ile Leu Asp Thr
      100      105      110

```

Leu Leu Leu Thr Val Met Ala Tyr Asp Arg Phe Val Ala Val Cys His
 115 120 125
 Pro Leu His Tyr Met Ile Ile Met Asn Pro His Leu Cys Gly Leu Leu
 130 135 140
 Val Phe Val Thr Trp Leu Ile Gly Val Met Thr Ser Leu Leu His Ile
 145 150 155 160
 Ser Leu Met Met His Leu Ile Phe Cys Lys Asp Phe Glu Ile Pro His
 165 170 175
 Phe Phe Cys Glu Leu Thr Tyr Ile Leu Gln Leu Ala Cys Ser Asp Thr
 180 185 190
 Phe Leu Asn Ser Thr Leu Ile Tyr Phe Met Thr Gly Val Leu Gly Val
 195 200 205
 Phe Pro Leu Leu Gly Ile Ile Phe Ser Tyr Ser Arg Ile Ala Ser Ser
 210 215 220
 Ile Arg Lys Met Ser Ser Ser Gly Gly Lys Gln Lys Ala Leu Ser Thr
 225 230 235 240
 Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Gly Ile
 245 250 255
 Gly Val His Phe Thr Ser Ala Val Thr His Ser Ser Gln Lys Ile Ser
 260 265 270
 Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Gly Ala Leu Gly Ser Leu
 290 295 300
 Leu Ser Arg Ala Ala Ser Cys Leu
 305 310

<210> 1358

<211> 320

<212> PRT

<213> Unknown (H38g275 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(320)

<223> Xaa = Any Amino Acid

<400> 1358

Met Thr Ala Cys Asn Ala Ser Gln Gly His Pro Ser Phe Phe Ile Leu
 1 5 10 15
 Gln Gly Ile Pro Gly Met Glu Asp Lys His Arg Trp Ile Ser Ile Pro
 20 25 30
 Phe Ser Ser Met Tyr Phe Ile Met Val Leu Gly Asn Cys Thr Ile Leu
 35 40 45
 Leu Thr Ile Ser Thr Glu Arg Ser Leu His Lys Pro Met Phe Leu Leu
 50 55 60
 Leu Cys Leu Leu Ala Leu Thr Asp Leu Gly Met Ser Thr Thr Thr Ile
 65 70 75 80
 Pro Lys Val Leu Cys Ile Phe Trp Phe Gly Gln Ser Glu Ile Ser Tyr
 85 90 95
 Glu Gly Cys Leu Val Gln Leu Phe Phe Ile His Ser Ile Ser Ala Met
 100 105 110
 Gln Ser Ala Val Leu Met Thr Met Ala Phe Asp His Tyr Val Ala Ile
 115 120 125
 Cys Lys Pro Leu Arg Tyr Ala Thr Ile Leu Ser Asn Ser Cys Thr Gly
 130 135 140
 Leu Ile Gly Leu Val Ser Leu Val Arg Ala Ile Leu Phe Ile Leu Pro
 145 150 155 160
 Met Pro Ile Leu Leu Gln Gln Met Pro Tyr His Ala Asn Arg Val Ile

Pro	Thr	Thr	Ser	165	Cys	Glu	His	Met	170	Ala	Val	Val	Lys	Met	175	Val	Cys	Val
Asp	Thr	Thr	Val	180	Asn	Arg	Ile	Tyr	185	Gly	Leu	Val	Val	Ala	190	Leu	Leu	Val
Ala	Gly	Tyr	Asp	195	Leu	Ser	Ala	Ile	200	Ala	Ser	Ser	Tyr	205	Val	Leu	Ile	Ile
Gln	Ala	Ile	Met	210	His	Leu	Ser	Ser	215	Lys	Glu	Ala	His	His	220	Lys	Ala	Val
Asn	Thr	Cys	Thr	225	Thr	His	Ile	Cys	230	Val	Met	Leu	Ile	Ser	235	Tyr	Thr	Pro
Ser	Leu	Phe	Ser	245	Phe	Leu	Ala	His	250	Arg	Phe	Gly	Gln	Gly	255	Ile	Pro	Pro
His	Val	His	Ile	260	Ile	Leu	Gly	Asn	265	Leu	Tyr	Phe	Leu	Val	270	Pro	Pro	Met
Leu	Ser	Pro	Ile	275	Ile	Tyr	Gly	Val	280	Lys	Thr	Lys	Glu	Phe	285	Trp	Asp	Lys
Val	Thr	Lys	Xaa	290	Val	Ala	Gly	Lys	295	Lys	Asn	Pro	Gln	Pro	300	Leu	Thr	Met
305				310								315						320

<210> 1359

<211> 316

<212> PRT

<213> Unknown (H38g276 protein)

<220>

<223> Synthetic construct

<400> 1359

Met	Glu	Leu	Trp	Asn	Phe	Thr	Leu	Gly	Ser	Gly	Phe	Ile	Leu	Val	Gly
1				5					10					15	
Ile	Leu	Asn	Asp	Ser	Gly	Ser	Pro	Glu	Leu	Leu	Cys	Ala	Thr	Ile	Thr
		20						25					30		
Ile	Leu	Tyr	Leu	Leu	Ala	Leu	Ile	Ser	Asn	Gly	Leu	Leu	Leu	Leu	Ala
		35					40					45			
Ile	Thr	Met	Glu	Ala	Arg	Leu	His	Met	Pro	Met	Tyr	Leu	Leu	Leu	Gly
	50				55					60					
Gln	Leu	Ser	Leu	Met	Asp	Leu	Leu	Phe	Thr	Ser	Val	Val	Thr	Pro	Lys
65				70					75					80	
Ala	Leu	Ala	Asp	Phe	Leu	Arg	Arg	Glu	Asn	Thr	Ile	Ser	Phe	Gly	Gly
			85					90						95	
Cys	Ala	Leu	Gln	Met	Phe	Leu	Ala	Leu	Thr	Met	Gly	Gly	Ala	Glu	Asp
		100					105						110		
Leu	Leu	Leu	Ala	Phe	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Cys	His
		115					120					125			
Pro	Leu	Thr	Tyr	Met	Thr	Leu	Met	Ser	Ser	Arg	Ala	Cys	Trp	Leu	Met
	130					135					140				
Val	Ala	Thr	Ser	Trp	Ile	Leu	Ala	Ser	Leu	Ser	Ala	Leu	Ile	Tyr	Thr
145					150					155				160	
Val	Tyr	Thr	Met	His	Tyr	Pro	Phe	Cys	Arg	Ala	Gln	Glu	Ile	Arg	His
			165						170					175	
Leu	Leu	Cys	Glu	Ile	Pro	His	Leu	Leu	Lys	Val	Ala	Cys	Ala	Asp	Thr
		180					185						190		
Ser	Arg	Tyr	Glu	Leu	Met	Val	Tyr	Val	Met	Gly	Val	Thr	Phe	Leu	Ile
		195					200					205			
Pro	Ser	Leu	Ala	Ala	Ile	Leu	Ala	Ser	Tyr	Thr	Gln	Ile	Leu	Leu	Thr
	210					215					220				
Val	Leu	His	Met	Pro	Ser	Asn	Glu	Gly	Arg	Lys	Lys	Ala	Leu	Val	Thr
225					230					235				240	
Cys	Ser	Ser	His	Leu	Thr	Val	Val	Gly	Met	Phe	Tyr	Gly	Ala	Ala	Thr
			245						250					255	

Phe Met Tyr Val Leu Pro Ser Ser Phe His Ser Thr Arg Gln Asp Asn
 260 265 270
 Ile Ile Ser Val Phe Tyr Thr Ile Val Thr Pro Ala Leu Asn Pro Leu
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Glu Val Met Arg Ala Leu Arg Arg Val
 290 295 300
 Leu Gly Lys Tyr Met Leu Pro Ala His Ser Thr Leu
 305 310 315

<210> 1360

<211> 312

<212> PRT

<213> Unknown (H38g277 protein)

<220>

<223> Synthetic construct

<400> 1360

Met Lys Ala Gly Asn Phe Ser Asp Thr Pro Glu Phe Phe Leu Leu Gly
 1 5 10 15
 Leu Ser Gly Asp Pro Glu Leu Gln Pro Ile Leu Phe Met Leu Phe Leu
 20 25 30
 Ser Met Tyr Leu Ala Thr Met Leu Gly Asn Leu Leu Ile Ile Leu Ala
 35 40 45
 Val Asn Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Leu Leu Ser
 50 55 60
 Ile Leu Ser Leu Val Asp Ile Cys Phe Thr Ser Thr Thr Met Pro Lys
 65 70 75 80
 Met Leu Val Asn Ile Gln Ala Gln Ala Gln Ser Ile Asn Tyr Thr Gly
 85 90 95
 Cys Leu Thr Gln Ile Cys Phe Val Leu Val Phe Val Gly Leu Glu Asn
 100 105 110
 Gly Ile Leu Val Met Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His
 115 120 125
 Pro Leu Arg Tyr Asn Val Ile Met Asn Pro Lys Leu Cys Gly Leu Leu
 130 135 140
 Leu Leu Leu Ser Phe Ile Val Ser Val Leu Asp Ala Leu Leu His Thr
 145 150 155 160
 Leu Met Val Leu Gln Leu Thr Phe Cys Ile Asp Leu Glu Ile Pro His
 165 170 175
 Phe Phe Cys Glu Leu Ala His Ile Leu Lys Leu Ala Cys Ser Asp Val
 180 185 190
 Leu Ile Asn Asn Ile Leu Val Tyr Leu Val Thr Ser Leu Leu Gly Val
 195 200 205
 Val Pro Leu Ser Gly Ile Ile Phe Ser Tyr Thr Arg Ile Val Ser Ser
 210 215 220
 Val Met Lys Ile Pro Ser Ala Gly Gly Lys Tyr Lys Ala Phe Ser Ile
 225 230 235 240
 Cys Gly Ser His Leu Ile Val Val Ser Leu Phe Tyr Gly Thr Gly Phe
 245 250 255
 Gly Val Tyr Leu Ser Ser Gly Ala Thr His Ser Ser Arg Lys Gly Ala
 260 265 270
 Ile Ala Ser Val Met Tyr Thr Val Thr Pro Met Leu Asn Pro Leu
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Asp Met Leu Lys Ala Leu Arg Lys Leu
 290 295 300
 Ile Ser Arg Ile Pro Ser Phe His
 305 310

<210> 1361

<211> 328

<212> PRT
 <213> Unknown (H38g278 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(328)
 <223> Xaa = Any Amino Acid

<400> 1361
 Lys Ile Ser Asn Ser Ser Lys Phe Gln Val Ser Glu Phe Ile Leu Leu
 1 5 10 15
 Gly Phe Pro Gly Ile His Ser Trp Gln His Trp Leu Ser Leu Pro Leu
 20 25 30
 Ala Leu Leu Tyr Leu Ser Ala Leu Ala Ala Asn Thr Leu Ile Leu Ile
 35 40 45
 Ile Ile Trp Gln Asn Pro Ser Leu Gln Gln Pro Met Tyr Ile Phe Leu
 50 55 60
 Gly Ile Leu Cys Met Val Asp Met Gly Leu Ala Thr Thr Ile Ile Pro
 65 70 75 80
 Lys Ile Leu Ala Ile Phe Trp Phe Asp Ala Lys Val Ile Ser Leu Pro
 85 90 95
 Glu Cys Phe Ala Gln Ile Tyr Ala Ile His Phe Phe Val Gly Met Glu
 100 105 110
 Ser Gly Ile Leu Leu Cys Met Ala Phe Asp Arg Tyr Val Ala Ile Cys
 115 120 125
 His Pro Leu Arg Tyr Pro Ser Ile Val Thr Ser Ser Leu Ile Leu Lys
 130 135 140
 Ala Thr Leu Phe Met Val Leu Arg Asn Gly Leu Phe Val Thr Pro Val
 145 150 155 160
 Pro Val Leu Ala Ala Gln Arg Asp Tyr Cys Ser Lys Asn Glu Ile Glu
 165 170 175
 His Cys Leu Cys Ser Asn Leu Gly Val Thr Ser Leu Ala Cys Asp Asp
 180 185 190
 Arg Arg Pro Asn Ser Ile Cys Gln Leu Val Leu Ala Trp Leu Gly Met
 195 200 205
 Gly Ser Asp Leu Ser Leu Ile Ile Leu Ser Tyr Ile Leu Ile Leu Tyr
 210 215 220
 Ser Val Leu Arg Leu Asn Ser Ala Glu Ala Ala Lys Ala Leu Ser
 225 230 235 240
 Thr Cys Ser Ser His Leu Thr Leu Ile Leu Phe Phe Tyr Thr Ile Val
 245 250 255
 Val Val Ile Ser Val Thr His Leu Thr Glu Met Lys Ala Thr Leu Ile
 260 265 270
 Pro Val Leu Leu Asn Val Leu His Asn Ile Ile Pro Pro Ser Leu Asn
 275 280 285
 Pro Thr Val Tyr Ala Leu Gln Thr Lys Glu Leu Arg Ala Ala Phe Gln
 290 295 300
 Lys Val Leu Phe Ala Leu Thr Lys Glu Ile Arg Ser Xaa Arg Pro Ser
 305 310 315 320
 Pro Xaa Cys Thr Xaa Thr Ser Ala
 325

<210> 1362
 <211> 316
 <212> PRT
 <213> Unknown (H38g279 protein)

<220>
 <223> Synthetic construct

<400> 1362

```

Met Glu Leu Arg Asn Ser Thr Leu Gly Ser Gly Phe Ile Leu Val Gly
 1           5           10           15
Ile Leu Asn Asp Ser Gly Ser Pro Glu Leu Leu Tyr Ala Thr Phe Thr
      20           25           30
Ile Leu Tyr Met Leu Ala Leu Thr Ser Asn Gly Leu Leu Leu Leu Ala
      35           40           45
Ile Thr Ile Glu Ala Arg Leu His Met Pro Met Tyr Leu Leu Leu Gly
      50           55           60
Gln Leu Ser Leu Met Asp Leu Leu Phe Thr Ser Val Val Thr Pro Lys
      65           70           75           80
Ala Leu Ala Asp Phe Leu Arg Arg Glu Asn Thr Ile Ser Phe Gly Gly
      85           90           95
Cys Ala Leu Gln Met Phe Leu Ala Leu Thr Met Gly Ser Ala Glu Asp
      100          105          110
Leu Leu Leu Ala Phe Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His
      115          120          125
Pro Leu Lys Tyr Met Thr Leu Met Ser Pro Arg Val Cys Trp Ile Met
      130          135          140
Val Ala Thr Ser Trp Ile Leu Ala Ser Leu Ile Ala Ile Gly His Thr
      145          150          155          160
Met Tyr Thr Met His Leu Pro Phe Cys Val Ser Trp Glu Ile Arg His
      165          170          175
Leu Leu Cys Glu Ile Pro Pro Leu Leu Lys Leu Ala Cys Ala Asp Thr
      180          185          190
Ser Arg Tyr Glu Leu Ile Ile Tyr Val Thr Gly Val Thr Phe Leu Leu
      195          200          205
Leu Pro Ile Ser Ala Ile Val Ala Ser Tyr Thr Leu Val Leu Phe Thr
      210          215          220
Val Leu Arg Met Pro Ser Asn Glu Gly Arg Lys Lys Ala Leu Val Thr
      225          230          235          240
Cys Ser Ser His Leu Ile Val Val Gly Met Phe Tyr Gly Ala Ala Thr
      245          250          255
Phe Met Tyr Val Leu Pro Ser Ser Phe His Ser Pro Lys Gln Asp Asn
      260          265          270
Ile Ile Ser Val Phe Tyr Thr Ile Val Thr Pro Ala Leu Asn Pro Leu
      275          280          285
Ile Tyr Ser Leu Arg Asn Lys Glu Val Met Arg Ala Leu Arg Arg Val
      290          295          300
Leu Gly Lys Tyr Ile Leu Leu Ala His Ser Thr Leu
      305          310          315

```

<210> 1363

<211> 299

<212> PRT

<213> Unknown (H38g280 protein)

<220>

<223> Synthetic construct

<400> 1363

```

Met Gly Phe Pro Gly Ile His Ser Trp Gln His Trp Leu Ser Leu Pro
 1           5           10           15
Leu Ala Leu Leu Tyr Leu Leu Ala Leu Ser Ala Asn Ile Leu Ile Leu
      20           25           30
Ile Ile Ile Asn Lys Glu Ala Ala Leu His Gln Pro Met Tyr Tyr Phe
      35           40           45
Leu Gly Ile Leu Ala Met Ala Asp Ile Gly Leu Ala Thr Thr Ile Met
      50           55           60
Pro Lys Ile Leu Ala Ile Leu Trp Phe Asn Ala Lys Thr Ile Ser Leu

```

```

65          70          75          80
Leu Glu Cys Phe Ala Gln Met Tyr Ala Ile His Cys Phe Val Ala Met
      85          90          95
Glu Ser Ser Thr Phe Val Cys Met Ala Ile Asp Arg Tyr Val Ala Ile
      100         105         110
Cys Arg Pro Leu Arg Tyr Pro Ser Ile Ile Thr Glu Ser Phe Val Phe
      115         120         125
Lys Ala Asn Gly Phe Met Ala Leu Arg Asn Ser Leu Cys Leu Ile Ser
      130         135         140
Val Pro Leu Leu Ala Ala Gln Arg His Tyr Cys Ser Gln Asn Gln Ile
      145         150         155
Glu His Cys Leu Cys Ser Asn Leu Gly Val Thr Ser Leu Ser Cys Asp
      165         170         175
Asp Arg Arg Ile Asn Ser Ile Asn Gln Val Leu Leu Ala Trp Thr Leu
      180         185         190
Met Gly Ser Asp Leu Gly Leu Ile Ile Leu Ser Tyr Ala Leu Ile Leu
      195         200         205
Tyr Ser Val Leu Lys Leu Asn Ser Pro Glu Ala Ala Ser Lys Ala Leu
      210         215         220
Ser Thr Cys Thr Ser His Leu Ile Leu Ile Leu Phe Phe Tyr Thr Val
      225         230         235
Ile Ile Val Ile Ser Ile Thr Arg Ser Thr Gly Met Arg Val Pro Leu
      245         250         255
Ile Pro Val Leu Leu Asn Val Leu His Asn Val Ile Pro Pro Ala Leu
      260         265         270
Asn Pro Met Val Tyr Ala Leu Lys Asn Lys Glu Leu Arg Gln Gly Leu
      275         280         285
Tyr Lys Val Leu Arg Leu Gly Val Lys Gly Thr
      290         295

```

<210> 1364

<211> 327

<212> PRT

<213> Unknown (H38g281 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(327)

<223> Xaa = Any Amino Acid

<400> 1364

```

Met Thr Trp Ser Gly Gly Thr Leu Val Gly Glu Xaa Gly Glu Phe Val
1          5          10          15
Leu Leu Gly Phe Pro Ala Pro Ala Pro Leu Gln Val Leu Ser Phe Ala
      20          25          30
Arg Xaa Ser Ala Ala Tyr Ala Leu Val Leu Thr Glu Asn Thr Leu Ile
      35          40          45
Ile Met Ala Ser Arg Asn His Ser Thr Leu His Lys Pro Met Tyr Phe
      50          55          60
Val Leu Ala Asn Met Ser Ser Leu Glu Ile Trp Tyr Val Thr Val Thr
      65          70          75          80
Ile Pro Lys Met Leu Ala Gly Phe Val Gly Ser Lys Gln Asp His Gly
      85          90          95
Gln Leu Ile Ser Phe Glu Gly Cys Met Thr Gln Leu Tyr Phe Phe Leu
      100         105         110
Gly Leu Gly Cys Thr Glu Cys Val Leu Leu Ala Val Met Ala Tyr Asp
      115         120         125
Arg Tyr Met Ala Ile Cys Tyr Pro Leu His Tyr Pro Val Ile Val Ser
      130         135         140

```

Gly Arg Leu Cys Val Gln Met Ala Ala Gly Ser Trp Ala Gly Gly Phe
 145 150 155 160
 Gly Ile Ser Met Val Lys Val Phe Leu Ile Ser Gly Leu Ser Tyr Cys
 165 170 175
 Gly Pro Asn Ile Ile Asn His Phe Phe Cys Asp Val Ser Pro Leu Leu
 180 185 190
 Asn Leu Ser Cys Thr Asp Met Ser Thr Ala Glu Leu Thr Asp Phe Ile
 195 200 205
 Leu Ala Ile Phe Ile Leu Leu Gly Pro Leu Ser Val Thr Gly Ala Ser
 210 215 220
 Tyr Val Ala Ile Thr Gly Ala Val Met His Thr Ser Ser Ala Ala Gly
 225 230 235 240
 Arg Tyr Lys Ala Phe Ser Thr Cys Ala Ser His Leu Thr Val Val Ile
 245 250 255
 Ile Phe Tyr Ala Ala Ser Ile Phe Ile Tyr Ala Arg Pro Lys Ala Leu
 260 265 270
 Ser Ala Phe Asp Thr Asn Lys Leu Val Ser Val Leu Tyr Ala Val Ile
 275 280 285
 Val Pro Leu Leu Asn Pro Ile Ile Tyr Cys Leu Arg Asn Gln Glu Val
 290 295 300
 Lys Arg Ala Leu Cys Cys Thr Leu His Leu Tyr Gln His Gln Asp Pro
 305 310 315 320
 Asp Pro Lys Lys Ala Ser Arg
 325

<210> 1365

<211> 333

<212> PRT

<213> Unknown (H38g282 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(333)

<223> Xaa = Any Amino Acid

<400> 1365

Met Asp Gly Glu Asn His Ser Val Val Ser Glu Phe Leu Phe Leu Gly
 1 5 10 15
 Leu Thr His Ser Trp Glu Ile Gln Leu Leu Leu Leu Val Phe Ser Ser
 20 25 30
 Val Leu Tyr Val Ala Ser Ile Thr Gly Asn Ile Leu Ile Val Phe Ser
 35 40 45
 Val Thr Thr Asp Pro His Leu His Ser Pro Met Tyr Phe Leu Leu Val
 50 55 60
 Ser Leu Ser Phe Ile Asp Leu Gly Ala Cys Ser Val Thr Ser Pro Lys
 65 70 75 80
 Met Ile Tyr Asp Leu Phe Arg Lys Arg Lys Val Ile Ser Phe Gly Gly
 85 90 95
 Cys Ile Ala Gln Ile Phe Phe Ile His Val Ile Gly Gly Val Glu Met
 100 105 110
 Val Leu Leu Ile Ala Met Ala Phe Asp Ser Tyr Val Ala Leu Cys Lys
 115 120 125
 Pro Leu His Tyr Leu Thr Ile Met Ser Pro Arg Met Cys Leu Ser Phe
 130 135 140
 Leu Ala Val Ala Trp Thr Leu Val Val Ser His Ser Leu Phe Gln Leu
 145 150 155 160
 Ala Phe Leu Val Asn Leu Pro Phe Cys Gly Pro Asn Val Leu Asp Ser
 165 170 175
 Phe Tyr Cys Asp Leu Pro Gln Leu Leu Arg Leu Ala Cys Thr Asp Thr

Met 1	Leu	Leu	Gly	Asn 5	Leu	Ala	Ile	Ile	Ser 10	Phe	Ile	Cys	Leu	Asp 15	Ser
Arg	Leu	His	Ser 20	Pro	Met	Tyr	Phe	Phe 25	Leu	Cys	Asn	Phe	Ser 30	Leu	Met
Glu	Met	Val 35	Val	Thr	Ser	Thr	Val 40	Val	His	Arg	Met	Leu 45	Ala	Asp	Leu
Leu	Ser 50	Thr	His	Lys	Thr	Met 55	Ser	Leu	Ala	Lys	Cys 60	Leu	Thr	Gln	Ser
Phe 65	Phe	Tyr	Phe	Ser 70	Leu	Gly	Ser	Ala	Asn	Phe 75	Leu	Ile	Leu	Met	Val 80
Met	Ala	Phe	Asp 85	Arg	Tyr	Val	Ala	Ile	Cys 90	His	Pro	Leu	Arg	Tyr 95	Pro
Thr	Ile	Thr	Asn 100	Gly	Pro	Val	Cys	Val 105	Lys	Leu	Val	Val 110	Ala	Cys	Trp
Val	Val	Gly 115	Phe	Leu	Ser	Ile	Val 120	Ser	Pro	Thr	Leu	Gln 125	Lys	Thr	Arg
Leu	Trp 130	Phe	Cys	Gly	Pro	Asn 135	Ile	Ile	Gly	His	Tyr 140	Phe	Cys	Asp	Ser
Ala 145	Pro	Leu	Leu	Lys 150	Leu	Ala	Cys	Ser	Asp	Thr 155	Arg	His	Ile	Glu	Arg 160
Met	Asp	Leu	Phe 165	Leu	Ser	Leu	Leu	Phe	Val 170	Leu	Thr	Thr 175	Met	Leu	Leu
Ile	Ile	Leu	Ser 180	Tyr	Ile	Leu	Ile	Val 185	Ala	Ala	Val	Leu 190	His	Ile	Pro
Ser	Ser	Ser 195	Gly	Cys	Gln	Lys	Ala 200	Phe	Ser	Thr	Cys	Ala 205	Ser	His	Leu
Thr	Val 210	Val	Val	Leu	Gly	Tyr 215	Gly	Ser	Ala	Ile	Phe 220	Ile	Tyr	Val	Arg
Pro 225	Gly	Lys	Gly	His 230	Ser	Thr	Tyr	Leu	Asn	Lys 235	Ala	Val	Ala	Met	Val
Thr	Ala	Met	Val 245	Thr	Pro	Phe	Leu	Asn 250	Pro	Phe	Ile	Phe	Thr	Phe 255	Arg

Asn Glu Lys Val Lys Glu Val Ile Glu Asp Val Thr Lys Arg Ile Phe
 260 265 270
 Leu Gly Asp Pro Ala Ala Cys Arg
 275 280

<210> 1367
 <211> 313
 <212> PRT
 <213> Unknown (H38g284 protein)

<220>
 <223> Synthetic construct

<400> 1367
 Met Glu Thr Ala Asn Tyr Thr Lys Val Thr Glu Phe Val Leu Thr Gly
 1 5 10 15
 Leu Ser Gln Thr Pro Glu Val Gln Leu Val Leu Phe Val Ile Phe Leu
 20 25 30
 Ser Phe Tyr Leu Phe Ile Leu Pro Gly Asn Ile Leu Ile Ile Cys Thr
 35 40 45
 Ile Ser Leu Asp Pro His Leu Thr Ser Pro Met Tyr Phe Leu Leu Ala
 50 55 60
 Asn Leu Ala Phe Leu Asp Ile Trp Tyr Ser Ser Ile Thr Ala Pro Glu
 65 70 75 80
 Met Leu Ile Asp Phe Phe Val Glu Arg Lys Ile Ile Ser Phe Asp Gly
 85 90 95
 Cys Ile Ala Gln Leu Phe Phe Leu His Phe Ala Gly Ala Ser Glu Met
 100 105 110
 Phe Leu Leu Thr Val Met Ala Phe Asp Leu Tyr Thr Ala Ile Cys Arg
 115 120 125
 Pro Leu His Tyr Ala Thr Ile Met Asn Gln Arg Leu Cys Cys Ile Leu
 130 135 140
 Val Ala Leu Ser Trp Arg Gly Gly Phe Ile His Ser Ile Ile Gln Val
 145 150 155 160
 Ala Leu Ile Val Arg Leu Pro Phe Cys Gly Pro Asn Glu Leu Asp Ser
 165 170 175
 Tyr Phe Cys Asp Ile Thr Gln Val Val Arg Ile Ala Cys Ala Asn Thr
 180 185 190
 Phe Pro Glu Glu Leu Val Met Ile Cys Ser Ser Gly Leu Ile Ser Val
 195 200 205
 Val Trp Leu Ile Ala Leu Leu Met Ser Tyr Ala Phe Leu Leu Ala Leu
 210 215 220
 Phe Lys Lys Leu Ser Gly Ser Gly Glu Asn Thr Asn Arg Ala Met Ser
 225 230 235 240
 Thr Cys Tyr Ser His Ile Thr Ile Val Val Leu Met Phe Gly Pro Ser
 245 250 255
 Ile Tyr Ile Tyr Ala Arg Pro Phe Asp Ser Phe Ser Leu Asp Lys Val
 260 265 270
 Val Ser Val Phe Asn Thr Leu Ile Phe Pro Leu Arg Asn Pro Ile Ile
 275 280 285
 Tyr Thr Leu Arg Asn Lys Glu Val Lys Ala Ala Met Arg Lys Leu Val
 290 295 300
 Thr Lys Tyr Ile Leu Cys Lys Glu Lys
 305 310

<210> 1368
 <211> 214
 <212> PRT
 <213> Unknown (H38g285 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(214)

<223> Xaa = Any Amino Acid

<400> 1368

```

Cys Leu Leu Xaa Leu Tyr Gln Val Cys Leu Leu Thr Arg Asp Pro Ile
 1           5           10           15
Leu Gln Asp Leu His Xaa Lys Pro Arg Ile Tyr Cys Ser Pro Cys Leu
          20           25           30
Xaa Val Tyr Ser Leu Gly Leu Asp Arg Xaa Xaa Val Phe Leu Thr Met
          35           40           45
Thr Gln Ser Val Leu Trp Asn Glu Pro Val Cys Phe Met Phe Ser Xaa
          50           55           60
Met Pro Phe Cys Leu Ser Xaa Ile Leu Pro Xaa Thr Tyr Tyr Glu Gln
65           70           75           80
Val Val Met Leu Asn Leu Val Cys Ala Asp Ile Thr Tyr Ile Val His
          85           90           95
Thr Cys Gly Leu Phe Met Ala Phe Ser Val Asp Gly Phe Asp Ile Phe
          100          105          110
Gly Ile Ile Ile His Arg Tyr Gln Thr Leu Gln Ala Val Leu Xaa Leu
          115          120          125
Pro Ala Lys Glu Ser Val Pro Lys Val Phe Ser Ile Tyr Ala Phe His
          130          135          140
Ile Cys Val Thr Leu Tyr Leu Leu Met Ile Gly Phe Tyr Ser Phe Phe
145           150           155           160
Ser Cys Cys Phe Ser Tyr His Thr Leu Thr Val Ile Pro Ile Ser Phe
          165          170          175
Ser Ser Phe Tyr Ser Leu Val Pro Ser Met Phe Asn Thr Ile Thr Cys
          180          185          190
Gly Val Lys Ser Lys His Ile Gln Glu Asn Met Val Gln Arg Phe Cys
          195          200          205
Gly Lys Ile Ser Cys His
          210

```

<210> 1369

<211> 330

<212> PRT

<213> Unknown (H38g286 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(330)

<223> Xaa = Any Amino Acid

<400> 1369

```

Met Cys Leu Leu Thr Leu Gln Val Thr Gly Pro Met Asn Val Ser Glu
 1           5           10           15
Pro Asn Ser Ser Phe Ala Leu Val Asn Glu Phe Ile Leu Gln Asp Leu
          20           25           30
Ser Phe Glu Trp Thr Ile Gln Ile Phe Leu Phe Ser Leu Phe Thr Thr
          35           40           45
Thr Tyr Ala Leu Thr Ile Thr Gly Asn Gly Ala Ile Ala Cys Ala Leu
          50           55           60
Trp Cys Asp Arg Arg Arg His Thr Pro Met Tyr Met Phe Leu Gly Asn
65           70           75           80
Phe Ser Phe Leu Glu Ile Trp Tyr Val Ser Ser Thr Val Pro Lys Met
          85           90           95

```

Leu Val Asn Phe Leu Ser Glu Lys Lys Thr Ile Ser Phe Ala Gly Cys
 100 105 110
 Phe Leu Gln Phe Tyr Phe Phe Phe Ser Leu Gly Thr Ser Glu Cys Leu
 115 120 125
 Ile Leu Thr Val Met Ala Phe Asp Gln Tyr Leu Val Ile Cys His Pro
 130 135 140
 Leu His Tyr Pro Asn Ile Ile Met Thr Gly His Leu Cys Ala Lys Leu
 145 150 155 160
 Val Ile Leu Cys Trp Val Cys Gly Phe Leu Trp Phe Leu Ile Pro Thr
 165 170 175
 Val Leu Ile Ser Gln Met Pro Phe Cys Gly Pro Asn Ile Asn Asp His
 180 185 190
 Val Val Cys Asp Pro Gly Pro Leu Phe Ala Leu Ala Cys Val Ser Ala
 195 200 205
 Pro Arg Ile Gln Leu Phe Cys Tyr Thr Leu Ser Ser Leu Val Ile Phe
 210 215 220
 Gly Asn Phe Leu Phe Ile Ile Gly Ser Tyr Thr Leu Val Leu Lys Ala
 225 230 235 240
 Val Leu Gly Met Pro Ser Ser Thr Gly Lys His Lys Ala Phe Ser Thr
 245 250 255
 Cys Gly Ser His Leu Ala Val Val Ser Leu Phe Tyr Gly Ser Leu Met
 260 265 270
 Val Met Cys Val Ser Pro Gly Leu Gly His Ser Met Gly Met Gln Lys
 275 280 285
 Ile Lys Thr Leu Phe Tyr Ala Met Val Thr Pro Leu Phe Asn Pro Leu
 290 295 300
 Ile Tyr Ser Leu Gln Asn Lys Glu Ile Lys Ala Ala Leu Arg Lys Val
 305 310 315 320
 Leu Gly Ser Ser Asn Ile Ile Xaa Ala Ile
 325 330

<210> 1370

<211> 310

<212> PRT

<213> Unknown (H38g287 protein)

<220>

<223> Synthetic construct

<400> 1370

Met Met Asp Asn His Ser Ser Ala Thr Glu Phe His Leu Leu Gly Phe
 1 5 10 15
 Pro Gly Ser Gln Gly Leu His His Ile Leu Phe Ala Ile Phe Phe
 20 25 30
 Phe Tyr Leu Val Thr Leu Met Gly Asn Thr Val Ile Ile Val Ile Val
 35 40 45
 Cys Val Asp Lys Arg Leu Gln Ser Pro Met Tyr Phe Phe Leu Ser His
 50 55 60
 Leu Ser Thr Leu Glu Ile Leu Val Thr Thr Ile Ile Val Pro Met Met
 65 70 75 80
 Leu Trp Gly Leu Leu Phe Leu Gly Cys Arg Gln Tyr Leu Ser Leu His
 85 90 95
 Val Ser Leu Asn Phe Ser Cys Gly Thr Met Glu Phe Ala Leu Leu Gly
 100 105 110
 Val Met Ala Val Asp Arg Tyr Val Ala Val Cys Asn Pro Leu Arg Tyr
 115 120 125
 Asn Ile Ile Met Asn Ser Ser Thr Cys Ile Trp Val Val Ile Val Ser
 130 135 140
 Trp Val Phe Gly Phe Leu Ser Glu Ile Trp Pro Ile Tyr Ala Thr Phe
 145 150 155 160
 Gln Phe Thr Phe Arg Lys Ser Asn Ser Leu Asp His Phe Tyr Cys Asp

```

      165      170      175
Arg Gly Gln Leu Leu Lys Leu Ser Cys Asp Asn Thr Leu Leu Thr Glu
      180      185      190
Phe Ile Leu Phe Leu Met Ala Val Phe Ile Leu Ile Gly Ser Leu Ile
      195      200      205
Pro Thr Ile Val Ser Tyr Thr Tyr Ile Ile Ser Thr Ile Leu Lys Ile
      210      215      220
Pro Ser Ala Ser Gly Arg Arg Lys Ala Phe Ser Thr Phe Ala Ser His
      225      230      235      240
Phe Thr Cys Val Val Ile Gly Tyr Gly Ser Cys Leu Phe Leu Tyr Val
      245      250      255
Lys Pro Lys Gln Thr Gln Gly Val Glu Tyr Asn Lys Ile Val Ser Leu
      260      265      270
Leu Val Ser Val Leu Thr Pro Phe Leu Asn Pro Phe Ile Phe Thr Leu
      275      280      285
Arg Asn Asp Lys Val Lys Glu Ala Leu Arg Asp Gly Met Lys Arg Cys
      290      295      300
Cys Gln Leu Leu Lys Asp
      305      310

```

<210> 1371

<211> 305

<212> PRT

<213> Unknown (H38g288 protein)

<220>

<223> Synthetic construct

<400> 1371

```

Met Ser Asn Thr Asn Gly Ser Ala Ile Thr Glu Phe Ile Leu Leu Gly
  1      5      10      15
Leu Thr Asp Cys Pro Glu Leu Gln Ser Leu Leu Phe Val Leu Phe Leu
      20      25      30
Val Val Tyr Leu Val Thr Leu Leu Gly Asn Leu Gly Met Ile Met Leu
      35      40      45
Met Arg Leu Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Thr
      50      55      60
Asn Leu Ala Phe Val Asp Leu Cys Tyr Thr Ser Asn Ala Thr Pro Gln
      65      70      75      80
Met Ser Thr Asn Ile Val Ser Glu Lys Thr Ile Ser Phe Ala Gly Cys
      85      90      95
Phe Thr Gln Cys Tyr Ile Phe Ile Ala Leu Leu Leu Thr Glu Phe Tyr
      100      105      110
Met Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Tyr Asp Pro
      115      120      125
Leu Arg Tyr Ser Val Lys Thr Ser Arg Arg Val Cys Ile Cys Leu Ala
      130      135      140
Thr Phe Pro Tyr Val Tyr Gly Phe Ser Asp Gly Leu Phe Gln Ala Ile
      145      150      155      160
Leu Thr Phe Arg Leu Thr Phe Cys Arg Ser Ser Val Ile Asn His Phe
      165      170      175
Tyr Cys Ala Asp Pro Pro Leu Ile Lys Leu Ser Cys Ser Asp Thr Tyr
      180      185      190
Val Lys Glu His Ala Met Phe Ile Ser Ala Gly Phe Asn Leu Ser Ser
      195      200      205
Ser Leu Thr Ile Val Leu Val Ser Tyr Ala Phe Ile Leu Ala Ala Ile
      210      215      220
Leu Arg Ile Lys Ser Ala Glu Gly Arg His Lys Ala Phe Ser Thr Cys
      225      230      235      240
Gly Ser His Met Met Ala Val Thr Leu Phe Tyr Gly Thr Leu Phe Cys
      245      250      255

```

Met Tyr Ile Arg Pro Pro Thr Asp Lys Thr Val Glu Glu Ser Lys Ile
 260 265 270
 Ile Ala Val Phe Tyr Thr Phe Val Ser Pro Val Leu Asn Pro Leu Ile
 275 280 285
 Tyr Ser Leu Arg Asn Lys Asp Val Lys Gln Ala Leu Lys Asn Val Leu
 290 295 300

Arg
 305

<210> 1372

<211> 313

<212> PRT

<213> Unknown (H38g289 protein)

<220>

<223> Synthetic construct

<400> 1372

Met Ala Asn Leu Ser Gln Pro Ser Glu Phe Val Leu Leu Gly Phe Ser
 1 5 10 15
 Ser Phe Gly Glu Leu Gln Ala Leu Leu Tyr Gly Pro Phe Leu Met Leu
 20 25 30
 Tyr Leu Leu Ala Phe Met Gly Asn Thr Ile Ile Ile Val Met Val Ile
 35 40 45
 Ala Asp Thr His Leu His Thr Pro Met Tyr Phe Phe Leu Gly Asn Phe
 50 55 60
 Ser Leu Leu Glu Ile Leu Val Thr Met Thr Ala Val Pro Arg Met Leu
 65 70 75 80
 Ser Asp Leu Leu Val Pro His Lys Val Ile Thr Phe Thr Gly Cys Met
 85 90 95
 Val Gln Phe Tyr Phe His Phe Ser Leu Gly Ser Thr Ser Phe Leu Ile
 100 105 110
 Leu Thr Asp Met Ala Leu Asp Arg Phe Val Ala Ile Cys His Pro Leu
 115 120 125
 Arg Tyr Gly Thr Leu Met Ser Arg Ala Met Cys Val Gln Leu Ala Gly
 130 135 140
 Ala Ala Trp Ala Ala Pro Phe Leu Ala Met Val Pro Thr Val Leu Ser
 145 150 155 160
 Arg Ala His Leu Asp Tyr Cys His Gly Asp Val Ile Asn His Phe Phe
 165 170 175
 Cys Asp Asn Glu Pro Leu Leu Gln Leu Ser Cys Ser Asp Thr Arg Leu
 180 185 190
 Leu Glu Phe Trp Asp Phe Leu Met Ala Leu Thr Phe Val Leu Ser Ser
 195 200 205
 Phe Leu Val Thr Leu Ile Ser Tyr Gly Tyr Ile Val Thr Thr Val Leu
 210 215 220
 Arg Ile Pro Ser Ala Ser Ser Cys Gln Lys Ala Phe Ser Thr Cys Gly
 225 230 235 240
 Ser His Leu Thr Leu Val Phe Ile Gly Tyr Ser Ser Thr Ile Phe Leu
 245 250 255
 Tyr Val Arg Pro Gly Lys Ala His Ser Val Gln Val Arg Lys Val Val
 260 265 270
 Ala Leu Val Thr Ser Val Leu Thr Pro Phe Leu Asn Pro Phe Ile Leu
 275 280 285
 Thr Phe Cys Asn Gln Thr Val Lys Thr Val Leu Gln Gly Gln Met Gln
 290 295 300
 Arg Leu Lys Gly Leu Cys Lys Ala Gln
 305 310

<210> 1373

<211> 316

<212> PRT

<213> Unknown (H38g290 protein)

<220>

<223> Synthetic construct

<400> 1373

```

Met Lys Ile Ala Asn Asn Thr Val Val Thr Glu Phe Ile Leu Leu Gly
 1           5           10           15
Leu Thr Gln Ser Gln Asp Ile Gln Leu Leu Val Phe Val Leu Ile Leu
      20           25           30
Ile Phe Tyr Leu Ile Ile Leu Pro Gly Asn Phe Leu Ile Ile Phe Thr
      35           40           45
Ile Arg Ser Asp Pro Gly Leu Thr Ala Pro Leu Tyr Leu Phe Leu Gly
      50           55           60
Asn Leu Ala Phe Leu Asp Ala Ser Tyr Ser Phe Ile Val Ala Pro Arg
65           70           75           80
Met Leu Val Asp Phe Leu Ser Glu Lys Lys Val Ile Ser Tyr Arg Gly
      85           90           95
Cys Ile Thr Gln Leu Phe Phe Leu His Phe Leu Gly Gly Gly Glu Gly
      100           105           110
Leu Leu Leu Val Val Met Ala Phe Asp Arg Tyr Ile Ala Ile Cys Arg
      115           120           125
Pro Leu His Cys Ser Thr Val Met Asn Pro Arg Ala Cys Tyr Ala Met
      130           135           140
Met Leu Ala Leu Trp Leu Gly Gly Phe Val His Ser Ile Ile Gln Val
145           150           155           160
Val Leu Ile Leu Arg Leu Pro Phe Cys Gly Pro Asn Gln Leu Asp Asn
      165           170           175
Phe Phe Cys Asp Val Arg Gln Val Ile Lys Leu Ala Cys Thr Asp Met
      180           185           190
Phe Val Val Glu Leu Leu Met Val Phe Asn Ser Gly Leu Met Thr Leu
      195           200           205
Leu Cys Phe Leu Gly Leu Leu Ala Ser Tyr Ala Val Ile Leu Cys His
      210           215           220
Val Arg Arg Ala Ala Ser Glu Gly Lys Asn Lys Ala Met Ser Thr Cys
225           230           235           240
Thr Thr Arg Val Ile Ile Ile Leu Leu Met Phe Gly Pro Ala Ile Phe
      245           250           255
Ile Tyr Met Cys Pro Phe Arg Ala Leu Pro Ala Asp Lys Met Val Ser
      260           265           270
Leu Phe His Thr Val Ile Phe Pro Leu Met Asn Pro Met Ile Tyr Thr
      275           280           285
Leu Arg Asn Gln Glu Val Lys Thr Ser Met Lys Arg Leu Leu Ser Arg
      290           295           300
His Val Val Cys Gln Val Asp Phe Ile Ile Arg Asn
305           310           315

```

<210> 1374

<211> 345

<212> PRT

<213> Unknown (H38g291 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(345)

<223> Xaa = Any Amino Acid

<400> 1374

```

Met His Leu Pro Asn Ser Ser Glu Ile Ala Ile Thr Thr Phe Phe Leu
 1          5          10          15
Ile Gly Ile Pro Gly Leu Glu His Ala His Ile Trp Ile Ser Val Pro
          20          25          30
Ile Cys Leu Met Tyr Leu Val Ala Ile Leu Gly Asn Cys Thr Ile Leu
          35          40          45
Phe Val Ile Arg Thr Glu Pro Ser Leu His Ala Pro Met Tyr Tyr Phe
          50          55          60
Leu Ser Met Leu Ala Val Ser Asp Leu Gly Leu Ser Leu Ser Tyr Leu
65          70          75          80
Pro Thr Met Leu Arg Ile Phe Val Phe Asn Ala Thr Gly Ile Ser Ser
          85          90          95
Asn Ala Arg Phe Ala Gln Glu Phe Phe Ile His Gly Phe Thr Asp Met
          100          105          110
Glu Ser Ser Val Leu Leu Val Met Ser Phe Asp Arg Phe Leu Ala Ile
          115          120          125
Cys His Pro Leu Arg Tyr Ile Ser Glu Val Leu Val Ser Cys Ile Leu
          130          135          140
Thr Ser Ala Arg Val Ala Lys Met Gly Leu Leu Phe Leu Ile Lys Arg
          145          150          155          160
Glu Thr Thr Leu Asn Ser Leu Lys Glu Thr Thr Asn Ser Val Leu Leu
          165          170          175
Val Leu Pro Phe Pro Phe Thr Leu Thr Arg Leu Thr Tyr Cys Arg Lys
          180          185          190
Ser Leu Leu Ser His Ser Tyr Cys Leu His Gln Asp Val Arg Lys Leu
          195          200          205
Ala Cys Ser Asp Asn Thr Val Asn Phe Phe Tyr Gly Phe Phe Leu Ala
          210          215          220
Leu Cys Met Met Ser Glu Ser Val Phe Ile Thr Val Ser Tyr Val Leu
          225          230          235          240
Ile Leu Lys Thr Ile Met Gly Ile Gly Ser His Arg Glu Arg Leu Lys
          245          250          255
Ala Leu Asn Thr Cys Val Ser His Ile Cys Ala Val Leu Ile Phe Tyr
          260          265          270
Ala Pro Val Ile Ala Leu Ala Ser Met His Cys Phe Ala Ser Met Asn
          275          280          285
Cys Phe Gly Lys His Arg Ser Pro Leu Ala Met Ile Leu Ile Ala Asp
          290          295          300
Val Phe Leu Leu Val Pro Pro Leu Met Asn Pro Ile Val Tyr Cys Val
          305          310          315          320
Lys Thr Gln Gln Ile His Glu Lys Val Leu Gly Lys Leu Gly Leu Gln
          325          330          335
Gln Arg Cys Gln Xaa Thr Trp Tyr Lys
          340          345

```

<210> 1375

<211> 238

<212> PRT

<213> Unknown (H38g292 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(238)

<223> Xaa = Any Amino Acid

<400> 1375

```

Pro Leu Ile Xaa Pro Asp Pro Phe Ile Phe Thr Gln Leu Cys Ser Phe
 1          5          10          15
Leu Asn Lys Tyr Val Ala Ser Thr Arg Leu Asn Asp His Asn Ile Asp

```

```

      20      25      30
Gln Ala Pro Xaa Ser Arg Ser Ile Ile Leu Asn Leu Cys Leu Ile Ser
      35      40      45
Phe Gly Ile Lys Gly Met Trp Ser Asn Val Asn Ser Cys Phe Leu Ser
      50      55      60
Ser Leu Pro Arg Glu Lys Glu Leu Gly Leu Lys Ser Glu Gly Asn Tyr
      65      70      75      80
Ser Ser Ala Thr Gln Phe Cys Leu Leu Gly Phe Pro Gly Phe Glu Glu
      85      90      95
Leu Pro His Phe Leu Leu Val Asn Phe Phe His Leu Met Arg Leu
      100      105      110
Met Gly Asn Ala Val Ile Tyr Met Val Arg Ile Asp Xaa Ser Leu Gln
      115      120      125
Ser Pro Gly Asp Phe Phe Leu Ser Gln Leu Phe Ile Phe Ser His Ser
      130      135      140
Leu Leu Met Asp Ile Ser Ile Val Ile Ala Ser Leu Ile Gln Ile Asp
      145      150      155      160
Ser Tyr Ser Ser Ile Pro Ser Ala Ser Gly Gln Lys Lys Ser Phe Ser
      165      170      175
Thr His Ala Ser His Phe Thr Cys Val Gly Ile Asp Tyr Asp Ser Cys
      180      185      190
Leu Phe Leu Tyr Val Lys Pro Lys Gln Ile Trp Ala Ala Glu Xaa Asn
      195      200      205
Lys Val Val Phe Leu Phe Ile Phe Leu Leu Thr Pro Phe Leu Asn Leu
      210      215      220
Leu Thr Gly Gln Ile Tyr Xaa Pro Lys Ser Val Leu Gly Gly
      225      230      235

```

<210> 1376

<211> 311

<212> PRT

<213> Unknown (H38g293 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(311)

<223> Xaa = Any Amino Acid

<400> 1376

```

Pro Met Lys Val Ala Asn Asn Val Thr Glu Phe Ile Phe Leu Gly Leu
1      5      10      15
Ser Gln Asp Ser Gly Met Gln Leu Met Phe Phe Val Leu Phe Leu Leu
      20      25      30
Phe Tyr Val Val Ile Met Val Gly Asn Leu Leu Ile Leu Leu Met Val
      35      40      45
Phe Ser Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser Asn
      50      55      60
Leu Ser Phe Val Asp Ile Ala Cys Ser Ser Ala Thr Ala Pro Lys Met
      65      70      75      80
Ile Glu Asp Phe Val Ser Glu Lys Lys Thr Ile Ser Tyr Trp Gly Cys
      85      90      95
Ile Thr Gln Met Phe Thr Phe His Phe Gly Cys Ala Glu Ile Phe
      100      105      110
Val Leu Thr Val Met Ala Phe Asp Arg Tyr Ala Ala Ile Cys Gln Pro
      115      120      125
Leu Arg Tyr Thr Val Ile Met Ser Ala Asn Ala Tyr Thr Val Leu Ala
      130      135      140
Ser Leu Ser Trp Leu Gly Ala Leu Gly His Ser Phe Val Gln Thr Leu
      145      150      155      160

```

Leu Thr Phe Gln Leu Pro Phe Cys Asn Ala Gln Val Ile Asp His Tyr
 165 170 175
 Phe Cys Asp Val His Pro Val Leu Lys Leu Ala Cys Ala Asp Thr Thr
 180 185 190
 Leu Val Asn Met Leu Val Val Ala Asn Ser Gly Leu Ile Ser Leu Gly
 195 200 205
 Cys Phe Leu Ile Leu Leu Ala Ser Tyr Thr Val Ile Leu Phe Ser Leu
 210 215 220
 Gln Lys Gln Ser Ala Glu Ser Xaa His Lys Val Leu Ser Thr Cys Gly
 225 230 235 240
 Ser His Leu Thr Ile Val Thr Phe Phe Phe Val Pro Cys Ile Phe Ile
 245 250 255
 Tyr Arg Pro Ser Thr Thr Phe Pro Leu Asp Lys Ala Val Ser Val Phe
 260 265 270
 Tyr Thr Thr Ile Thr Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg
 275 280 285
 Asn Glu Glu Val Lys Asn Ala Met Arg Arg Leu Trp Ser Ser Lys Ile
 290 295 300
 Ser Leu Lys Glu Lys Gln Arg
 305 310

<210> 1377

<211> 323

<212> PRT

<213> Unknown (H38g294 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(323)

<223> Xaa = Any Amino Acid

<400> 1377

Met Glu Ile Leu Ser Asn Ser Thr Ser Lys Phe Pro Thr Phe Leu Leu
 1 5 10 15
 Thr Gly Ile Pro Gly Leu Glu Ser Ala His Val Trp Ile Ser Ile Pro
 20 25 30
 Phe Cys Cys Phe Tyr Ala Ile Ala Leu Ser Gly Asn Ser Val Ile Leu
 35 40 45
 Phe Val Ile Ile Thr Gln Gln Ser Leu His Glu Pro Met Tyr Tyr Phe
 50 55 60
 Leu Ser Met Leu Ser Ala Thr Asp Leu Gly Leu Thr Val Ser Ser Leu
 65 70 75 80
 Ser Thr Thr Leu Gly Ile Leu Trp Phe Glu Ala Arg Glu Ile Ser Leu
 85 90 95
 Tyr Ser Cys Ile Val Gln Met Phe Phe Leu His Gly Phe Thr Phe Met
 100 105 110
 Glu Ser Gly Val Leu Val Ala Thr Ala Phe Asp Arg Tyr Val Ala Ile
 115 120 125
 Cys Asp Pro Leu Arg Tyr Thr Thr Ile Leu Thr Asn Ser Arg Ile Ile
 130 135 140
 Gln Met Gly Leu Leu Met Ile Thr Arg Ala Ile Val Leu Ile Leu Pro
 145 150 155 160
 Leu Leu Leu Leu Leu Lys Pro Leu Tyr Phe Cys Arg Met Asn Ala Leu
 165 170 175
 Ser His Ser Tyr Cys Tyr His Pro Asp Val Ile Gln Leu Ala Cys Ser
 180 185 190
 Asp Ile Arg Ala Asn Ser Ile Cys Gly Leu Ile Asp Leu Ile Leu Thr
 195 200 205
 Thr Gly Ile Asp Thr Pro Cys Ile Val Leu Ser Tyr Ile Leu Ile Ile

210	215	220
Arg Phe Val Leu Arg Ile	Ala Ser Pro Glu Glu Trp His Lys Val Phe	
225	230	235
Ser Thr Cys Val Ser His Val Gly Ala Val Ala Phe Phe Tyr Ile His		240
	245	250
Met Leu Ser Leu Ser Leu Val Tyr Arg Tyr Gly Arg Ser Ala Pro Arg		255
	260	265
Val Val His Ser Val Met Ala Asn Val Tyr Leu Leu Leu Pro Pro Val		270
	275	280
Leu Asn Pro Ile Ile Tyr Ser Val Lys Thr Lys Gln Ile Arg Lys Ala		285
	290	295
Met Leu Ser Leu Leu Leu Thr Lys Xaa Thr Asp Ile Val Leu Phe Asp		300
305	310	315
Thr Asn Leu		320

<210> 1378

<211> 321

<212> PRT

<213> Unknown (H38g295 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(321)

<223> Xaa = Any Amino Acid

<400> 1378

His Thr Glu Pro Arg Asn Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu	
1	5
Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Ile Leu Ala Leu Leu Ser	10
	15
	20
Leu Ser Leu Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ser	25
	30
	35
Ile Leu Ala Val Cys Ser Asp Ser Pro Leu His Thr Pro Arg Tyr Phe	40
	45
	50
Phe Leu Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Thr	55
	60
65	70
Val Pro Lys Met Ile Val Asp Met Gln Ser His Ser Arg Val Thr Ser	75
	80
	85
His Ala Gly Cys Leu Thr Gln Met Ser Phe Leu Val Leu Phe Ala Cys	90
	95
	100
Ile Glu Gly Met Leu Leu Thr Val Met Ala Tyr Asp Cys Phe Val Ala	105
	110
	115
Ile Cys Arg Pro Leu His Tyr Pro Val Ile Val Asn Pro His Leu Cys	120
	125
	130
Val Phe Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu	135
	140
145	150
His Ser Trp Ile Val Leu Gln Phe Thr Ile Val Xaa Asn Leu Glu Ile	155
	160
	165
Ser Asn Phe Val Cys Asp Pro Ser Gln Leu Leu Lys Leu Ala Cys Ser	170
	175
	180
Asp Ser Val Ile Asn Ser Ile Phe Ile Tyr Phe Asp Ser Thr Met Phe	185
	190
	195
Gly Phe Leu Pro Ile Ser Gly Ile Leu Trp Ser Tyr Tyr Lys Ile Ile	200
	205
	210
Pro Ser Ile Leu Arg Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala Phe	215
	220
225	230
Ser Thr Cys Gly Ser His Leu Ala Val Val Cys Xaa Phe Tyr Gly Thr	235
	240
	245
	250
	255

Gly Ile Gly Met Tyr Leu Thr Ser Ala Val Ser Gln Pro Pro Arg Asn
 260 265 270
 Gly Val Val Ala Ser Val Met Tyr Ala Val Val Thr Pro Met Leu Asn
 275 280 285
 Leu Phe Ile Tyr Ser Leu Arg Asn Arg Asn Ile Gln Ser Ala Leu Trp
 290 295 300
 Arg Leu His Ser Arg Thr Val Glu Ser His Asp Leu Phe His Pro Phe
 305 310 315 320
 Ser

<210> 1379

<211> 325

<212> PRT

<213> Unknown (H38g296 protein)

<220>

<223> Synthetic construct

<400> 1379

Met Ala Ile Phe Asn Asn Thr Thr Ser Ser Ser Ser Asn Phe Leu Leu
 1 5 10 15
 Thr Ala Phe Pro Gly Leu Glu Cys Ala His Val Trp Ile Ser Ile Pro
 20 25 30
 Val Cys Cys Leu Tyr Thr Ile Ala Leu Leu Gly Asn Ser Met Ile Phe
 35 40 45
 Leu Val Ile Ile Thr Lys Arg Arg Leu His Lys Pro Met Tyr Tyr Phe
 50 55 60
 Leu Ser Met Leu Ala Ala Val Asp Leu Cys Leu Thr Ile Thr Thr Leu
 65 70 75 80
 Pro Thr Val Leu Gly Val Leu Trp Phe His Ala Arg Glu Ile Ser Phe
 85 90 95
 Lys Ala Cys Phe Ile Gln Met Phe Phe Val His Ala Phe Ser Leu Leu
 100 105 110
 Glu Ser Ser Val Leu Val Ala Met Ala Phe Asp Arg Phe Val Ala Ile
 115 120 125
 Cys Asn Pro Leu Asn Tyr Ala Thr Ile Leu Thr Asp Arg Met Val Leu
 130 135 140
 Val Ile Gly Leu Val Ile Cys Ile Arg Pro Ala Val Phe Leu Leu Pro
 145 150 155 160
 Leu Leu Val Ala Ile Asn Thr Val Ser Phe His Gly Gly His Glu Leu
 165 170 175
 Ser His Pro Phe Cys Tyr His Pro Glu Val Ile Lys Tyr Thr Tyr Ser
 180 185 190
 Lys Pro Trp Ile Ser Ser Phe Trp Gly Leu Phe Leu Gln Leu Tyr Leu
 195 200 205
 Asn Gly Thr Asp Val Leu Phe Ile Leu Phe Ser Tyr Val Leu Ile Leu
 210 215 220
 Arg Thr Val Leu Gly Ile Val Ala Arg Lys Lys Gln Gln Lys Ala Leu
 225 230 235 240
 Ser Thr Cys Val Cys His Ile Cys Ala Val Thr Ile Phe Tyr Val Pro
 245 250 255
 Leu Ile Ser Leu Ser Leu Ala His Arg Leu Phe His Ser Thr Pro Arg
 260 265 270
 Val Leu Cys Ser Thr Leu Ala Asn Ile Tyr Leu Leu Leu Pro Pro Val
 275 280 285
 Leu Asn Pro Ile Ile Tyr Ser Leu Lys Thr Lys Thr Ile Arg Gln Ala
 290 295 300
 Met Phe Gln Leu Leu Gln Ser Lys Gly Ser Trp Gly Phe Asn Val Arg
 305 310 315 320
 Gly Leu Arg Gly Arg

325

<210> 1380
 <211> 315
 <212> PRT
 <213> Unknown (H38g297 protein)

<220>
 <223> Synthetic construct

<400> 1380
 Met Glu Thr Trp Val Asn Gln Ser Tyr Thr Asp Gly Phe Phe Leu Leu
 1 5 10 15
 Gly Ile Phe Ser His Ser Thr Ala Asp Leu Val Leu Phe Ser Val Val
 20 25 30
 Met Ala Val Phe Thr Val Ala Leu Cys Gly Asn Val Leu Leu Ile Phe
 35 40 45
 Leu Ile Tyr Met Asp Pro His Leu His Thr Pro Met Tyr Phe Phe Leu
 50 55 60
 Ser Gln Leu Ser Leu Met Asp Leu Met Leu Val Cys Thr Asn Val Pro
 65 70 75 80
 Lys Met Ala Ala Asn Phe Leu Ser Gly Arg Lys Ser Ile Ser Phe Val
 85 90 95
 Gly Cys Gly Ile Gln Ile Gly Leu Phe Val Cys Leu Val Gly Ser Glu
 100 105 110
 Gly Leu Leu Leu Gly Leu Met Ala Tyr Asp Arg Tyr Val Ala Ile Ser
 115 120 125
 His Pro Leu His Tyr Pro Ile Leu Met Asn Gln Arg Val Cys Leu Gln
 130 135 140
 Ile Thr Gly Ser Ser Trp Ala Phe Gly Ile Ile Asp Gly Leu Ile Gln
 145 150 155 160
 Met Val Val Val Met Asn Phe Pro Tyr Cys Gly Leu Arg Lys Val Asn
 165 170 175
 His Phe Phe Cys Glu Met Leu Ser Leu Leu Lys Leu Ala Cys Val Asp
 180 185 190
 Thr Ser Leu Phe Glu Lys Val Ile Phe Ala Cys Cys Val Phe Met Leu
 195 200 205
 Leu Phe Pro Phe Ser Ile Ile Val Ala Ser Tyr Ala Arg Ile Leu Gly
 210 215 220
 Thr Val Leu Gln Met His Ser Ala Gln Ala Trp Lys Lys Ala Leu Ala
 225 230 235 240
 Thr Cys Ser Ser His Leu Thr Ala Val Thr Leu Phe Tyr Gly Ala Ala
 245 250 255
 Met Phe Ile Tyr Leu Arg Pro Arg His Tyr Arg Ala Pro Ser His Asp
 260 265 270
 Lys Val Ala Ser Ile Phe Tyr Thr Val Leu Thr Pro Met Leu Asn Pro
 275 280 285
 Leu Ile Tyr Ser Leu Arg Asn Arg Glu Val Met Gly Ala Leu Arg Lys
 290 295 300
 Gly Leu Asp Arg Cys Arg Ile Gly Ser Gln His
 305 310 315

<210> 1381
 <211> 323
 <212> PRT
 <213> Unknown (H38g298 protein)

<220>
 <223> Synthetic construct

<221> VARIANT

<222> (1)...(323)

<223> Xaa = Any Amino Acid

<400> 1381

```

Met Ser Pro Leu Asn Gln Thr Thr Glu Asn His Gln Ser Phe Phe Thr
 1           5           10           15
Leu Thr Gly Ile Pro Gly Met Pro Glu Lys Asp Leu Trp Met Ala Leu
 20           25           30
Pro Leu Cys Leu Leu Tyr Ser Thr Thr Ile Leu Gly Asn Val Thr Ile
 35           40           45
Leu Val Val Ile Lys Val Glu Gln Ser Leu His Glu Pro Met Tyr Tyr
 50           55           60
Phe Leu Ala Met Leu Ala Ala Thr Asp Leu Ser Leu Ser Leu Ser Ser
 65           70           75           80
Met Pro Thr Met Val Ser Val His Trp Phe Asn Trp Arg Ser Ile Thr
 85           90           95
Phe Asn Gly Cys Leu Ile Gln Met Phe Phe Ile His Thr Phe Gly Gly
 100          105          110
Val Glu Ser Gly Val Leu Val Ala Met Ala Phe Asp Arg Phe Val Ala
 115          120          125
Ile Arg Phe Pro Leu His Tyr Ala Thr Ile Leu Thr His Ser Val Ile
 130          135          140
Ser Lys Ile Ala Ala Ile Leu Leu Arg Ser Val Gly Ala Val Leu
 145          150          155          160
Pro Val Pro Phe Leu Ile Lys Arg Leu Pro Phe Cys His Ser Asn Val
 165          170          175
Leu Ser His Ala Tyr Cys Leu His Gln Asp Ala Met Arg Leu Ala Cys
 180          185          190
Ala Asp Thr Gly Val Asn Ser Ile Tyr Gly Leu Leu Ala Val Ile Phe
 195          200          205
Ile Ile Val Leu Asp Ala Leu Ile Leu Leu Ala Ser Tyr Ile Leu Ile
 210          215          220
Leu Gln Ala Val Leu Ser Ile Ala Ser Gln Glu Asp Arg Leu Lys Ala
 225          230          235          240
Leu Asn Thr Cys Leu Ser His Met Ser Ala Val Leu Leu Phe Tyr Val
 245          250          255
Pro Leu Ile Gly Met Thr Leu Ile His Arg Tyr Gly Lys His Leu Ser
 260          265          270
Pro Leu Ile His Thr Phe Met Ala Asn Ile Tyr Leu Leu Leu Pro Pro
 275          280          285
Val Leu Asn Pro Ile Val Tyr Ser Val Arg Thr Lys Gln Ile Xaa Xaa
 290          295          300
Gln Ile Val Gln Ala Phe Cys Gly Ala Arg Val Ser Pro Xaa Trp His
 305          310          315          320
Leu Leu Phe

```

<210> 1382

<211> 312

<212> PRT

<213> Unknown (H38g299 protein)

<220>

<223> Synthetic construct

<400> 1382

```

Met Ser Val Leu Asn Asn Ser Glu Val Lys Leu Phe Leu Leu Ile Gly
 1           5           10           15
Ile Pro Gly Leu Glu His Ala His Ile Trp Phe Ser Ile Pro Ile Cys
 20           25           30
Leu Met Tyr Leu Leu Ala Ile Met Gly Asn Cys Thr Ile Leu Phe Ile

```

```

      35      40      45
Ile Lys Thr Glu Pro Ser Leu His Glu Pro Met Tyr Tyr Phe Leu Ala
 50      55      60
Met Leu Ala Val Ser Asp Met Gly Leu Ser Leu Ser Ser Leu Pro Thr
 65      70      75      80
Met Leu Arg Val Phe Leu Phe Asn Ala Met Gly Ile Ser Pro Asn Ala
      85      90      95
Cys Phe Ala Gln Glu Phe Phe Ile His Gly Phe Thr Val Met Glu Ser
      100      105      110
Ser Val Leu Leu Ile Met Ser Leu Asp Arg Phe Leu Ala Ile His Asn
      115      120      125
Pro Leu Arg Tyr Ser Ser Ile Leu Thr Ser Asn Arg Val Ala Lys Met
      130      135      140
Gly Leu Ile Leu Ala Ile Arg Ser Ile Leu Leu Val Ile Pro Phe Pro
      145      150      155      160
Phe Thr Leu Arg Arg Leu Lys Tyr Cys Gln Lys Asn Leu Leu Ser His
      165      170      175
Ser Tyr Cys Leu His Gln Asp Thr Met Lys Leu Ala Cys Ser Asp Asn
      180      185      190
Lys Thr Asn Val Ile Tyr Gly Phe Phe Ile Ala Leu Cys Thr Met Leu
      195      200      205
Asp Leu Ala Leu Ile Val Leu Ser Tyr Val Leu Ile Leu Lys Thr Ile
      210      215      220
Leu Ser Ile Ala Ser Leu Ala Glu Arg Leu Lys Ala Leu Asn Thr Cys
      225      230      235      240
Val Ser His Ile Cys Ala Val Leu Thr Phe Tyr Val Pro Ile Ile Thr
      245      250      255
Leu Ala Ala Met His His Phe Ala Lys His Lys Ser Pro Leu Val Val
      260      265      270
Ile Leu Ile Ala Asp Met Phe Leu Leu Val Pro Pro Leu Met Asn Pro
      275      280      285
Ile Val Tyr Cys Val Lys Thr Arg Gln Ile Trp Glu Lys Ile Leu Gly
      290      295      300
Lys Leu Leu Asn Val Cys Gly Arg
      305      310

```

<210> 1383

<211> 308

<212> PRT

<213> Unknown (H38g300 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(308)

<223> Xaa = Any Amino Acid

<400> 1383

```

Met Lys Ile Asn Asp Ser Ser Gly Glu Asp Phe Ile Leu Val Gly Phe
 1      5      10      15
Ser Glu Tyr Pro Gln Ala Glu Phe Ile Leu Ser Leu Phe Val Ser Gly
      20      25      30
Phe Tyr Thr Met Thr Phe Thr Gly Asn Thr Ala Ile Ile Leu Val Ser
      35      40      45
Leu Leu Asp Tyr Arg Leu Arg Thr Pro Met Tyr Phe Phe Leu Arg Lys
      50      55      60
Leu Ser Phe Leu Asp Met Cys Phe Thr Thr Cys Ile Val Leu Gln Met
      65      70      75      80
Leu Val Asn Ile Trp Gly Glu Ser Lys Lys Val Ser Tyr Val Gly Cys
      85      90      95

```

Met Val Gln Tyr Ser Val Ala Leu Ala Leu Gly Ser Thr Glu Cys Val
 100 105 110
 Leu Leu Ala Ile Met Ala Val Asp Arg Tyr Val Ala Val Arg Trp Pro
 115 120 125
 Leu His Tyr Val Thr Ile Met His Gln Gln Ile Cys His Phe Leu Ala
 130 135 140
 Ala Leu Ser Trp Phe Ser Gly Leu Ala Asn Ser Leu Phe His Ser Ser
 145 150 155 160
 Leu Thr Thr Ile Leu Pro Leu Cys Gly His Arg Arg Val Asp His Phe
 165 170 175
 Phe Cys Glu Val Leu Leu Ile Val Lys Leu Ser Cys Val Asp Thr Gly
 180 185 190
 Pro Thr Glu Leu Lys Met Leu Ile Ala Arg Val Ile Ile Leu Ala Leu
 195 200 205
 Pro Val Cys Thr Ile Leu Thr Ser Tyr Ala Cys Ile Ala Arg Ala Val
 210 215 220
 Leu Arg Leu Gln Ser Ala Glu Gly Gln Gln Lys Ala Phe Gly Thr Cys
 225 230 235 240
 Ala Ser His Leu Met Val Val Leu Leu Phe Tyr Gly Thr Ile Met Phe
 245 250 255
 Met Cys Leu Gln Leu Lys Ser Asn Tyr Ser Gln Ile Gln Gly Lys Leu
 260 265 270
 Leu Pro Leu Val Tyr Thr Ile Ala Ala Pro Thr Xaa Asn Pro Leu Ile
 275 280 285
 Tyr Ala Leu Arg Asn Lys Val Val Lys Arg Ala Ile Gly Lys Leu Ile
 290 295 300
 Trp Lys Asp Ser
 305

<210> 1384

<211> 317

<212> PRT

<213> Unknown (H38g301 protein)

<220>

<223> Synthetic construct

<400> 1384

Met Glu Ile Asp Asn Gln Thr Trp Val Arg Glu Phe Ile Leu Leu Gly
 1 5 10 15
 Leu Ser Ser Asp Trp Cys Thr Gln Ile Ser Leu Phe Ser Leu Phe Leu
 20 25 30
 Val Thr Tyr Leu Met Thr Val Leu Gly Asn Cys Leu Ile Val Leu Leu
 35 40 45
 Ile Arg Leu Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Thr
 50 55 60
 Asn Leu Ser Leu Val Asp Val Ser Tyr Ala Thr Ser Val Val Pro Gln
 65 70 75 80
 Leu Leu Ala His Phe Leu Ala Glu His Lys Ala Ile Pro Phe Gln Ser
 85 90 95
 Cys Ala Ala Gln Leu Phe Phe Ser Leu Ala Leu Gly Gly Ile Glu Phe
 100 105 110
 Val Leu Leu Ala Val Met Ala Tyr Asp Arg His Val Ala Val Ser Asp
 115 120 125
 Arg Leu Arg Tyr Ser Ala Ile Met His Gly Gly Leu Cys Ala Arg Leu
 130 135 140
 Ala Ile Thr Ser Trp Val Ser Gly Ser Ile Asn Ser Leu Val Gln Thr
 145 150 155 160
 Ala Ile Thr Phe Gln Leu Pro Met Cys Thr Asn Lys Phe Ile Asp His
 165 170 175
 Ile Ser Cys Glu Leu Leu Ala Val Val Arg Leu Ala Cys Val Asp Thr

```
<210> 1385
<211> 306
<212> PRT
<213> Unknown (H38g302 protein)
```

<400> 1385

688

Ala Ala Ser Val Ile Phe Met Val Val Ala Pro Val Leu Asn Pro Phe
 275 280 285
 Ile Tyr Ser Leu Arg Asn Asn Glu Leu Lys Gly Thr Leu Lys Lys Thr
 290 295 300
 Leu Ser
 305

<210> 1386

<211> 311

<212> PRT

<213> Unknown (H38g303 protein)

<220>

<223> Synthetic construct

<400> 1386

Met Gly Pro Arg Asn Gln Thr Ala Val Ser Glu Phe Leu Leu Met Lys
 1 5 10 15
 Val Thr Glu Asp Pro Glu Leu Lys Leu Ile Pro Phe Ser Leu Phe Leu
 20 25 30
 Ser Met Tyr Leu Val Thr Ile Leu Gly Asn Leu Leu Ile Leu Leu Ala
 35 40 45
 Val Ile Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Leu Leu Phe
 50 55 60
 Asn Leu Ser Phe Thr Asp Ile Cys Leu Thr Thr Thr Thr Val Pro Lys
 65 70 75 80
 Ile Leu Val Asn Ile Gln Ala Gln Asn Gln Ser Ile Thr Tyr Thr Gly
 85 90 95
 Cys Leu Thr Gln Ile Cys Leu Val Leu Val Phe Ala Gly Leu Glu Ser
 100 105 110
 Cys Phe Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His
 115 120 125
 Pro Leu Arg Tyr Thr Val Leu Met Asn Val His Phe Trp Gly Leu Leu
 130 135 140
 Ile Leu Leu Ser Met Phe Met Ser Thr Met Asp Ala Leu Val Gln Ser
 145 150 155 160
 Leu Met Val Leu Gln Leu Ser Phe Cys Lys Asn Val Glu Ile Pro Leu
 165 170 175
 Phe Phe Cys Glu Val Val Gln Val Ile Lys Leu Ala Cys Ser Asp Thr
 180 185 190
 Leu Ile Asn Asn Ile Leu Ile Tyr Phe Ala Ser Ser Val Phe Gly Ala
 195 200 205
 Ile Pro Leu Ser Gly Ile Ile Phe Ser Tyr Ser Gln Ile Val Thr Ser
 210 215 220
 Val Leu Arg Met Pro Ser Ala Arg Gly Lys Tyr Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Gly Cys His Leu Ser Val Phe Ser Leu Phe Tyr Gly Thr Ala Phe
 245 250 255
 Gly Val Tyr Ile Ser Ser Ala Val Ala Glu Ser Ser Arg Ile Thr Ala
 260 265 270
 Val Ala Ser Val Met Tyr Thr Val Val Pro Gln Met Met Asn Pro Phe
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Glu Met Lys Lys Ala Leu Arg Lys Leu
 290 295 300
 Ile Gly Arg Leu Phe Pro Phe
 305 310

<210> 1387

<211> 313

<212> PRT

<213> Unknown (H38g304 protein)

<220>

<223> Synthetic construct

<400> 1387

```

Met Glu Ala Arg Asn Gln Thr Ala Ile Ser Lys Phe Leu Leu Leu Gly
 1           5           10           15
Leu Ile Glu Asp Pro Glu Leu Gln Pro Val Leu Phe Ser Leu Phe Leu
      20           25           30
Ser Met Tyr Leu Val Thr Ile Leu Gly Asn Leu Leu Ile Leu Ala
      35           40           45
Val Ile Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ser
      50           55           60
Asn Leu Ser Phe Leu Asp Ile Cys Leu Ser Thr Thr Thr Ile Pro Lys
      65           70           75           80
Met Leu Val Asn Ile Gln Ala Gln Asn Arg Ser Ile Thr Tyr Ser Gly
      85           90           95
Cys Leu Thr Gln Ile Cys Phe Val Leu Phe Phe Ala Gly Leu Glu Asn
      100          105          110
Cys Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His
      115          120          125
Pro Leu Arg Tyr Thr Val Ile Met Asn Pro Arg Leu Cys Gly Leu Leu
      130          135          140
Ile Leu Leu Ser Leu Leu Thr Ser Val Val Asn Ala Leu Leu Leu Ser
      145          150          155          160
Leu Met Val Leu Arg Leu Ser Phe Cys Thr Asp Leu Glu Ile Pro Leu
      165          170          175
Phe Phe Cys Glu Leu Ala Gln Val Ile Gln Leu Thr Cys Ser Asp Thr
      180          185          190
Leu Ile Asn Asn Ile Leu Ile Tyr Phe Ala Ala Cys Ile Phe Gly Gly
      195          200          205
Val Pro Leu Ser Gly Ile Ile Leu Ser Tyr Thr Gln Ile Thr Ser Cys
      210          215          220
Val Leu Arg Met Pro Ser Ala Ser Gly Lys His Lys Ala Val Ser Thr
      225          230          235          240
Cys Gly Ser His Leu Ser Ile Val Leu Leu Phe Tyr Gly Ala Gly Leu
      245          250          255
Gly Val Tyr Ile Ser Ser Val Val Thr Asp Ser Pro Arg Lys Ala Ala
      260          265          270
Val Ala Ser Val Met Tyr Ser Val Phe Pro Gln Met Val Asn Pro Phe
      275          280          285
Ile Tyr Ser Leu Arg Asn Lys Asp Met Lys Gly Thr Leu Arg Lys Phe
      290          295          300
Ile Gly Arg Ile Pro Ser Leu Leu Trp
      305          310

```

<210> 1388

<211> 313

<212> PRT

<213> Unknown (H38g305 protein)

<220>

<223> Synthetic construct

<400> 1388

```

Met Glu Pro Arg Asn Gln Thr Ser Ala Ser Gln Phe Ile Leu Leu Gly
 1           5           10           15
Leu Ser Glu Lys Pro Glu Gln Glu Thr Leu Leu Phe Ser Leu Phe Phe
      20           25           30
Cys Met Tyr Leu Val Met Val Val Gly Asn Leu Leu Ile Ile Leu Ala
      35           40           45

```

```

Ile Ser Ile Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ala
 50          55          60
Asn Leu Ser Leu Val Asp Phe Cys Leu Ala Thr Asn Thr Ile Pro Lys
 65          70          75          80
Met Leu Val Ser Leu Gln Thr Gly Ser Lys Ala Ile Ser Tyr Pro Cys
          85          90          95
Cys Leu Ile Gln Met Tyr Phe Phe His Phe Phe Gly Ile Val Asp Ser
          100          105          110
Val Ile Ile Ala Met Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His
          115          120          125
Pro Leu His Tyr Ala Lys Ile Met Ser Leu Arg Leu Cys Arg Leu Leu
          130          135          140
Val Gly Ala Leu Trp Ala Phe Ser Cys Phe Ile Ser Leu Thr His Ile
 145          150          155          160
Leu Leu Met Ala Arg Leu Val Phe Cys Gly Ser His Glu Val Pro His
          165          170          175
Tyr Phe Cys Asp Leu Thr Pro Ile Leu Arg Leu Ser Cys Thr Asp Thr
          180          185          190
Ser Val Asn Arg Ile Phe Ile Leu Ile Val Ala Gly Met Val Ile Ala
          195          200          205
Thr Pro Phe Val Cys Ile Leu Ala Ser Tyr Ala Arg Ile Leu Val Ala
          210          215          220
Ile Met Lys Val Pro Ser Ala Gly Gly Arg Lys Lys Ala Phe Ser Thr
 225          230          235          240
Cys Ser Ser His Leu Ser Val Val Ala Leu Phe Tyr Gly Thr Thr Ile
          245          250          255
Gly Val Tyr Leu Cys Pro Ser Ser Val Leu Thr Thr Val Lys Glu Lys
          260          265          270
Ala Ser Ala Val Met Tyr Thr Ala Val Thr Pro Met Leu Asn Pro Phe
          275          280          285
Ile Tyr Ser Leu Arg Asn Arg Asp Leu Lys Gly Ala Leu Arg Lys Leu
          290          295          300
Val Asn Arg Lys Ile Thr Ser Ser Ser
305          310

```

<210> 1389

<211> 98

<212> PRT

<213> Unknown (H38g306 protein)

<220>

<223> Synthetic construct

<400> 1389

```

Met Ser Ala Ser Ser Ile Thr Ser Thr His Pro Thr Ser Phe Leu Leu
 1          5          10          15
Met Gly Ile Pro Gly Leu Glu His Leu His Ile Trp Ile Ser Ile Pro
          20          25          30
Phe Ser Ala Tyr Thr Leu Ala Leu Leu Gly Asn Cys Thr Leu Leu Leu
          35          40          45
Ile Ile Gln Ala Asp Ala Ala Leu His Glu Pro Met Tyr Leu Phe Leu
          50          55          60
Ala Met Leu Ala Ala Ile Asp Gln Leu Ser Ile Ser Ser Ala Leu Pro
 65          70          75          80
Pro Gly Gln Thr Val Phe Trp Phe Thr Asp Gln Lys Asn Lys Pro Phe
          85          90          95
Ala Gly

```

<210> 1390

<211> 320

<212> PRT

<213> Unknown (H38g307 protein)

<220>

<223> Synthetic construct

<400> 1390

```

Met Pro Ser Ala Ser Ala Met Ile Ile Phe Asn Leu Ser Ser Tyr Asn
 1           5           10           15
Pro Gly Pro Phe Ile Leu Val Gly Ile Pro Gly Leu Glu Gln Phe His
          20           25           30
Val Trp Ile Gly Ile Pro Phe Cys Ile Ile Tyr Ile Val Ala Val Val
          35           40           45
Gly Asn Cys Ile Leu Leu Tyr Leu Ile Val Val Glu His Ser Leu His
          50           55           60
Glu Pro Met Phe Phe Phe Leu Ser Met Leu Ala Met Thr Asp Leu Ile
 65           70           75           80
Leu Ser Thr Ala Gly Val Pro Lys Ala Leu Ser Ile Phe Trp Leu Gly
          85           90           95
Ala Arg Glu Ile Thr Phe Pro Gly Cys Leu Thr Gln Met Phe Phe Leu
          100          105          110
His Tyr Asn Phe Val Leu Asp Ser Ala Ile Leu Met Ala Met Ala Phe
          115          120          125
Asp His Tyr Val Ala Ile Cys Ser Pro Leu Arg Tyr Thr Thr Ile Leu
          130          135          140
Thr Pro Lys Thr Ile Ile Lys Ser Ala Met Gly Ile Ser Phe Arg Ser
          145          150          155          160
Phe Cys Ile Ile Leu Pro Asp Val Phe Leu Leu Thr Cys Leu Pro Phe
          165          170          175
Cys Arg Thr Arg Ile Ile Pro His Thr Tyr Cys Glu His Ile Gly Val
          180          185          190
Ala Gln Leu Ala Cys Ala Asp Ile Ser Ile Asn Phe Trp Tyr Gly Phe
          195          200          205
Cys Val Pro Ile Met Thr Val Ile Ser Asp Val Ile Leu Ile Ala Val
          210          215          220
Ser Tyr Ala His Ile Leu Cys Ala Val Phe Gly Leu Pro Ser Gln Glu
          225          230          235          240
Ala Cys Gln Lys Ala Leu Gly Thr Cys Gly Ser His Val Cys Val Ile
          245          250          255
Leu Met Phe Tyr Thr Pro Ala Phe Phe Ser Ile Leu Ala His Arg Phe
          260          265          270
Gly His Asn Val Ser Arg Thr Phe His Ile Met Phe Ala Asn Leu Tyr
          275          280          285
Ile Val Ile Pro Pro Ala Leu Asn Pro Met Val Tyr Gly Val Lys Thr
          290          295          300
Lys Gln Ile Arg Asp Lys Val Ile Leu Leu Phe Ser Lys Gly Thr Gly
          305          310          315          320

```

<210> 1391

<211> 312

<212> PRT

<213> Unknown (H38g308 protein)

<220>

<223> Synthetic construct

<400> 1391

```

Met Ser Gly Thr Asn Gln Ser Ser Val Ser Glu Phe Leu Leu Leu Gly
 1           5           10           15
Leu Ser Arg Gln Pro Gln Gln Gln His Leu Leu Phe Val Phe Phe Leu
          20           25           30

```

```

Ser Met Tyr Leu Ala Thr Val Leu Gly Asn Leu Leu Ile Ile Leu Ser
   35           40           45
Val Ser Ile Asp Ser Cys Leu His Thr Pro Met Tyr Phe Phe Leu Ser
   50           55           60
Asn Leu Ser Phe Val Asp Ile Cys Phe Ser Phe Thr Thr Val Pro Lys
   65           70           75           80
Met Leu Ala Asn His Ile Leu Glu Thr Gln Thr Ile Ser Phe Cys Gly
           85           90           95
Cys Leu Thr Gln Met Tyr Phe Val Phe Met Phe Val Asp Met Asp Asn
           100          105          110
Phe Leu Leu Ala Val Met Ala Tyr Asp His Phe Val Ala Val Cys His
           115          120          125
Pro Leu His Tyr Thr Ala Lys Met Thr His Gln Leu Cys Ala Leu Leu
           130          135          140
Val Ala Gly Leu Trp Val Val Ala Asn Leu Asn Val Leu Leu His Thr
           145          150          155          160
Leu Leu Met Ala Pro Leu Ser Phe Cys Ala Asp Asn Ala Ile Thr His
           165          170          175
Phe Phe Cys Asp Val Thr Pro Leu Leu Lys Leu Ser Cys Ser Asp Thr
           180          185          190
His Leu Asn Glu Val Ile Ile Leu Ser Glu Gly Ala Leu Val Met Ile
           195          200          205
Thr Pro Phe Leu Cys Ile Leu Ala Ser Tyr Met His Ile Thr Cys Thr
           210          215          220
Val Leu Lys Val Pro Ser Thr Lys Gly Arg Trp Lys Ala Phe Ser Thr
           225          230          235          240
Cys Gly Ser His Leu Ala Val Val Leu Leu Phe Tyr Ser Thr Ile Ile
           245          250          255
Ala Val Tyr Phe Asn Pro Leu Ser Ser His Ser Ala Glu Lys Asp Thr
           260          265          270
Met Ala Thr Val Leu Tyr Thr Val Thr Pro Met Leu Asn Pro Phe
           275          280          285
Ile Tyr Ser Leu Arg Asn Arg Tyr Leu Lys Gly Ala Leu Lys Lys Val
           290          295          300
Val Gly Arg Val Val Phe Ser Val
           305          310

```

<210> 1392

<211> 254

<212> PRT

<213> Unknown (H38g309 protein)

<220>

<223> Synthetic construct

<400> 1392

```

Met Tyr Phe Phe Leu Arg Gln Leu Ser Val Val Glu Leu Phe Tyr Thr
   1           5           10          15
Thr Asp Ile Val Pro Arg Thr Leu Ala Asn Leu Gly Ser Pro His Pro
           20           25           30
Gln Ala Ile Ser Phe Gln Gly Cys Ala Ala His Met Tyr Val Phe Ile
           35           40           45
Val Leu Gly Ile Ser Glu Cys Cys Leu Leu Thr Ala Met Ala Tyr Asp
           50           55           60
Arg Tyr Val Ala Ile Cys Gln Pro Leu Arg Tyr Ser Thr Leu Leu Ser
           65           70           75           80
Pro Arg Ala Cys Met Ala Met Val Gly Thr Ser Trp Leu Thr Gly Ile
           85           90           95
Ile Thr Ala Thr Thr His Ala Ser Leu Ile Phe Ser Leu Pro Phe Arg
           100          105          110
Ser His Pro Ile Ile Pro His Phe Leu Cys Asp Ile Leu Pro Val Leu

```

```

      115              120              125
Arg  Leu  Ala  Ser  Ala  Gly  Lys  His  Arg  Ser  Glu  Ile  Ser  Val  Met  Thr
 130              135              140
Ala  Thr  Ile  Val  Phe  Ile  Met  Ile  Pro  Phe  Ser  Leu  Ile  Val  Thr  Ser
145              150              155              160
Tyr  Ile  Arg  Ile  Leu  Gly  Ala  Ile  Leu  Ala  Met  Ala  Ser  Thr  Gln  Ser
      165              170              175
Arg  Arg  Lys  Val  Phe  Ser  Thr  Cys  Ser  Ser  His  Leu  Leu  Val  Val  Ser
      180              185              190
Leu  Phe  Phe  Gly  Thr  Ala  Ser  Ile  Thr  Tyr  Ile  Arg  Pro  Gln  Ala  Gly
      195              200              205
Ser  Ser  Val  Thr  Thr  Asp  Arg  Val  Leu  Ser  Leu  Phe  Tyr  Thr  Val  Ile
      210              215              220
Thr  Pro  Met  Leu  Asn  Pro  Ile  Ile  Tyr  Thr  Leu  Arg  Asn  Lys  Asp  Val
225              230              235              240
Arg  Arg  Ala  Leu  Arg  His  Leu  Val  Lys  Arg  Gln  Arg  Pro  Ser
      245              250

```

<210> 1393

<211> 333

<212> PRT

<213> Unknown (H38g310 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(333)

<223> Xaa = Any Amino Acid

<400> 1393

```

Met  Asp  Gly  Glu  Asn  His  Ser  Val  Val  Ser  Glu  Phe  Leu  Phe  Leu  Gly
 1              5              10              15
Leu  Thr  His  Ser  Trp  Glu  Ile  Gln  Leu  Leu  Leu  Leu  Val  Phe  Ser  Ser
      20              25              30
Val  Leu  Tyr  Val  Ala  Ser  Ile  Thr  Gly  Asn  Ile  Leu  Ile  Val  Phe  Ser
      35              40              45
Val  Thr  Thr  Asp  Pro  His  Leu  His  Ser  Pro  Met  Tyr  Phe  Leu  Leu  Val
      50              55              60
Ser  Leu  Ser  Phe  Ile  Asp  Leu  Gly  Ala  Cys  Ser  Val  Thr  Ser  Pro  Lys
65              70              75              80
Met  Ile  Tyr  Asp  Leu  Phe  Arg  Lys  Arg  Lys  Val  Ile  Ser  Phe  Gly  Gly
      85              90              95
Cys  Ile  Ala  Gln  Ile  Phe  Phe  Ile  His  Val  Ile  Gly  Gly  Val  Glu  Met
      100              105              110
Val  Leu  Leu  Ile  Ala  Met  Ala  Phe  Asp  Ser  Tyr  Val  Ala  Leu  Cys  Lys
      115              120              125
Pro  Leu  His  Tyr  Leu  Thr  Ile  Met  Ser  Pro  Arg  Met  Cys  Leu  Ser  Phe
      130              135              140
Leu  Ala  Val  Ala  Trp  Thr  Leu  Val  Val  Ser  His  Ser  Leu  Phe  Gln  Leu
145              150              155              160
Ala  Phe  Leu  Val  Asn  Leu  Pro  Phe  Cys  Gly  Pro  Asn  Val  Leu  Asp  Ser
      165              170              175
Phe  Tyr  Cys  Asp  Leu  Pro  Gln  Leu  Leu  Arg  Leu  Ala  Cys  Thr  Asp  Thr
      180              185              190
Tyr  Arg  Leu  Gln  Phe  Met  Val  Thr  Val  Asn  Ser  Gly  Phe  Ile  Cys  Val
      195              200              205
Gly  Thr  Phe  Phe  Ile  Leu  Leu  Ile  Ser  Tyr  Val  Phe  Ile  Leu  Phe  Thr
      210              215              220
Val  Trp  Lys  His  Ser  Ser  Gly  Gly  Ser  Ser  Lys  Ala  Leu  Ser  Thr  Leu
225              230              235              240

```

Ser Ala His Ser Thr Ala Val Leu Leu Phe Phe Gly Pro Pro Met Phe
 245 250 255
 Val Tyr Thr Trp Pro His Pro Asn Ser Gln Met Asp Lys Phe Leu Ala
 260 265 270
 Ile Phe Asp Ala Val Leu Thr Pro Phe Leu Asn Pro Val Val Tyr Thr
 275 280 285
 Phe Arg Asn Lys Glu Met Lys Ala Ala Ile Lys Arg Val Cys Lys Gln
 290 295 300
 Leu Val Ile Tyr Lys Lys Ile Ser Xaa Met Ile Gln Xaa Ala Leu Leu
 305 310 315 320
 Val Lys His Asp Met Ala Leu Cys Phe Phe Leu Xaa Tyr
 325 330

<210> 1394

<211> 311

<212> PRT

<213> Unknown (H38g311 protein)

<220>

<223> Synthetic construct

<400> 1394

Met Glu Glu Tyr Asn Thr Ser Ser Thr Asp Phe Thr Phe Met Gly Leu
 1 5 10 15
 Phe Asn Arg Lys Glu Thr Ser Gly Leu Ile Phe Ala Ile Ile Ser Ile
 20 25 30
 Ile Phe Phe Thr Ala Leu Met Ala Asn Gly Val Met Ile Phe Leu Ile
 35 40 45
 Gln Thr Asp Leu Arg Leu His Thr Pro Met Tyr Phe Leu Leu Ser His
 50 55 60
 Leu Ser Leu Ile Asp Met Tyr Ile Ser Thr Ile Val Pro Lys Met
 65 70 75 80
 Leu Val Asn Tyr Leu Leu Asp Gln Arg Thr Ile Ser Phe Val Gly Cys
 85 90 95
 Thr Ala Gln His Phe Leu Tyr Leu Thr Leu Val Gly Ala Glu Phe Phe
 100 105 110
 Leu Leu Gly Leu Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro
 115 120 125
 Leu Arg Tyr Pro Val Leu Met Ser Arg Arg Val Cys Trp Met Ile Ile
 130 135 140
 Ala Gly Ser Trp Phe Gly Gly Ser Leu Asp Gly Phe Leu Leu Thr Pro
 145 150 155 160
 Ile Thr Met Ser Phe Pro Phe Cys Asn Ser Arg Glu Ile Asn His Phe
 165 170 175
 Phe Cys Glu Ala Pro Ala Val Leu Lys Leu Ala Cys Ala Asp Thr Ala
 180 185 190
 Leu Tyr Glu Thr Val Met Tyr Val Cys Cys Val Leu Met Leu Leu Ile
 195 200 205
 Pro Phe Ser Val Val Leu Ala Ser Tyr Ala Arg Ile Leu Thr Thr Val
 210 215 220
 Gln Cys Met Ser Ser Val Glu Gly Arg Lys Lys Ala Phe Ala Thr Cys
 225 230 235 240
 Ser Ser His Met Thr Val Val Ser Leu Phe Tyr Gly Ala Ala Met Tyr
 245 250 255
 Thr Tyr Met Leu Pro His Ser Tyr His Lys Pro Ala Gln Asp Lys Val
 260 265 270
 Leu Ser Val Phe Tyr Thr Ile Leu Thr Pro Met Leu Asn Pro Leu Ile
 275 280 285
 Tyr Ser Leu Arg Asn Lys Asp Val Thr Gly Ala Leu Lys Arg Ala Leu
 290 295 300
 Gly Arg Phe Lys Gly Pro Gln

305

310

<210> 1395

<211> 295

<212> PRT

<213> Unknown (H38g312 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(295)

<223> Xaa = Any Amino Acid

<400> 1395

Ile	Gln	Cys	Lys	Gly	Xaa	Xaa	Lys	Xaa	Ile	Lys	Thr	Phe	Ser	Val	Thr
1				5					10					15	
Pro	Ile	Leu	Asn	Gly	Asn	Arg	Glu	Ile	Ala	Arg	Phe	Leu	Ser	Asn	Leu
			20					25					30		
Ser	Leu	Ala	Gly	Ile	Gly	Phe	Pro	Ser	Thr	Ile	Val	Ser	Lys	Met	Ile
		35					40					45			
Val	Asp	Ile	Gln	Ser	His	Ser	Arg	Val	Ile	Ser	Tyr	Ala	Gly	Cys	Leu
	50					55					60				
Thr	Gln	Val	Ser	Leu	Phe	Ala	Val	Phe	Gly	Cys	Met	Glu	Asp	Met	Leu
65					70					75				80	
Leu	Ser	Val	Met	Ala	Tyr	Asp	Arg	Phe	Val	Asp	Ile	Cys	His	Pro	Leu
			85						90					95	
Asp	Tyr	Pro	Val	Ile	Met	Asn	Pro	Cys	Phe	Cys	Gly	Phe	Leu	Val	Leu
			100					105					110		
Leu	Ser	Phe	Phe	Leu	Ser	Leu	Leu	Asp	Ser	Gln	Leu	His	Asn	Trp	Ile
		115					120					125			
Ala	Leu	Gln	Ile	Thr	Cys	Phe	Lys	Asp	Val	Glu	Ile	Pro	Asn	Phe	Phe
	130					135					140				
Cys	Asp	Pro	Ser	Gln	Leu	Pro	His	Leu	Ala	Cys	Cys	Asp	Thr	Phe	Thr
145					150					155				160	
Asn	Asp	Ile	Val	Met	Tyr	Phe	Leu	Ala	Ala	Ile	Phe	Gly	Phe	Leu	Pro
				165					170					175	
Ile	Ser	Gly	Thr	Phe	Phe	Ser	Tyr	Tyr	Lys	Ile	Val	Ser	Ser	Ile	Leu
			180					185					190		
Arg	Val	Ser	Ser	Ser	Gly	Gly	Lys	Tyr	Lys	Ala	Phe	Ser	Thr	Cys	Gly
		195					200					205			
Ser	His	Leu	Ser	Val	Val	Cys	Leu	Phe	Tyr	Gly	Thr	Gly	Phe	Gly	Gly
	210					215					220				
Asp	Leu	Ser	Ser	Asp	Met	Ser	Ser	Tyr	Pro	Arg	Lys	Gly	Ala	Val	Ala
225					230					235				240	
Ser	Val	Met	Tyr	Thr	Val	Val	Thr	Pro	Met	Leu	Asn	Pro	Phe	Ile	Tyr
				245					250					255	
Ser	Arg	Asn	Arg	Glu	Ile	Lys	Ser	Ala	Leu	Arg	Gln	Leu	His	Cys	Arg
			260					265					270		
Ile	Val	Xaa	Ser	His	Phe	Leu	Ile	Ile	Cys	Ser	Ile	Pro	Ser	Val	Val
		275					280						285		
Xaa	Val	Arg	Lys	Gly	Ser	Lys									
	290					295									

<210> 1396

<211> 314

<212> PRT

<213> Unknown (H38g313 protein)

<220>

<223> Synthetic construct

<400> 1396

```

Met Thr Leu Gly Ser Leu Gly Asn Ser Ser Ser Val Ser Ala Thr
 1           5           10           15
Phe Leu Leu Ser Gly Ile Pro Gly Leu Glu Arg Met His Ile Trp Ile
      20           25           30
Ser Ile Pro Leu Cys Phe Met Tyr Leu Val Ser Ile Pro Gly Asn Cys
      35           40           45
Thr Ile Leu Phe Ile Ile Lys Thr Glu Arg Ser Leu His Glu Pro Met
      50           55           60
Tyr Leu Phe Leu Ser Met Leu Ala Leu Ile Asp Leu Gly Leu Ser Leu
      65           70           75           80
Cys Thr Leu Pro Thr Val Leu Gly Ile Phe Trp Val Gly Ala Arg Glu
      85           90           95
Ile Ser His Asp Ala Cys Phe Ala Gln Leu Phe Phe Ile His Cys Phe
      100          105          110
Ser Phe Leu Glu Ser Ser Val Leu Leu Ser Met Ala Phe Asp Arg Phe
      115          120          125
Val Ala Ile Cys His Pro Leu His Tyr Val Ser Ile Leu Thr Asn Thr
      130          135          140
Val Ile Gly Arg Ile Gly Leu Val Ser Leu Gly Arg Ser Val Ala Leu
      145          150          155          160
Ile Phe Pro Leu Pro Phe Met Leu Lys Arg Phe Pro Tyr Cys Gly Ser
      165          170          175
Pro Val Leu Ser His Ser Tyr Cys Leu His Gln Glu Val Met Lys Leu
      180          185          190
Ala Cys Ala Asp Met Lys Ala Asn Ser Ile Tyr Gly Met Phe Val Ile
      195          200          205
Val Ser Thr Val Gly Ile Asp Ser Leu Leu Ile Leu Phe Ser Tyr Ala
      210          215          220
Leu Ile Leu Arg Thr Val Leu Ser Ile Ala Ser Arg Ala Glu Arg Phe
      225          230          235          240
Lys Ala Leu Asn Thr Cys Val Ser His Ile Cys Ala Val Leu Leu Phe
      245          250          255
Tyr Thr Pro Met Ile Gly Leu Ser Val Ile His Arg Phe Gly Lys Gln
      260          265          270
Ala Pro His Leu Val Gln Val Val Met Gly Phe Met Tyr Leu Leu Phe
      275          280          285
Pro Pro Val Met Asn Pro Ile Val Tyr Ser Val Lys Thr Lys Gln Ile
      290          295          300
Arg Asp Arg Val Thr His Ala Phe Cys Tyr
305          310

```

<210> 1397

<211> 330

<212> PRT

<213> Unknown (H38g314 protein)

<220>

<223> Synthetic construct

<400> 1397

```

Met Gly Leu Phe Arg Gln Ser Lys His Pro Met Ala Asn Ile Thr Trp
 1           5           10           15
Met Ala Asn His Thr Gly Trp Ser Asp Phe Ile Leu Leu Gly Leu Phe
      20           25           30
Arg Gln Ser Lys His Pro Ala Leu Cys Val Val Ile Phe Val Val
      35           40           45
Phe Leu Met Ala Leu Ser Gly Asn Ala Val Leu Ile Leu Leu Ile His
      50           55           60
Cys Asp Ala His Leu His Thr Pro Met Tyr Phe Phe Ile Ser Gln Leu

```

```

65          70          75          80
Ser Leu Met Asp Met Ala Tyr Ile Ser Val Thr Val Pro Lys Met Leu
      85
Leu Asp Gln Val Met Gly Val Asn Lys Ile Ser Ala Pro Glu Cys Gly
      100      105      110
Met Gln Met Phe Phe Tyr Val Thr Leu Ala Gly Ser Glu Phe Phe Leu
      115      120      125
Leu Ala Thr Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu
      130      135      140
Arg Tyr Pro Val Leu Met Asn His Arg Val Cys Leu Phe Leu Ser Ser
145      150      155      160
Gly Cys Trp Phe Leu Gly Ser Val Asp Gly Phe Thr Phe Thr Pro Ile
      165      170      175
Thr Met Thr Phe Pro Phe Arg Gly Ser Arg Glu Ile His His Phe Phe
      180      185      190
Cys Glu Val Pro Ala Val Leu Asn Leu Ser Cys Ser Asp Thr Ser Leu
      195      200      205
Tyr Glu Ile Phe Met Tyr Leu Cys Cys Val Leu Met Leu Leu Ile Pro
      210      215      220
Val Val Ile Ile Ser Ser Ser Tyr Leu Leu Ile Leu Leu Thr Ile His
225      230      235      240
Gly Met Asn Ser Ala Glu Gly Arg Lys Lys Ala Phe Ala Thr Cys Ser
      245      250      255
Ser His Leu Thr Val Val Ile Leu Phe Tyr Gly Ala Ala Ile Tyr Thr
      260      265      270
Tyr Met Leu Pro Ser Ser Tyr His Thr Pro Glu Lys Asp Met Met Val
      275      280      285
Ser Val Phe Tyr Thr Ile Leu Thr Pro Val Val Asn Pro Leu Ile Tyr
      290      295      300
Ser Leu Arg Asn Lys Asp Val Met Gly Ala Leu Lys Lys Met Leu Thr
305      310      315      320
Val Glu Pro Ala Phe Gln Lys Ala Met Glu
      325      330

```

<210> 1398

<211> 197

<212> PRT

<213> Unknown (H38g315 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(197)

<223> Xaa = Any Amino Acid

<400> 1398

```

Ala Ala Met Ala Xaa Asp Arg Tyr Ile Ala Ile Cys Asn Pro Leu Leu
1          5          10          15
Tyr Thr Val Ile Met Ser Lys Lys Val Cys Cys Gln Leu Ala Ile Gly
      20      25      30
Ala Phe Leu Gly Gly Thr Met Ser Ile Ile His Thr Thr Asn Thr
      35      40      45
Phe His Leu Ser Phe Cys Ser Arg Asp Ile Asn His Phe Phe Cys Asp
      50      55      60
Ile Ser Pro Leu Phe Ser Leu Ser Cys Thr Asp Thr Tyr Met His Asp
65      70      75      80
Ile Ile Leu Val Val Phe Ala Ser Phe Val Glu Ala Ile Cys Leu Leu
      85      90      95
Ser Val Leu Leu Ser Tyr Val Phe Ile Met Ala Ala Ile Leu Arg Thr
100      105      110

```

Gly Ser Val Glu Gly Arg Arg Arg Gly Phe Ser Thr Cys Ala Ser His
 115 120 125
 Leu Thr Val Val Thr Met Tyr His Gly Thr Leu Ile Phe Ile Tyr Leu
 130 135 140
 Arg Pro Ser Thr Gly His Ser Leu Asp Ile Asp Lys Val Thr Ser Val
 145 150 155 160
 Phe Tyr Thr Leu Ile Ile Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu
 165 170 175
 Arg Asn Lys Asp Val Lys Asn Ala Phe Arg Lys Val Ile Gly Arg Lys
 180 185 190
 Leu Leu Pro Xaa Gly
 195

<210> 1399

<211> 313

<212> PRT

<213> Unknown (H38g316 protein)

<220>

<223> Synthetic construct

<400> 1399

Met Met Thr Leu Lys Asn Cys Thr Val Phe Thr Asp Phe Ile Phe Leu
 1 5 10 15
 Gly Leu Ser Gly Thr Gln Asp Ile Gln Gln Gly Leu Phe Val Leu Phe
 20 25 30
 Phe Leu Ile Tyr Gly Ile Thr Val Ile Val Asn Leu Gly Met Ile Leu
 35 40 45
 Leu Ile Lys Met Asp Leu Arg Leu His Thr Pro Val Tyr Tyr Phe Leu
 50 55 60
 Ser Asn Leu Ser Phe Cys Asp Val Cys Tyr Ser Ser Val Ser Pro
 65 70 75 80
 Arg Met Leu Ala Asp Phe Leu Ser Asp Gln Lys Trp Ile Pro Tyr Asn
 85 90 95
 Leu Cys Ala Ile Gln Met Tyr Leu Phe Gly Val Phe Ala Asp Val Glu
 100 105 110
 Cys Leu Met Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys
 115 120 125
 Asn Pro Leu Leu Tyr Thr Ile Thr Met Pro Arg Arg Ile Cys Thr Gln
 130 135 140
 Leu Val Ala Leu Ala Tyr Val Val Gly Leu Val Asp Ser Ala Ile His
 145 150 155 160
 Thr Cys Cys Thr Phe Arg Leu Ser Phe Cys Asn Ser Asn Val Ile Asn
 165 170 175
 His Phe Phe Cys Asp Ile Pro Pro Leu Ala Leu Asn Pro Thr Ile
 180 185 190
 Asn Ser Ile Asn Glu Ile Val Met Phe Thr Phe Val Gly Cys Val Ala
 195 200 205
 Gly Cys Ser Ile Val Thr Val Phe Leu Ser Tyr Ser Tyr Ile Ile Ile
 210 215 220
 Thr Ile Leu Lys Met Ser Ser Ala Glu Gly Arg Arg Lys Ala Phe Ser
 225 230 235 240
 Thr Cys Thr Ser His Leu Met Ala Val Ala Val Phe His Gly Thr Leu
 245 250 255
 Leu Phe Met Tyr Phe Arg Pro Ser Ser Ser Tyr Ser Met Glu Thr Asp
 260 265 270
 Lys Met Ala Ser Val Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro
 275 280 285
 Leu Ile Tyr Ser Leu Arg Asn Arg Asp Val Lys Gly Ala Leu Lys Lys
 290 295 300
 Ala Ile Ser Thr Lys Leu Tyr Ser Val

305

310

<210> 1400

<211> 323

<212> PRT

<213> Unknown (H38g317 protein)

<220>

<223> Synthetic construct

<400> 1400

```

Met Ser Thr Leu Pro Thr Gln Ile Ala Pro Asn Ser Ser Thr Ser Met
 1           5           10           15
Ala Pro Thr Phe Leu Leu Val Gly Met Pro Gly Leu Ser Gly Ala Pro
      20           25           30
Ser Trp Trp Thr Leu Pro Leu Ile Ala Val Tyr Leu Leu Ser Ala Leu
      35           40           45
Gly Asn Gly Thr Ile Leu Trp Ile Ile Ala Leu Gln Pro Ala Leu His
      50           55           60
Arg Pro Met His Phe Phe Leu Phe Leu Leu Ser Val Ser Asp Ile Gly
      65           70           75           80
Leu Val Thr Ala Leu Met Pro Thr Leu Leu Gly Ile Ala Leu Ala Gly
      85           90           95
Ala His Thr Val Pro Ala Ser Ala Cys Leu Leu Gln Met Val Phe Ile
      100          105          110
His Val Phe Ser Val Met Glu Ser Ser Val Leu Leu Ala Met Ser Ile
      115          120          125
Asp Arg Ala Leu Ala Ile Cys Arg Pro Leu His Tyr Pro Ala Leu Leu
      130          135          140
Thr Asn Gly Val Ile Ser Lys Ile Ser Leu Ala Ile Ser Phe Arg Cys
      145          150          155          160
Leu Gly Leu His Leu Pro Leu Pro Phe Leu Leu Ala Tyr Met Pro Tyr
      165          170          175
Cys Leu Pro Gln Val Leu Thr His Ser Tyr Cys Leu His Pro Asp Val
      180          185          190
Ala Arg Leu Ala Cys Pro Glu Ala Trp Gly Ala Ala Tyr Ser Leu Phe
      195          200          205
Val Val Leu Ser Ala Met Gly Leu Asp Pro Leu Leu Ile Phe Phe Ser
      210          215          220
Tyr Gly Leu Ile Gly Lys Val Leu Gln Gly Val Glu Ser Arg Glu Asp
      225          230          235          240
Arg Trp Lys Ala Gly Gln Thr Cys Ala Ala His Leu Ser Ala Val Leu
      245          250          255
Leu Phe Tyr Ile Pro Met Ile Leu Leu Ala Leu Ile Asn His Pro Glu
      260          265          270
Leu Pro Ile Thr Gln His Thr His Thr Leu Leu Ser Tyr Val His Phe
      275          280          285
Leu Leu Pro Pro Leu Ile Asn Pro Ile Leu Tyr Ser Val Lys Met Lys
      290          295          300
Glu Ile Arg Lys Arg Ile Leu Asn Arg Leu Gln Pro Arg Lys Val Gly
      305          310          315          320
Gly Ala Gln

```

<210> 1401

<211> 128

<212> PRT

<213> Unknown (H38g318 protein)

<220>

<223> Synthetic construct

<221> VARIANT
 <222> (1)...(128)
 <223> Xaa = Any Amino Acid

<400> 1401
 Ser Arg Ser Asp Thr Gln Val Asn Glu Leu Val Leu Phe Thr Val Phe
 1 5 10 15
 Gly Phe Ile Glu Leu Ser Thr Ile Ser Gly Val Phe Ile Ser Tyr Cys
 20 25 30
 Tyr Ile Ile Leu Ser Val Leu Glu Ile His Ser Ala Glu Gly Arg Phe
 35 40 45
 Lys Ala Leu Ser Thr Cys Thr Ser His Leu Ser Ala Val Ala Ile Phe
 50 55 60
 Gln Gly Thr Leu Leu Phe Met Tyr Phe Arg Pro Ser Ser Ser Tyr Ser
 65 70 75 80
 Leu Asp Gln Asp Lys Met Thr Ser Leu Phe Tyr Thr Leu Val Val Pro
 85 90 95
 Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Glu
 100 105 110
 Ala Leu Lys Lys Leu Lys Asn Lys Ile Leu Phe Xaa Gly Asn Ser Lys
 115 120 125

<210> 1402
 <211> 316
 <212> PRT
 <213> Unknown (H38g319 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(316)
 <223> Xaa = Any Amino Acid

<400> 1402
 Met Phe Leu Leu Asn Thr Ser Glu Val Glu Val Ser Thr Phe Leu Leu
 1 5 10 15
 Ile Gly Ile Pro Gly Leu Glu His Ala His Ile Trp Ile Ser Ile Pro
 20 25 30
 Ile Cys Leu Met Tyr Leu Met Ala Ile Leu Gly Asn Cys Thr Ile Leu
 35 40 45
 Phe Val Ile Arg Thr Glu His Ser Leu Gln Glu Pro Met Tyr Tyr Phe
 50 55 60
 Leu Ser Met Leu Ala Leu Ser Asp Leu Gly Leu Ser Phe Ser Ser Leu
 65 70 75 80
 Pro Thr Met Leu Arg Ile Phe Leu Phe Asn Asn Met Gly Ile Ser Ala
 85 90 95
 Asp Thr Cys Ile Ala Gln Glu Phe Phe Ile His Gly Phe Thr Asp Met
 100 105 110
 Glu Ser Ser Val Leu Leu Ile Met Ser Phe Asp His Leu Val Ala Ile
 115 120 125
 Cys Asn Pro Leu Arg Tyr Ser Ser Ile Leu Thr Ser Phe Arg Val Leu
 130 135 140
 Gln Ile Gly Leu Ala Phe Ala Ile Lys Ser Ile Leu Leu Val Leu Pro
 145 150 155 160
 Pro Phe Thr Leu Lys Arg Leu Arg Tyr Cys Asn Lys His Leu Leu Ser
 165 170 175
 His Ser Tyr Cys Leu His Gln Asp Val Met Lys Leu Ala Cys Ser Asp
 180 185 190
 Asn Arg Val Asn Phe Tyr Tyr Gly Leu Phe Val Ala Leu Cys Met Met

		195					200					205						
Ser	Asp	Ser	Val	Phe	Ile	Ala	Ile	Ser	Tyr	Met	Leu	Phe	Ile	Leu	Lys			
	210					215					220							
Thr	Val	Leu	Gly	Ile	Ala	Ser	His	Gly	Glu	Cys	Leu	Glu	Ala	Leu	Asp			
225					230					235					240			
Thr	Cys	Val	Ser	His	Ile	Cys	Ala	Val	Leu	Val	Phe	Tyr	Val	Pro	Ile			
				245					250					255				
Ile	Thr	Leu	Ala	Thr	Met	Arg	Arg	Phe	Ala	Lys	His	Lys	Ser	Pro	Leu			
			260					265					270					
Ala	Met	Ile	Leu	Ile	Ala	Asp	Ala	Phe	Leu	Leu	Val	Pro	Pro	Leu	Met			
		275					280					285						
Asn	Pro	Ile	Val	Tyr	Cys	Val	Lys	Thr	Arg	Gln	Ile	Arg	Val	Lys	Val			
	290					295					300							
Leu	Glu	Lys	Leu	Ala	Leu	Lys	Pro	Lys	Xaa	Trp	Gly							
305					310					315								

<210> 1403

<211> 314

<212> PRT

<213> Unknown (H38g320 protein)

<220>

<223> Synthetic construct

<400> 1403

Met 1	Met	Ala	Ser	Glu 5	Arg	Asn	Gln	Ser	Ser 10	Thr	Pro	Thr	Phe	Ile 15	Leu
Leu	Gly	Phe	Ser	Glu	Tyr	Pro	Glu	Ile	Gln	Val	Pro	Leu	Phe	Leu	Val
			20					25					30		
Phe	Leu	Phe	Val	Tyr	Thr	Val	Thr	Val	Val	Gly	Asn	Leu	Gly	Met	Ile
			35				40					45			
Ile	Ile	Ile	Arg	Leu	Asn	Ser	Lys	Leu	His	Thr	Ile	Met	Cys	Phe	Phe
	50					55					60				
Leu	Ser	His	Leu	Ser	Leu	Thr	Asp	Phe	Cys	Phe	Ser	Thr	Val	Val	Thr
65					70					75					80
Pro	Lys	Leu	Leu	Glu	Asn	Leu	Val	Val	Glu	Tyr	Arg	Thr	Ile	Ser	Phe
				85					90					95	
Ser	Gly	Cys	Ile	Met	Gln	Phe	Cys	Phe	Ala	Cys	Ile	Phe	Gly	Val	Thr
			100					105					110		
Glu	Thr	Phe	Met	Leu	Ala	Ala	Met	Ala	Tyr	Asp	Arg	Phe	Val	Ala	Val
			115				120					125			
Cys	Lys	Pro	Leu	Leu	Tyr	Thr	Thr	Ile	Met	Ser	Gln	Lys	Leu	Cys	Ala
	130					135					140				
Leu	Leu	Val	Ala	Gly	Ser	Tyr	Thr	Trp	Gly	Ile	Val	Cys	Ser	Leu	Ile
145					150					155					160
Leu	Thr	Tyr	Phe	Leu	Leu	Asp	Leu	Ser	Phe	Cys	Glu	Ser	Thr	Phe	Ile
				165					170					175	
Asn	Asn	Phe	Ile	Cys	Asp	His	Ser	Val	Ile	Val	Ser	Ala	Ser	Tyr	Ser
			180					185					190		
Asp	Pro	Tyr	Ile	Ser	Gln	Arg	Leu	Cys	Phe	Ile	Ile	Ala	Ile	Phe	Asn
			195				200					205			
Glu	Val	Ser	Ser	Leu	Ile	Ile	Ile	Leu	Thr	Ser	Tyr	Met	Leu	Ile	Phe
	210					215					220				
Thr	Thr	Ile	Met	Lys	Met	Arg	Ser	Ala	Ser	Gly	Arg	Gln	Lys	Thr	Phe
225					230					235					240
Ser	Thr	Cys	Ala	Ser	His	Leu	Thr	Ala	Ile	Thr	Ile	Phe	His	Gly	Thr
			245						250					255	
Ile	Leu	Phe	Leu	Tyr	Cys	Val	Pro	Asn	Pro	Lys	Thr	Ser	Ser	Leu	Ile
			260					265					270		
Val	Thr	Val	Ala	Ser	Val	Phe	Tyr	Thr	Val	Ala	Ile	Pro	Met	Leu	Asn
		275					280					285			

Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Ile Asn Asn Met Phe Glu
 290 295 300
 Lys Leu Val Val Thr Lys Leu Ile Tyr His
 305 310

<210> 1404

<211> 322

<212> PRT

<213> Unknown (H38g321 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(322)

<223> Xaa = Any Amino Acid

<400> 1404

His Thr Glu Pro Arg Asn His Thr Gly Val Xaa Glu Phe Leu Leu Leu
 1 5 10 15
 Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Leu Leu Ser
 20 25 30
 Leu Ser Leu Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ser
 35 40 45
 Ile Leu Ala Val Arg Ser Asp Ser Pro Leu His Asn Pro Met Tyr Phe
 50 55 60
 Phe Leu Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Thr
 65 70 75 80
 Val Ala Lys Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser
 85 90 95
 His Ala Gly Cys Leu Thr Gln Met Ser Phe Leu Val Leu Phe Ala Cys
 100 105 110
 Ile Glu Gly Met Leu Leu Thr Val Met Ala Tyr Asp Cys Phe Val Ala
 115 120 125
 Ile Cys Arg Pro Leu His Tyr Pro Val Ile Val Asn Pro His Leu Cys
 130 135 140
 Val Phe Phe Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln
 145 150 155 160
 Leu His Ser Ser Ile Val Leu Gln Phe Thr Ile Ile Lys Asn Val Glu
 165 170 175
 Ile Ser His Phe Val Cys Asp Pro Ser His Leu Leu Lys Leu Ala Cys
 180 185 190
 Ser Asp Ser Val Ile Asn Ser Ile Phe Ile Tyr Phe Asp Ser Thr Met
 195 200 205
 Phe Gly Phe Leu Pro Ile Ser Gly Ile Leu Trp Ser Tyr Tyr Lys Ile
 210 215 220
 Val Pro Ser Ile Leu Arg Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala
 225 230 235 240
 Phe Ala Thr Cys Gly Ser His Leu Ala Val Val Cys Xaa Phe Asp Gly
 245 250 255
 Thr Gly Ile Gly Met Tyr Leu Thr Ser Ala Val Ala Pro Pro Pro Arg
 260 265 270
 Asn Gly Val Val Ala Ser Val Met Xaa Ala Val Val Thr Pro Met Leu
 275 280 285
 Asn Leu Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu
 290 295 300
 Arg Arg Leu Leu Ser Arg Thr Val Glu Phe His Asp Leu Phe His Ser
 305 310 315 320
 Phe Ser

<210> 1405
 <211> 330
 <212> PRT
 <213> Unknown (H38g322 protein)

<220>
 <223> Synthetic construct

<400> 1405
 Met Ser Val Leu Asn Asn Thr Ile Ala Glu Pro Leu Ile Phe Leu Leu
 1 5 10 15
 Met Gly Ile Pro Gly Leu Lys Ala Thr Gln Tyr Trp Ile Ser Ile Pro
 20 25 30
 Phe Cys Leu Leu Tyr Val Val Ala Val Ser Gly Asn Ser Met Ile Leu
 35 40 45
 Phe Val Val Leu Cys Glu Arg Ser Leu His Lys Pro Met Tyr Tyr Phe
 50 55 60
 Leu Ser Met Leu Ser Ala Thr Asp Leu Ser Leu Ser Leu Cys Thr Leu
 65 70 75 80
 Ser Thr Thr Leu Gly Val Phe Trp Phe Glu Ala Arg Glu Ile Asn Leu
 85 90 95
 Asn Ala Cys Ile Ala Gln Met Phe Phe Leu His Gly Phe Thr Phe Met
 100 105 110
 Glu Ser Gly Val Leu Leu Ala Met Ala Phe Asp Arg Phe Val Ala Ile
 115 120 125
 Cys Tyr Pro Leu Arg Tyr Thr Thr Ile Leu Thr Asn Ala Arg Ile Ala
 130 135 140
 Lys Ile Gly Met Ser Met Leu Ile Arg Asn Val Ala Val Met Leu Pro
 145 150 155 160
 Val Met Leu Phe Val Lys Arg Leu Ser Phe Cys Ser Ser Met Val Leu
 165 170 175
 Ser His Ser Tyr Cys Tyr His Val Asp Leu Ile Gln Leu Ser Cys Thr
 180 185 190
 Asp Asn Arg Ile Asn Ser Ile Leu Gly Leu Phe Ala Leu Leu Ser Thr
 195 200 205
 Thr Gly Phe Asp Cys Pro Cys Ile Leu Leu Ser Tyr Ile Leu Ile Ile
 210 215 220
 Arg Ser Val Leu Ser Ile Ala Ser Ser Glu Glu Arg Arg Lys Ala Phe
 225 230 235 240
 Asn Thr Cys Thr Ser His Ile Ser Ala Val Ser Ile Phe Tyr Leu Pro
 245 250 255
 Leu Ile Ser Leu Ser Leu Val His Arg Tyr Gly His Ser Ala Pro Pro
 260 265 270
 Phe Val His Ile Ile Met Ala Asn Val Phe Leu Leu Ile Pro Pro Val
 275 280 285
 Leu Asn Pro Ile Ile Tyr Ser Val Lys Ile Lys Gln Ile Gln Lys Ala
 290 295 300
 Ile Ile Lys Val Leu Ile Gln Lys His Ser Lys Ser Asn His Gln Leu
 305 310 315 320
 Phe Leu Ile Arg Asp Lys Ala Ile Tyr Glu
 325 330

<210> 1406
 <211> 314
 <212> PRT
 <213> Unknown (H38g323 protein)

<220>
 <223> Synthetic construct

<400> 1406

```

Met Met Met Val Leu Arg Asn Leu Ser Met Glu Pro Thr Phe Ala Leu
 1          5          10          15
Leu Gly Phe Thr Asp Tyr Pro Lys Leu Gln Ile Pro Leu Phe Leu Val
          20          25          30
Phe Leu Leu Met Tyr Val Ile Thr Val Val Gly Asn Leu Gly Met Ile
          35          40          45
Ile Ile Ile Lys Ile Asn Pro Lys Phe His Thr Pro Met Tyr Phe Phe
          50          55          60
Leu Ser His Leu Ser Phe Val Asp Phe Cys Tyr Ser Ser Ile Val Thr
65          70          75          80
Pro Lys Leu Leu Glu Asn Leu Val Met Ala Asp Lys Ser Ile Phe Tyr
          85          90          95
Phe Ser Cys Met Met Gln Tyr Phe Leu Ser Cys Thr Ala Val Val Thr
          100          105          110
Glu Ser Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile
          115          120          125
Cys Asn Pro Leu Leu Tyr Thr Val Ala Met Ser Gln Arg Leu Cys Ala
          130          135          140
Leu Leu Val Ala Gly Ser Tyr Leu Trp Gly Met Phe Gly Pro Leu Val
145          150          155          160
Leu Leu Cys Tyr Ala Leu Arg Leu Asn Phe Ser Gly Pro Asn Val Ile
          165          170          175
Asn His Phe Phe Cys Glu Tyr Thr Ala Leu Ile Ser Val Ser Gly Ser
          180          185          190
Asp Ile Leu Ile Pro His Leu Leu Leu Phe Ser Phe Ala Thr Phe Asn
          195          200          205
Glu Met Cys Thr Leu Leu Ile Ile Leu Thr Ser Tyr Val Phe Ile Phe
210          215          220
Val Thr Val Leu Lys Ile Arg Ser Val Ser Gly Arg His Lys Ala Phe
225          230          235          240
Ser Thr Trp Ala Ser His Leu Thr Ala Ile Thr Ile Phe His Gly Thr
          245          250          255
Ile Leu Phe Leu Tyr Cys Val Pro Asn Ser Lys Asn Ser Arg Gln Thr
          260          265          270
Val Lys Val Ala Ser Val Phe Tyr Thr Val Val Asn Pro Met Leu Asn
          275          280          285
Pro Pro Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Asp Ala Phe Trp
290          295          300
Lys Leu Ile His Thr Gln Val Pro Phe His
305          310

```

<210> 1407

<211> 314

<212> PRT

<213> Unknown (H38g324 protein)

<220>

<223> Synthetic construct

<400> 1407

```

Met Val Leu Ala Ser Gly Asn Ser Ser Ser His Pro Val Ser Phe Ile
 1          5          10          15
Leu Leu Gly Ile Pro Gly Leu Glu Ser Phe Gln Leu Trp Ile Ala Phe
          20          25          30
Pro Phe Cys Ala Thr Tyr Ala Val Ala Val Val Gly Asn Ile Thr Leu
          35          40          45
Leu His Val Ile Arg Ile Asp His Thr Leu His Glu Pro Met Tyr Leu
          50          55          60
Phe Leu Ala Met Leu Ala Ile Thr Asp Leu Val Leu Ser Ser Ser Thr
65          70          75          80
Gln Pro Lys Met Leu Ala Ile Phe Trp Phe His Ala His Glu Ile Gln

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```

      85      90      95
Tyr His Ala Cys Leu Ile Gln Val Phe Phe Ile His Ala Phe Ser Ser
      100      105      110
Val Glu Ser Gly Val Leu Met Ala Met Ala Leu Asp Cys Tyr Val Ala
      115      120      125
Thr Cys Phe Pro Leu Arg His Ser Ser Ile Leu Thr Pro Ser Val Val
      130      135      140
Ile Lys Leu Gly Thr Ile Val Met Leu Arg Gly Leu Leu Trp Val Ser
      145      150      155      160
Pro Phe Cys Phe Met Val Ser Arg Met Pro Phe Cys Gln His Gln Ala
      165      170      175
Ile Pro Gln Ser Tyr Cys Glu His Met Ala Val Leu Lys Leu Val Cys
      180      185      190
Ala Asp Thr Ser Ile Ser Arg Gly Tyr Gly Leu Phe Val Ala Phe Ser
      195      200      205
Val Ala Gly Phe Asp Met Ile Val Ile Gly Met Ser Tyr Val Met Ile
      210      215      220
Leu Arg Ala Val Leu Gln Leu Pro Ser Gly Glu Ala Arg Leu Lys Ala
      225      230      235      240
Phe Ser Thr Arg Ala Ser His Ile Cys Val Ile Leu Ala Leu Tyr Ile
      245      250      255
Pro Ala Leu Phe Ser Phe Leu Thr Tyr Arg Phe Gly His Asp Val Pro
      260      265      270
Arg Val Val His Ile Leu Phe Ala Asn Leu Tyr Leu Leu Ile Pro Pro
      275      280      285
Met Leu Asn Pro Ile Ile Tyr Gly Val Arg Thr Lys Gln Ile Gly Asp
      290      295      300
Arg Val Ile Gln Gly Cys Cys Gly Asn Ile
      305      310

```

<210> 1408

<211> 287

<212> PRT

<213> Unknown (H38g325 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(287)

<223> Xaa = Any Amino Acid

<400> 1408

```

Tyr Ile Leu Leu Asp Ile Tyr Ile Cys Leu Asn Asn Thr His Val Xaa
  1      5      10
Leu Cys Val Glu Ser Gln Arg Gln Phe Lys Ile Ser Phe Tyr Phe Ser
      20      25      30
Phe Phe Leu Leu Ala Ile Thr Xaa Phe Xaa Xaa Xaa Ile Leu Ile Ile
      35      40      45
Met Lys Thr Xaa Gln Tyr Phe Leu Lys His Lys His Leu Lys Lys Lys
      50      55      60
Phe Ser Xaa Cys Leu Val Tyr Ile Leu Thr Tyr Ile Leu Ser Leu Xaa
      65      70      75      80
Ser Lys Phe Phe Ala Leu Cys Xaa Ile Phe Ala Asp Lys Ala Phe Gln
      85      90      95
Glu Gln Val Ser Gly Asn Xaa Xaa Ser Arg Ser Xaa Glu Ser Pro Val
      100      105      110
His Tyr Thr Leu Thr Met Ser Gln Lys Phe Cys Ser Ile His Pro Ala
      115      120      125
Gly Cys Tyr Asp Gln Gly Ile Xaa Ser Ile Pro Gly His Ser Phe Ser
      130      135      140

```

His Cys Ile Ala Tyr Cys Gly His Asn Val Val Asn Ile Phe Xaa Asn
 145 150 155 160
 Lys Tyr Ser Val Ala Ile Ser Asp Ser Cys Ser Ser Ser Trp Ile Ala
 165 170 175
 Asp Phe Cys Leu Phe Val Cys Phe Ala Leu Val Asn Phe Asp Xaa Leu
 180 185 190
 Arg Asn Leu Arg Val Leu Leu Leu Ser Phe His Phe Gln Leu Val Xaa
 195 200 205
 Lys Ala Leu Ser Ala Ser Ala His Gln Pro Ser Pro Pro Ile Ser His
 210 215 220
 Ile Ser Thr Ile Phe Leu Thr Leu Val Pro Asn Ser Lys Asn Ser Gln
 225 230 235 240
 Ala Thr Val Lys Ala His Ser Val Cys Tyr Ala Met Leu Ile Pro Met
 245 250 255
 Leu Asn Ser Gln Thr Cys Ser Met Arg Tyr Lys Asn Val Asn Glu Ser
 260 265 270
 Leu Gln Lys Leu Met Asp Phe Lys Ile Phe Xaa His Xaa Lys Gln
 275 280 285

<210> 1409

<211> 323

<212> PRT

<213> Unknown (H38g326 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(323)

<223> Xaa = Any Amino Acid

<400> 1409

Ser His Thr Glu Pro Xaa Asn Leu Thr Ser Val Ser Glu Phe Leu Leu
 1 5 10 15
 Gln Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Gly Leu
 20 25 30
 Ser Leu Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu Ile Ile
 35 40 45
 Leu Ala Val Ser Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe
 50 55 60
 Leu Ser Asn Leu Ser Trp Ala Asp Ile Gly Phe Thr Ser Ala Met Val
 65 70 75 80
 Pro Lys Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser Xaa
 85 90 95
 Ala Gly Cys Leu Thr Gln Met Ser Phe Phe Val Leu Phe Ala Cys Ile
 100 105 110
 Glu Asp Met Leu Leu Thr Val Met Ala Tyr Asp Gln Phe Val Ala Ile
 115 120 125
 Cys His Pro Leu His Tyr Pro Val Ile Met Asn Pro His Leu Cys Val
 130 135 140
 Phe Leu Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu
 145 150 155 160
 His Ser Trp Ile Val Leu Gln Phe Thr Phe Phe Lys Asn Val Glu Ile
 165 170 175
 Ser Asn Phe Phe Cys Asp Pro Ser Gln Leu Leu Asn Leu Ala Cys Ser
 180 185 190
 Asp Gly Ile Ile Asn Ser Ile Phe Ile Tyr Leu Asp Ser Ile Leu Phe
 195 200 205
 Ser Phe Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys Ile Val
 210 215 220
 Pro Ser Ile Leu Arg Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala Phe

225		230		235		240
Ser Ile Cys Gly	Ser His Leu Ala Val	Val Cys Leu Phe Tyr Gly Thr				
	245	250				
Gly Ile Gly Val	Tyr Leu Thr Ser Ala Val Ser Pro Pro Pro Gly Asn					
	260	265				
Gly Val Val Ala	Ser Val Met Tyr Ala Val Gly Thr Pro Met Leu Asn					
	275	280				
Ser Phe Ile Tyr	Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu Trp					
	290	295				
Arg Leu Arg Ser Arg	Thr Val Glu Ser Pro Xaa Ser Val Pro Ser Leu					
	305	310				
Phe Leu Cys		315				
		320				

<210> 1410

<211> 317

<212> PRT

<213> Unknown (H38g327 protein)

<220>

<223> Synthetic construct

<400> 1410

Met Gln Pro Tyr	Thr Lys Asn Trp	Thr Gln Val Thr Glu Phe Val Met
1	5	10
Met Gly Phe Ala	Gly Ile His Glu Ala His Leu Leu Phe Phe Ile Leu	15
	20	25
Phe Leu Thr Met	Tyr Leu Phe Thr Leu Val Glu Asn Leu Ala Ile Ile	30
	35	40
Leu Val Val Gly	Leu Asp His Arg Leu Arg Arg Pro Met Tyr Phe Phe	45
	50	55
Leu Thr His Leu	Ser Cys Leu Glu Ile Trp Tyr Thr Ser Val Thr Val	60
	65	70
Pro Lys Met Leu	Ala Gly Phe Ile Gly Val Asp Gly Gly Lys Asn Ile	75
	85	90
Ser Tyr Ala Gly	Cys Leu Ser Gln Leu Phe Ile Phe Thr Phe Leu Gly	95
	100	105
Ala Thr Glu Cys	Phe Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Val	110
	115	120
Ala Ile Cys Met	Pro Leu His Tyr Gly Ala Phe Val Ser Trp Gly Thr	125
	130	135
Cys Ile Arg Leu	Ala Ala Ala Cys Trp Leu Val Gly Phe Leu Thr Pro	140
	145	150
Ile Leu Pro Ile	Tyr Leu Leu Ser Gln Leu Thr Phe Cys Gly Pro Asn	155
	165	170
Val Ile Asp His	Phe Ser Cys Asp Ala Ser Pro Leu Leu Ala Leu Ser	175
	180	185
Cys Ser Asp Val	Thr Trp Lys Glu Thr Val Asp Phe Leu Val Ser Leu	190
	195	200
Ala Val Leu Leu	Ala Ser Ser Met Val Ile Ala Val Ser Tyr Gly Asn	205
	210	215
Ile Val Trp Thr	Leu Leu His Ile Arg Ser Ala Ala Glu Arg Trp Lys	220
	225	230
Ala Phe Ser Thr	Cys Ala Ala His Leu Thr Val Val Ser Leu Phe Tyr	235
	245	250
Gly Thr Leu Phe	Phe Met Tyr Val Gln Thr Lys Val Thr Ser Ser Ile	255
	260	265
Asn Phe Asn Lys	Val Val Ser Val Phe Tyr Ser Val Val Thr Pro Met	270
	275	280
Leu Asn Pro Leu	Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Gly Ala	285
	290	295
		300

Leu Gly Arg Val Phe Ser Leu Asn Phe Trp Lys Gly Gln
 305 310 315

<210> 1411

<211> 312

<212> PRT

<213> Unknown (H38g328 protein)

<220>

<223> Synthetic construct

<400> 1411

Met Asp Gly Glu Asn His Ser Val Val Ser Glu Phe Leu Phe Leu Gly
 1 5 10 15
 Leu Thr His Ser Trp Glu Ile Gln Leu Leu Leu Val Phe Ser Ser
 20 25 30
 Val Leu Tyr Val Ala Ser Ile Thr Gly Asn Ile Leu Ile Val Phe Ser
 35 40 45
 Val Thr Thr Asp Pro His Leu His Ser Pro Met Tyr Phe Leu Leu Ala
 50 55 60
 Ser Leu Ser Phe Ile Asp Leu Gly Ala Cys Ser Val Thr Ser Pro Lys
 65 70 75 80
 Met Ile Tyr Asp Leu Phe Arg Lys Arg Lys Val Ile Ser Phe Gly Gly
 85 90 95
 Cys Ile Ala Gln Ile Phe Phe Ile His Val Val Gly Gly Val Glu Met
 100 105 110
 Val Leu Leu Ile Ala Met Ala Phe Asp Arg Tyr Val Ala Leu Cys Lys
 115 120 125
 Pro Leu His Tyr Leu Thr Ile Met Ser Pro Arg Met Cys Leu Ser Phe
 130 135 140
 Leu Ala Val Ala Trp Thr Leu Gly Val Ser His Ser Leu Phe Gln Leu
 145 150 155 160
 Ala Phe Leu Val Asn Leu Pro Phe Cys Gly Pro Asn Val Leu Asp Ser
 165 170 175
 Phe Tyr Cys Asp Leu Pro Gln Leu Leu Arg Leu Ala Cys Thr Asp Thr
 180 185 190
 Tyr Arg Leu Gln Phe Met Val Thr Val Asn Ser Gly Phe Ile Cys Val
 195 200 205
 Gly Thr Phe Phe Ile Leu Leu Ile Ser Tyr Ile Phe Ile Leu Phe Thr
 210 215 220
 Val Trp Lys His Ser Ser Gly Gly Ser Ser Lys Ala Leu Ser Thr Leu
 225 230 235 240
 Ser Ala His Ser Thr Ala Val Leu Leu Phe Phe Gly Pro Pro Met Phe
 245 250 255
 Val Tyr Thr Trp Pro His Pro Asn Ser Gln Met Asp Lys Phe Leu Ala
 260 265 270
 Ile Phe Asp Ala Val Leu Thr Pro Phe Leu Asn Pro Val Val Tyr Thr
 275 280 285
 Phe Arg Asn Lys Glu Met Lys Ala Ala Ile Lys Arg Val Cys Lys Gln
 290 295 300
 Leu Val Ile Tyr Lys Lys Ile Ser
 305 310

<210> 1412

<211> 223

<212> PRT

<213> Unknown (H38g329 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(223)

<223> Xaa = Any Amino Acid

<400> 1412

```

Val Arg His Pro Leu Arg Cys Gly Lys Xaa Glu Pro Ala Pro Leu Pro
 1           5           10           15
Pro Leu Ala Leu Arg Asn Pro Ile Met Thr Ser Cys Phe Cys Gly Phe
 20           25           30
Leu Val Leu Phe Phe Phe Phe Phe Leu Ser Pro Leu Asp Ala Gln
 35           40           45
Leu His Asn Leu Ile Ala Leu Gln Met Thr Cys Phe Gln Asp Ala Glu
 50           55           60
Ile Pro Ser Phe Phe Trp Asp Pro Ser Gln Leu Pro His Leu Ala Cys
 65           70           75           80
Cys Asp Thr Phe Thr Asn Asn Ile Ile Met Tyr Leu Pro Ala Ala Ile
 85           90           95
Phe Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser Tyr Tyr Lys Ile
100          105          110
Val Ser Ser Ile Leu Arg Val Ser Ser Ser Arg Gly Lys Tyr Lys Ala
115          120          125
Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Cys Xaa Phe Tyr Gly
130          135          140
Thr Gly Phe Gly Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser Pro Arg
145          150          155          160
Lys Ala Ala Val Ala Ser Val Met Tyr Thr Val Ile Thr Ser Met Leu
165          170          175
Asn Pro Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Lys Gly Val Leu
180          185          190
Arg Gln Pro His Gly Ser Thr Val Gln Phe Gln Tyr Leu Leu Ile Cys
195          200          205
Ser Ile Pro Phe Val Val Trp Val Lys Lys Gly Ser Lys Val Lys
210          215          220

```

<210> 1413

<211> 280

<212> PRT

<213> Unknown (H38g330 protein)

<220>

<223> Synthetic construct

<400> 1413

```

Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Ile Ile Leu Ala Val
 1           5           10           15
Ser Ser Asp Ser His Leu His Thr Pro Met Cys Phe Phe Leu Ser Asn
 20           25           30
Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Met Val Pro Lys Met
 35           40           45
Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser Tyr Ala Gly Cys
 50           55           60
Leu Thr Gln Met Ser Phe Phe Val Leu Phe Ala Cys Ile Glu Asp Met
 65           70           75           80
Leu Leu Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro
 85           90           95
Leu His Tyr Pro Val Ile Met Asn Pro His Leu Gly Val Phe Leu Val
100          105          110
Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His Ser Trp
115          120          125
Ile Val Leu Gln Phe Thr Phe Phe Lys Asn Val Glu Ile Ser Asn Phe
130          135          140

```

Val Cys Asp Pro Ser Gln Leu Leu Asn Leu Ala Cys Ser Asp Ser Val
 145 150 155 160
 Ile Asn Ser Ile Phe Ile Tyr Leu Asp Ser Ile Met Phe Gly Phe Leu
 165 170 175
 Pro Ile Ser Gly Ile Leu Leu Ser Tyr Ala Asn Asn Val Pro Ser Ile
 180 185 190
 Leu Arg Ile Ser Ser Ser Asp Arg Lys Ser Lys Ala Phe Ser Thr Cys
 195 200 205
 Gly Ser His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Gly Ile Gly
 210 215 220
 Val Tyr Leu Thr Ser Ala Val Ser Pro Pro Pro Arg Asn Gly Val Val
 225 230 235 240
 Ala Ser Val Met Tyr Ala Val Val Thr Pro Met Leu Asn Pro Phe Ile
 245 250 255
 Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu Trp Arg Leu Arg
 260 265 270
 Ser Arg Thr Val Glu Ser His Asp
 275 280

<210> 1414

<211> 308

<212> PRT

<213> Unknown (H38g331 protein)

<220>

<223> Synthetic construct

<400> 1414

Met Glu Thr Gln Asn Leu Thr Val Val Thr Glu Phe Ile Leu Leu Gly
 1 5 10 15
 Leu Thr Gln Ser Gln Asp Ala Gln Leu Val Phe Val Leu Val Leu
 20 25 30
 Ile Phe Tyr Leu Ile Ile Leu Pro Gly Asn Phe Leu Ile Ile Phe Thr
 35 40 45
 Ile Lys Ser Asp Pro Gly Leu Thr Ala Pro Leu Tyr Phe Phe Leu Gly
 50 55 60
 Asn Leu Ala Leu Leu Asp Ala Ser Tyr Ser Phe Ile Val Val Pro Arg
 65 70 75 80
 Met Leu Val Asp Phe Leu Ser Glu Lys Lys Val Ile Ser Tyr Arg Ser
 85 90 95
 Cys Ile Thr Gln Leu Phe Phe Leu His Phe Leu Gly Ala Gly Glu Met
 100 105 110
 Phe Leu Leu Val Val Met Ala Phe Asp Arg Tyr Ile Ala Ile Cys Arg
 115 120 125
 Pro Leu His Tyr Ser Thr Ile Met Asn Pro Arg Ala Cys Tyr Ala Leu
 130 135 140
 Ser Leu Val Leu Trp Leu Gly Gly Phe Ile His Ser Ile Val Gln Val
 145 150 155 160
 Ala Leu Ile Leu His Leu Pro Phe Cys Gly Pro Asn Gln Leu Asp Asn
 165 170 175
 Phe Phe Cys Asp Val Pro Gln Val Ile Lys Leu Ala Cys Thr Asn Thr
 180 185 190
 Phe Val Val Glu Leu Leu Met Val Ser Asn Ser Gly Leu Leu Ser Leu
 195 200 205
 Leu Cys Phe Leu Gly Leu Leu Ala Ser Tyr Ala Val Ile Leu Cys Arg
 210 215 220
 Ile Arg Glu His Ser Ser Glu Gly Lys Ser Lys Ala Ile Ser Thr Cys
 225 230 235 240
 Thr Thr His Ile Ile Ile Phe Leu Met Phe Gly Pro Ala Ile Phe
 245 250 255
 Ile Tyr Thr Cys Pro Phe Gln Ala Phe Pro Ala Asp Lys Val Val Ser

260 265 270
 Leu Phe His Thr Val Ile Phe Pro Leu Met Asn Pro Val Ile Tyr Thr
 275 280 285
 Leu Arg Asn Gln Glu Val Lys Ala Ser Met Arg Lys Leu Leu Ser Gln
 290 295 300
 His Met Phe Cys
 305

<210> 1415

<211> 154

<212> PRT

<213> Unknown (H38g332 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(154)

<223> Xaa = Any Amino Acid

<400> 1415

Gly Met Arg Lys Glu Gln Ala Val Cys Gly Ser His Arg Met Ile Glu
 1 5 10 15
 Met Met Cys Gly Pro Xaa Val Arg Leu Pro Gly Ser Asn Ala Gly Ser
 20 25 30
 Leu Leu Phe Thr His Leu Ile Leu Ala Cys Gly Ser Leu Leu Leu Ile
 35 40 45
 Pro Phe His Leu Gly Leu Val Ala Ser His Thr Ser Ile Phe Leu Thr
 50 55 60
 Val Leu His Met Lys Ser Pro Xaa Ser Arg Asn Lys Ala Leu Ala Asn
 65 70 75 80
 Cys Ser Ser His Leu Ser Val Gly Leu Tyr Leu Gly Thr Val Cys Leu
 85 90 95
 Ile Tyr Val Thr Gln Gly Phe Ser His Ile Pro Glu Gln Lys Gln Ala
 100 105 110
 Val Ser Val Phe Cys Thr Val Leu Thr Pro Met Leu Asn Pro Leu Ile
 115 120 125
 Tyr Ile Leu Arg Asn Lys Asp Val Val Arg Ala Leu Gln Lys Val Leu
 130 135 140
 Gly Thr His Gln Val Ser Lys Gln Asn Thr
 145 150

<210> 1416

<211> 324

<212> PRT

<213> Unknown (H38g333 protein)

<220>

<223> Synthetic construct

<400> 1416

Met Ser Phe Phe Val Asp Leu Arg Pro Met Asn Arg Ser Ala Thr
 1 5 10 15
 His Ile Val Thr Glu Phe Ile Leu Leu Gly Phe Pro Gly Cys Trp Lys
 20 25 30
 Ile Gln Ile Phe Leu Phe Ser Leu Phe Leu Val Ile Tyr Val Leu Thr
 35 40 45
 Leu Leu Gly Asn Gly Ala Ile Ile Tyr Ala Val Arg Cys Asn Pro Leu
 50 55 60
 Leu His Thr Pro Met Tyr Phe Leu Leu Gly Asn Phe Ala Phe Leu Glu
 65 70 75 80

Ile Trp Tyr Val Ser Ser Thr Ile Pro Asn Met Leu Val Asn Ile Leu
 85 90 95
 Ser Lys Thr Lys Ala Ile Ser Phe Ser Gly Cys Phe Leu Gln Phe Tyr
 100 105 110
 Phe Phe Phe Ser Leu Gly Thr Thr Glu Cys Leu Phe Leu Ala Val Met
 115 120 125
 Ala Tyr Asp Arg Tyr Leu Ala Ile Cys His Pro Leu Gln Tyr Pro Ala
 130 135 140
 Ile Met Thr Val Arg Phe Cys Gly Lys Leu Val Ser Phe Cys Trp Leu
 145 150 155 160
 Ile Gly Phe Leu Gly Tyr Pro Ile Pro Ile Phe Tyr Ile Ser Gln Leu
 165 170 175
 Pro Phe Cys Gly Pro Asn Ile Ile Asp His Phe Leu Cys Asp Met Asp
 180 185 190
 Pro Leu Met Ala Leu Ser Cys Ala Pro Ala Pro Ile Thr Glu Cys Ile
 195 200 205
 Phe Tyr Thr Gln Ser Ser Leu Val Leu Phe Phe Thr Ser Met Tyr Ile
 210 215 220
 Leu Arg Ser Tyr Ile Leu Leu Leu Thr Ala Val Phe Gln Val Pro Ser
 225 230 235 240
 Ala Ala Gly Arg Arg Lys Ala Phe Ser Thr Cys Gly Ser His Leu Val
 245 250 255
 Val Val Ser Leu Phe Tyr Gly Thr Val Met Val Met Tyr Val Ser Pro
 260 265 270
 Thr Tyr Gly Ile Pro Thr Leu Leu Gln Lys Ile Leu Thr Leu Val Tyr
 275 280 285
 Ser Val Thr Thr Pro Leu Phe Asn Pro Leu Ile Tyr Thr Leu Arg Asn
 290 295 300
 Lys Asp Met Lys Leu Ala Leu Arg Asn Val Leu Phe Gly Met Arg Ile
 305 310 315 320
 Arg Gln Asn Ser

<210> 1417

<211> 315

<212> PRT

<213> Unknown (H38g334 protein)

<220>

<223> Synthetic construct

<400> 1417

Met Ala Asn Ile Thr Arg Met Ala Asn His Thr Gly Lys Leu Asp Phe
 1 5 10 15
 Ile Leu Met Gly Leu Phe Arg Arg Ser Lys His Pro Ala Leu Leu Ser
 20 25 30
 Val Val Ile Phe Val Val Phe Leu Lys Ala Leu Ser Gly Asn Ala Val
 35 40 45
 Leu Ile Leu Leu Ile His Cys Asp Ala His Leu His Ser Pro Met Tyr
 50 55 60
 Phe Phe Ile Ser Gln Leu Ser Leu Met Asp Met Ala Tyr Ile Ser Val
 65 70 75 80
 Thr Val Pro Lys Met Leu Leu Asp Gln Val Met Gly Val Asn Lys Val
 85 90 95
 Ser Ala Pro Glu Cys Gly Met Gln Met Phe Leu Tyr Leu Thr Leu Ala
 100 105 110
 Gly Ser Glu Phe Phe Leu Leu Ala Thr Met Ala Tyr Asp Arg Tyr Val
 115 120 125
 Ala Ile Cys His Pro Leu Arg Tyr Pro Val Leu Met Asn His Arg Val
 130 135 140
 Cys Leu Phe Leu Ala Ser Gly Cys Trp Phe Leu Gly Ser Val Asp Gly

```

145          150          155          160
Phe Met Leu Thr Pro Ile Thr Met Ser Phe Pro Phe Cys Arg Ser Trp
          165          170          175
Glu Ile His His Phe Phe Cys Glu Val Pro Ala Val Thr Ile Leu Ser
          180          185          190
Cys Ser Asp Thr Ser Leu Tyr Glu Thr Leu Met Tyr Leu Cys Cys Val
          195          200          205
Leu Met Leu Leu Ile Pro Val Thr Ile Ile Ser Ser Ser Tyr Leu Leu
          210          215          220
Ile Leu Leu Thr Val His Arg Met Asn Ser Ala Glu Gly Arg Lys Lys
225          230          235          240
Ala Phe Ala Thr Cys Ser Ser His Leu Thr Val Val Ile Leu Phe Tyr
          245          250          255
Gly Ala Ala Val Tyr Thr Tyr Met Leu Pro Ser Ser Tyr His Thr Pro
          260          265          270
Glu Lys Asp Met Met Val Ser Val Phe Tyr Thr Ile Leu Thr Pro Val
          275          280          285
Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Met Gly Ala
          290          295          300
Leu Lys Lys Met Leu Thr Val Arg Phe Val Leu
305          310          315

```

<210> 1418

<211> 253

<212> PRT

<213> Unknown (H38g335 protein)

<220> .

<223> Synthetic construct

<221> VARIANT

<222> (1)...(253)

<223> Xaa = Any Amino Acid

<400> 1418

```

Ser His Leu Ser Val Ile Asp Thr Leu Tyr Ile Ser Thr Ile Val Pro
1          5          10          15
Lys Met Leu Val Asp Tyr Leu Met Gly Glu Gly Thr Ile Ser Phe Ile
          20          25          30
Ala Cys Thr Ala Gln Cys Phe Leu Tyr Met Gly Phe Met Gly Ala Glu
          35          40          45
Phe Phe Leu Leu Gly Leu Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys
          50          55          60
Asn Pro Leu Arg Tyr Pro Val Leu Ile Ser Trp Arg Val Cys Trp Met
65          70          75          80
Ile Leu Ala Ser Ser Trp Phe Gly Gly Ala Leu Asp Ser Phe Leu Leu
          85          90          95
Thr Pro Ile Thr Met Ser Leu Pro Phe Cys Ala Ser His Gln Ile Asn
          100          105          110
His Phe Phe Cys Glu Ala Pro Thr Met Leu Arg Leu Ala Cys Gly Asp
          115          120          125
Lys Thr Thr Tyr Glu Thr Val Met Tyr Val Cys Cys Val Ala Met Leu
          130          135          140
Leu Ile Pro Phe Ser Val Val Thr Ala Ser Tyr Thr Arg Ile Leu Ile
145          150          155          160
Thr Val His Gln Met Thr Ser Ala Glu Gly Arg Lys Lys Ala Phe Ala
          165          170          175
Thr Cys Ser Ser His Met Met Val Val Thr Leu Phe Tyr Gly Ala Ala
          180          185          190
Leu Tyr Thr Tyr Thr Leu Pro Gln Ser Tyr His Thr Pro Ile Lys Asp
          195          200          205

```

Lys Val Phe Ser Ala Phe Tyr Thr Ile Leu Thr Pro Leu Leu Asn Pro
 210 215 220
 Leu Ile Tyr Ser Leu Arg Asn Arg Asp Val Met Gly Ala Leu Lys Arg
 225 230 235 240
 Val Val Ala Arg Cys Xaa Gly Thr Cys Gly Val Met Arg
 245 250

<210> 1419

<211> 285

<212> PRT

<213> Unknown (H38g336 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(285)

<223> Xaa = Any Amino Acid

<400> 1419

Val Phe Ser Arg Thr Arg Val Arg Leu Asn Cys Lys Arg Ile Phe Trp
 1 5 10 15
 Leu Thr Pro Val Phe Phe Leu Ser Pro Ser Cys Pro Ser Pro Ile Ala
 20 25 30
 Val Ser Lys Ser Ala Val Ser Phe Val Ser Gln Ser Arg Arg Ile Arg
 35 40 45
 Phe Leu Gly Cys Asp Ile Gln Thr Tyr Val Phe Leu Ala Pro Gly Gly
 50 55 60
 Thr Glu Ala Leu Leu Phe Gly Phe Met Ser Tyr Asp Arg Tyr Val Ala
 65 70 75 80
 Ile Cys His Pro Leu His Tyr Pro Met Leu Met Ser Lys Lys Ile Cys
 85 90 95
 Cys Leu Met Val Ala Cys Ala Trp Ala Ser Gly Ser Ile Asn Ala Phe
 100 105 110
 Ile His Thr Leu Tyr Val Phe Gln Leu Pro Phe Cys Arg Ser Arg Leu
 115 120 125
 Ile Asn His Phe Phe Cys Glu Val Pro Ala Leu Leu Ser Leu Val Cys
 130 135 140
 Gln Asp Thr Ser Gln Tyr Glu Tyr Thr Val Leu Leu Ser Gly Leu Ile
 145 150 155 160
 Ile Leu Leu Leu Pro Phe Leu Ala Ile Leu Ala Ser Tyr Ala Arg Val
 165 170 175
 Leu Ile Val Val Phe Gln Met Ser Ser Gly Lys Gly Gln Ala Lys Ala
 180 185 190
 Val Ser Thr Cys Ser Ser His Leu Ile Val Ala Ser Leu Phe Tyr Ala
 195 200 205
 Thr Thr Leu Phe Thr Tyr Thr Arg Pro His Ser Leu Arg Ser Pro Ser
 210 215 220
 Arg Asp Lys Ala Val Ala Val Phe Tyr Thr Ile Val Thr Pro Leu Leu
 225 230 235 240
 Asn Pro Phe Ile Tyr Ser Leu Arg Asn Lys Glu Val Thr Gly Ala Val
 245 250 255
 Arg Arg Leu Leu Gly Tyr Trp Ile Cys Cys Arg Lys Tyr Asp Phe Arg
 260 265 270
 Ser Leu Tyr Xaa Leu Ser Ile Asn Asn Ile Lys Ser Cys
 275 280 285

<210> 1420

<211> 271

<212> PRT

<213> Unknown (H38g337 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(271)

<223> Xaa = Any Amino Acid

<400> 1420

```

Arg Arg Asp Ile Phe Tyr Phe Ala Phe Ile Cys Ser Tyr Ser Xaa Leu
 1           5           10           15
Thr Leu Arg Ser Phe Val Tyr Leu Phe Ile Arg Pro Ser Ile His Pro
          20           25           30
Ser Ile His Ser Ala Ile Leu Leu Phe Asn Ser Asp Leu Leu Asn Ser
          35           40           45
Leu Leu Cys Ser Ser Ile Phe Asp Met Pro His Asp Val Gln Gln Xaa
          50           55           60
Leu Leu Leu Lys Ser Xaa Phe Leu Val Ser His Cys Phe Ser Leu Val
          65           70           75           80
Leu Tyr Leu Leu Leu Leu Xaa Leu Arg Thr Glu Lys Ser Ile Glu Lys
          85           90           95
Ile Leu Leu Pro Gly Tyr Gly Thr Leu Leu Ser Met Ala Ile Ser Tyr
          100          105          110
Cys Leu Cys Val Phe Gly Leu Ser Asn Pro Ala Ala Cys Val Tyr Ala
          115          120          125
Gln Xaa Cys Ser Trp Asn Lys Met Val Trp Phe Leu Phe Gln Glu Val
          130          135          140
Leu Pro Ser Leu Phe Xaa Leu Arg Ile Gly Leu Pro Arg Cys Ile Thr
          145          150          155          160
Ser Leu Thr Leu Tyr Ser Cys Asp Phe Phe Leu Met Ile Gly Gln Ile
          165          170          175
Cys Thr Lys Lys Ser Lys Ile Ile Tyr Tyr Ile Met Pro Phe Leu Leu
          180          185          190
Leu Phe Met Pro Asp Xaa Ile Phe Leu Val Leu Gln Cys Pro Leu Leu
          195          200          205
Ile Ser Ile Asn Lys Xaa Pro Phe Pro Asn Leu Leu Lys Ser Pro Cys
          210          215          220
Gly Ile Gly His Leu Ser Val Asp Ser Ile Ser Ser Pro Ser Phe Phe
          225          230          235          240
Cys Leu Pro Val Cys Pro Ser Ile Tyr Pro Ser Thr Xaa Leu Phe Val
          245          250          255
Arg Ser Thr Met Ile Xaa Xaa Ile Pro Thr Tyr Cys Asp Pro Ile
          260          265          270

```

<210> 1421

<211> 310

<212> PRT

<213> Unknown (H38g338 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(310)

<223> Xaa = Any Amino Acid

<400> 1421

```

Met Ser Leu Ala Glu Gly Asn Gln Ser Ser Gly Ala Val Phe Thr Leu
 1           5           10           15
Leu Gly Phe Ser Glu Tyr Ala Asp Leu Gln Val Pro Leu Phe Leu Val
          20           25           30

```

```

Phe Leu Thr Ile Tyr Thr Ile Thr Val Leu Gly Asn Leu Gly Met Ile
  35                               40                               45
Met Ile Ile Arg Ile Asn Pro Lys Leu His Thr Arg Met Tyr Phe Phe
  50                               55                               60
Leu Ser His Leu Ser Phe Val Asp Phe Cys Tyr Ser Thr Thr Val Thr
  65                               70                               75                               80
Pro Lys Leu Leu Glu Asn Leu Val Val Glu Asp Arg Thr Ile Ser Phe
  85                               90                               95
Thr Gly Cys Ile Met Gln Phe Phe Leu Ala Cys Ile Cys Ala Val Ala
 100                               105                               110
Glu Thr Phe Met Leu Ala Val Met Ala Tyr Asp Xaa Tyr Val Ala Val
 115                               120                               125
Cys Asn Pro Leu Leu Tyr Thr Val Val Arg Ser Gln Lys Leu Cys Ala
 130                               135                               140
Ser Leu Val Ala Gly Pro Tyr Thr Trp Gly Ile Ile Ser Ser Leu Thr
 145                               150                               155                               160
Leu Thr Tyr Phe Leu Leu Ser Leu Ser Phe Cys Gly Ser Asn Ile Ile
 165                               170                               175
Asn Asn Phe Val Cys Glu His Ser Val Ile Ile Ser Val Ser Cys Ser
 180                               185                               190
Asp Pro Tyr Ile Ser Gln Met Leu Cys Phe Val Ile Ala Ile Phe Asn
 195                               200                               205
Glu Val Ser Ser Leu Gly Val Ile Leu Thr Thr Tyr Ile Phe Ile Phe
 210                               215                               220
Ile Ala Val Ile Lys Met Pro Ser Ala Val Gly His Gln Lys Ala Phe
 225                               230                               235                               240
Ser Thr Cys Ala Ser His Leu Thr Ala Ile Thr Ile Phe His Gly Thr
 245                               250                               255
Val Leu Phe Leu Tyr Cys Val Pro Asn Ser Lys Asn Ser Trp Leu Ile
 260                               265                               270
Val Lys Val Gly Ser Val Phe Tyr Thr Val Ile Ile Pro Thr Leu Asn
 275                               280                               285
Pro Leu Thr Tyr Ser Leu Arg Asn Lys Asp Val Lys Glu Met Phe Glu
 290                               295                               300
Ser Xaa Xaa Ile Thr Gln
305                               310

```

<210> 1422

<211> 217

<212> PRT

<213> Unknown (H38g339 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(217)

<223> Xaa = Any Amino Acid

<400> 1422

```

Phe Leu Val Leu Phe Ala Cys Ile Glu Asp Met Phe Leu Thr Val Met
  1                               5                               10                               15
Ala Tyr Asp Cys Phe Ile Ala Ile Cys His Pro Leu His Tyr Pro Val
  20                               25                               30
Ile Val Asn Pro His Leu Cys Val Phe Phe Ile Leu Val Ser Phe Phe
  35                               40                               45
Leu Ser Leu Leu Asp Ser Gln Leu His Ser Trp Ile Val Leu Gln Phe
  50                               55                               60
Thr Ile Ile Lys Asn Val Glu Val Ser Asn Phe Val Cys Asp Pro Ser
  65                               70                               75                               80
Gln Leu Leu Lys Leu Ala Cys Ser Asp Ser Val Ile Asn Ser Ile Phe

```

<4000> 1423															
Met	Gly	Lys	Glu	Asn	Cys	Thr	Thr	Val	Ala	Glu	Phe	Ile	Leu	Leu	Gly
1				5					10					15	
Leu	Ser	Asp	Val	Pro	Glu	Leu	Arg	Val	Cys	Leu	Phe	Leu	Leu	Phe	Leu
			20					25					30		
Leu	Ile	Tyr	Gly	Val	Thr	Leu	Leu	Ala	Asn	Leu	Gly	Met	Thr	Ala	Leu
		35					40					45			
Ile	Gln	Val	Ser	Ser	Arg	Leu	His	Thr	Pro	Val	Tyr	Phe	Phe	Leu	Ser
	50					55					60				
His	Leu	Ser	Phe	Val	Asp	Phe	Cys	Tyr	Ser	Ser	Ile	Ile	Val	Pro	Lys
65					70					75					80
Met	Leu	Ala	Asn	Ile	Phe	Asn	Lys	Asp	Lys	Ala	Ile	Ser	Phe	Leu	Gly
				85					90					95	
Cys	Met	Val	Gln	Phe	Tyr	Leu	Phe	Cys	Thr	Cys	Gly	Val	Thr	Glu	Val
			100					105					110		
Phe	Leu	Leu	Ala	Val	Met	Ala	Tyr	Asp	Arg	Phe	Val	Ala	Ile	Cys	Asn
			115				120					125			
Pro	Leu	Leu	Tyr	Met	Val	Thr	Met	Ser	Gln	Lys	Leu	Arg	Val	Glu	Leu
	130					135					140				
Thr	Ser	Cys	Cys	Tyr	Phe	Cys	Gly	Thr	Val	Cys	Ser	Leu	Ile	His	Ser
145					150					155					160
Ser	Leu	Ala	Leu	Arg	Ile	Leu	Phe	Tyr	Arg	Ser	Asn	Val	Ile	Asn	His
				165					170					175	
Phe	Phe	Cys	Asp	Leu	Pro	Pro	Leu	Leu	Ser	Leu	Ala	Cys	Ser	Asp	Val
			180					185					190		
Thr	Val	Asn	Glu	Thr	Leu	Leu	Phe	Leu	Val	Ala	Thr	Leu	Asn	Glu	Ser
		195					200					205			
Val	Thr	Ile	Met	Ile	Ile	Leu	Thr	Ser	Tyr	Leu	Leu	Ile	Leu	Thr	Thr
	210					215					220				
Ile	Leu	Lys	Ile	His	Ser	Ala	Glu	Ser	Arg	His	Lys	Ala	Phe	Ser	Thr
225					230					235					240
Cys	Ala	Ser	His	Leu	Thr	Ala	Ile	Thr	Val	Ser	His	Gly	Thr	Ile	Leu
				245					250					255	
Tyr	Ile	Tyr	Cys	Arg	Pro	Ser	Ser	Gly	Asn	Ser	Gly	Asp	Val	Asp	Lys
			260					265					270		

Val Ala Thr Val Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro Leu
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Asp Val Asn Lys Ala Leu Arg Lys Val
 290 295 300
 Met Gly Ser Lys Ile His Ser
 305 310

<210> 1424

<211> 321

<212> PRT

<213> Unknown (H38g341 protein)

<220>

<223> Synthetic construct

<400> 1424

Met Phe Leu Thr Glu Arg Asn Thr Thr Ser Glu Ala Thr Phe Thr Leu
 1 5 10 15
 Leu Gly Phe Ser Asp Tyr Leu Glu Leu Gln Ile Pro Leu Phe Phe Val
 20 25 30
 Phe Leu Ala Val Tyr Gly Phe Ser Val Val Gly Asn Leu Gly Met Ile
 35 40 45
 Val Ile Ile Lys Ile Asn Pro Lys Leu His Thr Pro Met Tyr Phe Phe
 50 55 60
 Leu Asn His Leu Ser Phe Val Asp Phe Cys Tyr Ser Ser Ile Ile Ala
 65 70 75 80
 Pro Met Met Leu Val Asn Leu Val Val Glu Asp Arg Thr Ile Ser Phe
 85 90 95
 Ser Gly Cys Leu Val Gln Phe Phe Phe Phe Cys Thr Phe Val Val Thr
 100 105 110
 Glu Leu Ile Leu Phe Ala Val Met Ala Tyr Asp His Phe Val Ala Ile
 115 120 125
 Cys Asn Pro Leu Leu Tyr Thr Val Ala Ile Ser Gln Lys Leu Cys Ala
 130 135 140
 Met Leu Val Val Val Leu Tyr Ala Trp Gly Val Ala Cys Ser Leu Thr
 145 150 155 160
 Leu Ala Cys Ser Ala Leu Lys Leu Ser Phe His Gly Phe Asn Thr Ile
 165 170 175
 Asn His Phe Phe Cys Glu Leu Ser Ser Leu Ile Ser Leu Ser Tyr Pro
 180 185 190
 Asp Ser Tyr Leu Ser Gln Leu Leu Leu Phe Thr Val Ala Thr Phe Asn
 195 200 205
 Glu Ile Ser Thr Leu Leu Ile Ile Leu Thr Ser Tyr Ala Phe Ile Ile
 210 215 220
 Val Thr Thr Leu Lys Met Pro Ser Ala Ser Gly His Arg Lys Val Phe
 225 230 235 240
 Ser Thr Cys Ala Ser His Leu Thr Ala Ile Thr Ile Phe His Gly Thr
 245 250 255
 Ile Leu Phe Leu Tyr Cys Val Pro Asn Ser Lys Asn Ser Arg His Thr
 260 265 270
 Val Lys Val Ala Ser Val Phe Tyr Thr Val Val Ile Pro Leu Leu Asn
 275 280 285
 Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Asp Ala Ile Arg
 290 295 300
 Lys Ile Ile Asn Thr Lys Tyr Phe His Ile Lys His Arg His Trp Tyr
 305 310 315 320
 Pro

<210> 1425

<211> 101

<212> PRT

<213> Unknown (H38g342 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(101)

<223> Xaa = Any Amino Acid

<400> 1425

Cys	Cys	Pro	Leu	His	His	His	Tyr	Leu	Pro	Arg	Gln	Ser	Leu	Asp	Gln
1				5				10						15	
Leu	Thr	Tyr	Leu	Ile	Ala	Leu	Ile	Phe	Asn ¹	Phe	Leu	Phe	Val	Phe	Gly
			20					25					30		
Leu	Gln	Ser	Ser	Phe	Ile	Phe	Leu	Lys	Ala	Xaa	Gln	Cys	Phe	Pro	Lys
		35					40					45			
Asp	Ile	His	Tyr	Ile	Phe	Val	Lys	Ala	Arg	Arg	Ala	Ser	Gly	Tyr	Leu
	50					55					60				
Thr	Tyr	His	Ile	Ala	Gly	Asn	Arg	Ser	Xaa	Thr	Val	Phe	Phe	Leu	Val
65				70					75					80	
Cys	Asn	Cys	His	Tyr	Tyr	Gly	Asp	Asp	Ile	Gly	Xaa	Val	Xaa	Ile	Phe
			85					90						95	
Tyr	Val	Asn	Ile	Leu											
			100												

<210> 1426

<211> 319

<212> PRT

<213> Unknown (H38g343 protein)

<220>

<223> Synthetic construct

<400> 1426

Met	Pro	Val	Gly	Lys	Leu	Val	Phe	Asn	Gln	Ser	Glu	Pro	Thr	Glu	Phe
1				5				10						15	
Val	Phe	Arg	Ala	Phe	Thr	Thr	Ala	Thr	Glu	Phe	Gln	Val	Leu	Leu	Phe
			20					25					30		
Leu	Leu	Phe	Leu	Leu	Leu	Tyr	Leu	Met	Ile	Leu	Cys	Gly	Asn	Thr	Ala
		35					40					45			
Ile	Ile	Trp	Val	Val	Cys	Thr	His	Ser	Thr	Leu	Arg	Thr	Pro	Met	Tyr
	50				55					60					
Phe	Phe	Leu	Ser	Asn	Leu	Ser	Phe	Leu	Glu	Leu	Cys	Tyr	Thr	Thr	Val
65				70					75					80	
Val	Val	Pro	Leu	Met	Leu	Ser	Asn	Ile	Leu	Gly	Ala	Gln	Lys	Pro	Ile
			85					90						95	
Ser	Leu	Ala	Gly	Cys	Gly	Ala	Gln	Met	Phe	Phe	Phe	Val	Thr	Leu	Gly
		100						105					110		
Ser	Thr	Asp	Cys	Phe	Leu	Leu	Ala	Ile	Met	Ala	Tyr	Asp	Arg	Tyr	Val
	115						120					125			
Ala	Ile	Cys	His	Pro	Leu	His	Tyr	Thr	Leu	Ile	Met	Thr	Arg	Glu	Leu
	130				135						140				
Cys	Thr	Gln	Met	Leu	Gly	Ala	Leu	Gly	Leu	Ala	Leu	Phe	Pro	Ser	
145				150					155					160	
Leu	Gln	Leu	Thr	Ala	Leu	Ile	Phe	Thr	Leu	Pro	Phe	Cys	Gly	His	His
			165					170						175	
Gln	Glu	Ile	Asn	His	Phe	Leu	Cys	Asp	Val	Pro	Pro	Val	Leu	Arg	Leu
		180						185					190		
Ala	Cys	Ala	Asp	Ile	Arg	Val	His	Gln	Ala	Val	Leu	Tyr	Val	Val	Ser
		195					200					205			

```

Ile Leu Val Leu Thr Ile Pro Phe Leu Leu Ile Cys Val Ser Tyr Val
  210                215                220
Phe Ile Thr Cys Ala Ile Leu Ser Ile Arg Ser Ala Glu Gly Arg Arg
225                230                235                240
Arg Ala Phe Ser Thr Cys Ser Phe His Leu Thr Val Val Leu Leu Gln
                245                250                255
Tyr Gly Cys Cys Ser Leu Val Tyr Leu Arg Pro Arg Ser Ser Thr Ser
                260                265                270
Glu Asp Glu Asp Ser Gln Ile Ala Leu Val Tyr Thr Phe Val Thr Pro
                275                280                285
Leu Leu Asn Pro Leu Leu Tyr Ser Leu Arg Asn Lys Asp Val Lys Gly
                290                295                300
Ala Leu Arg Ser Ala Ile Ile Arg Lys Ala Ala Ser Asp Ala Asn
305                310                315

```

<210> 1427

<211> 208

<212> PRT

<213> Unknown (H38g344 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(208)

<223> Xaa = Any Amino Acid

<400> 1427

```

Met Glu Leu Glu Asn Gly Thr Val Lys Thr Gly Phe Phe Leu Leu Gly
  1                5                10                15
Phe Ser Asp His Leu Glu Leu Gln Ser Leu Leu Phe Ala Glu Phe Phe
                20                25                30
Ser Ile Tyr Ser Val Thr Leu Met Gly Asn Leu Gly Met Ile Leu Leu
                35                40                45
Ile Thr Ile Ser Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Cys
                50                55                60
Val Leu Ser Phe Ile Asp Ala Cys Tyr Ser Ser Val Ile Ala Pro Lys
65                70                75                80
Leu Leu Val Asn Leu Val Ser Glu Lys Lys Thr Ile Ser Tyr Asn Gly
                85                90                95
Cys Val Ala Gln Leu Tyr Phe Phe Cys Ser Leu Val Asp Thr Glu Ser
                100                105                110
Phe Leu Leu Ala Ala Met Ala Xaa Asp Arg Tyr Ile Ala Ile Cys Asn
                115                120                125
Pro Leu Leu Tyr Thr Val Ile Met Ser Lys Lys Val Cys Cys Gln Leu
130                135                140
Ala Ile Gly Ala Phe Leu Gly Gly Thr Met Ser Ser Ile Ile His Thr
145                150                155                160
Thr Asn Thr Phe His Leu Ser Phe Cys Ser Arg Asp Ile Asn His Phe
                165                170                175
Phe Cys Asp Ile Ser Pro Leu Phe Ser Leu Ser Cys Thr Asp Thr Tyr
                180                185                190
Met His Asp Ile Ile Leu Val Val Phe Ala Ser Phe Val Glu Ala Ile
195                200                205

```

<210> 1428

<211> 321

<212> PRT

<213> Unknown (H38g345 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(321)

<223> Xaa = Any Amino Acid

<400> 1428

His	Thr	Glu	Pro	Arg	Asn	Leu	Thr	Gly	Val	Ser	Glu	Phe	Leu	Leu	Leu
1				5					10					15	
Gly	Leu	Ser	Glu	Asp	Pro	Glu	Leu	Gln	Pro	Val	Leu	Pro	Gly	Leu	Ser
			20					25					30		
Leu	Ser	Met	Tyr	Leu	Leu	Thr	Val	Leu	Arg	Asn	Leu	Leu	Ile	Ile	Leu
		35				40						45			
Ala	Val	Ser	Ser	Asp	Ser	His	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu
	50					55					60				
Ser	Asn	Pro	Ser	Trp	Ala	Asp	Ile	Ala	Phe	Thr	Ser	Ala	Thr	Val	Pro
65				70						75					80
Lys	Met	Ile	Val	Asp	Met	Gln	Ser	His	Arg	Val	Ile	Ser	Tyr	Ala	Ser
			85						90					95	
Cys	Leu	Thr	Gln	Met	Ser	Phe	Phe	Ala	Leu	Phe	Ala	Cys	Ile	Glu	Asp
			100					105					110		
Met	Leu	Leu	Ile	Val	Met	Ala	Tyr	Asp	Arg	Phe	Val	Ala	Val	Cys	His
		115					120					125			
Ser	Pro	His	Tyr	Pro	Val	Ile	Met	Asn	Pro	Arg	Leu	Gly	Val	Phe	Phe
	130					135					140				
Val	Leu	Val	Ser	Phe	Phe	Leu	Ser	Leu	Leu	Asp	Ser	Gln	Leu	His	Ser
145					150					155					160
Trp	Thr	Val	Leu	Gln	Phe	Thr	Phe	Phe	Lys	Asn	Val	Glu	Ile	Ser	Asn
				165					170					175	
Phe	Val	Cys	Asp	Pro	Ser	Gln	Leu	Leu	Asn	Leu	Ala	Cys	Ser	Asp	Ser
			180					185					190		
Val	Ile	Asp	Ser	Ile	Phe	Ile	Tyr	Leu	Asp	Ser	Thr	Met	Phe	Arg	Phe
	195						200					205			
Leu	Pro	Ile	Ser	Gly	Ile	Leu	Leu	Ser	Tyr	Ser	Asn	Ile	Val	Pro	Ser
	210					215					220				
Ile	Leu	Arg	Ile	Ser	Ser	Ser	Asp	Gly	Lys	Ser	Lys	Ala	Phe	Ser	Thr
225					230					235					240
Cys	Arg	Ser	His	Leu	Ala	Val	Val	Cys	Leu	Phe	Tyr	Gly	Thr	Gly	Ile
			245						250					255	
Gly	Val	Tyr	Leu	Thr	Ser	Ala	Val	Ala	Pro	Pro	Pro	Gly	Asp	Gly	Val
			260					265					270		
Val	Val	Ser	Val	Met	Tyr	Thr	Val	Val	Thr	Pro	Met	Leu	Asn	Pro	Phe
		275					280					285			
Ile	Tyr	Cys	Leu	Arg	Asn	Arg	Asp	Ile	Gln	Ser	Ala	Leu	Trp	Arg	Leu
	290					295					300				
Arg	Ser	Arg	Thr	Val	Glu	Ser	Pro	Xaa	Ser	Val	Pro	Ser	Phe	Phe	Leu
305					310					315					320
Cys															

<210> 1429

<211> 310

<212> PRT

<213> Unknown (H38g346 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(310)

<223> Xaa = Any Amino Acid

<400> 1429

```

Glu Lys Asn Leu Ile Ser Met Asn Gly Phe Met Asn Phe Thr Asp Tyr
 1           5           10           15
Pro Glu Leu Glu Met Pro Leu Phe Leu Val Phe Leu Ser Cys Phe Leu
      20           25           30
Ala Ile Ile Leu Arg Asn Met Glu Trp Val Ile Leu Thr Gln Val Asn
      35           40           45
Val His Leu Phe Thr Pro Ile Tyr Phe Phe Leu Thr Asn Val Thr Leu
      50           55           60
Trp Asp Thr Ser Val Ile Met Pro Gln Ile Leu Ala Ile Leu Ala Thr
      65           70           75           80
Gly Lys Thr Thr Ile Ser Tyr Val Pro Leu Ile Lys Ala Met Arg Ser
      85           90           95
Phe Phe Phe Ile Cys Val Gly Thr Xaa Cys Phe Leu Pro Thr Ala Met
      100          105          110
Thr Ile Ser Ser His Cys Pro Thr Leu Gln Ala Met Asn Phe Lys Thr
      115          120          125
Cys Trp Gly Phe Phe Leu Val Gly Ile Cys Cys Cys Thr Cys Trp Val
      130          135          140
Leu Met Val Asn Val Val Asn Ala Tyr Thr Xaa Gly Leu Ser Gly Ala
      145          150          155          160
Thr Phe Asn Thr Ile Cys Thr Phe Ala Arg Phe Phe Cys Asp Asp Asn
      165          170          175
Xaa Ile Lys Phe Cys His Ile Leu Pro Leu Leu Lys Leu Ile Xaa Asn
      180          185          190
Thr Ser Gly Asn Ser Lys Ile Ile Ile Val Ile Leu Thr Ala Phe Met
      195          200          205
Ile Ile Ala Gly Thr Arg Val Ile Leu Ile Ser Tyr Leu Leu Ile Ile
      210          215          220
Arg Ala Leu Arg Met Lys Ser Ser Ser Gly Arg Ser Gln Xaa Phe Tyr
      225          230          235          240
Pro Ser Thr Cys Ala Ser His Leu Thr Ala Met Thr Phe Phe Gly Ile
      245          250          255
Pro Ile Phe Arg His Val Lys Tyr Leu Arg Xaa Ile Thr Asp Arg Arg
      260          265          270
Gln Val Gly Ile Met Thr Cys Thr Ile Phe Ile Pro Met Leu Glu Leu
      275          280          285
Leu Ile Gln Ser Leu Lys Lys Asp Ile Gln Val Ala Phe Lys Lys Ala
      290          295          300
Ile Gly Asn Phe Trp Val
      305          310

```

<210> 1430

<211> 336

<212> PRT

<213> Unknown (H38g347 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(336)

<223> Xaa = Any Amino Acid

<400> 1430

```

Ser Thr Asp Pro Gln Asn Leu Thr Asp Val Ser Ile Phe Leu Leu Arg
 1           5           10           15
Gly Thr Ser Glu Asp Pro Glu Trp Gln Leu Val Leu Ala Gly Leu Phe
      20           25           30
Leu Ser Met Cys Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Leu

```

```

      35      40      45
Ala Val Ser Pro Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu
  50      55      60
Ser Asn Leu Ser Leu Pro Asp Ile Gly Phe Thr Ser Thr Thr Val Ala
  65      70      75      80
Lys Met Ile Val Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala
      85      90      95
Gly Cys Leu Thr Gln Met Ser Pro Phe Ala Ile Phe Gly Val Met Glu
      100      105      110
Glu Asn Thr Leu Leu Ser Val Met Ala Ser Asp Arg Phe Val Ala Ile
      115      120      125
Cys His Pro Leu Tyr His Ser Ala Ile Met Asn Pro Cys Phe Cys Gly
      130      135      140
Phe Leu Val Leu Leu Ser Phe Phe Phe Phe Cys Cys Leu Leu Asp Ala
      145      150      155      160
Gln Leu His Asn Leu Ile Ala Leu Gln Met Thr Cys Phe Lys Asp Val
      165      170      175
Glu Ile Pro Asn Phe Phe Trp Asp Pro Ser Gln Leu Pro His Leu Ala
      180      185      190
Cys Cys Asp Thr Phe Thr Asn Asn Ile Ile Met Tyr Phe Pro Ala Ala
      195      200      205
Ile Phe Gly Phe Leu Pro Ile Ser Gly Ser Leu Phe Ser Tyr Tyr Lys
      210      215      220
Ile Val Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Lys Tyr Xaa
      225      230      235      240
Ala Phe Ser Ser Cys Trp Ser His Leu Ser Val Val Cys Xaa Phe Tyr
      245      250      255
Gly Thr Gly Val Gly Gly Tyr Leu Ser Xaa Asp Val Ser Ser Ser Pro
      260      265      270
Arg Lys Val Ala Val Ala Ser Val Met Tyr Met Val Val Thr Pro Met
      275      280      285
Leu Asn Pro Phe Val Tyr Ser Leu Arg Asn Arg Asp Ile Lys Ser Val
      290      295      300
Leu Arg Trp Pro His Gly Ser Thr Val Xaa Ser Gln Tyr Leu Leu Ile
      305      310      315      320
Cys Ser Ile Pro Phe Val Val Xaa Val Lys Lys Gly Ser Lys Val Lys
      325      330      335

```

<210> 1431

<211> 325

<212> PRT

<213> Unknown (H38g348 protein)

<220>

<223> Synthetic construct

<400> 1431

```

Met Lys Thr Phe Ser Ser Phe Leu Gln Ile Gly Arg Asn Met His Gln
  1      5      10      15
Gly Asn Gln Thr Thr Ile Thr Glu Phe Ile Leu Leu Gly Phe Phe Lys
      20      25      30
Gln Asp Glu His Gln Asn Leu Leu Phe Val Leu Phe Leu Gly Met Tyr
      35      40      45
Leu Val Thr Val Ile Gly Asn Gly Leu Ile Ile Val Ala Ile Ser Leu
      50      55      60
Asp Thr Tyr Leu His Thr Pro Met Tyr Leu Phe Leu Ala Asn Leu Ser
      65      70      75      80
Phe Ala Asp Ile Ser Ser Ile Ser Asn Ser Val Pro Lys Met Leu Val
      85      90      95
Asn Ile Gln Thr Lys Ser Gln Ser Ile Ser Tyr Glu Ser Cys Ile Thr
      100      105      110

```

Gln Met Tyr Phe Ser Ile Val Phe Val Val Ile Asp Asn Leu Leu Leu
 115 120 125
 Gly Thr Met Ala Tyr Asp His Phe Val Ala Ile Cys His Pro Leu Asn
 130 135 140
 Tyr Thr Ile Leu Met Arg Pro Arg Phe Gly Ile Leu Leu Thr Val Ile
 145 150 155 160
 Ser Trp Phe Leu Ser Asn Ile Ile Ala Leu Thr His Thr Leu Leu Leu
 165 170 175
 Ile Gln Leu Leu Phe Cys Asn His Asn Thr Leu Pro His Phe Phe Cys
 180 185 190
 Asp Leu Ala Pro Leu Leu Lys Leu Ser Cys Ser Asp Thr Leu Ile Asn
 195 200 205
 Glu Leu Val Leu Phe Ile Val Gly Leu Ser Val Ile Ile Phe Pro Phe
 210 215 220
 Thr Leu Ser Phe Phe Ser Tyr Val Cys Ile Ile Arg Ala Val Leu Arg
 225 230 235 240
 Val Ser Ser Thr Gln Gly Lys Trp Lys Ala Phe Ser Thr Cys Gly Ser
 245 250 255
 His Leu Thr Val Val Leu Leu Phe Tyr Gly Thr Ile Val Gly Val Tyr
 260 265 270
 Phe Phe Pro Ser Ser Thr His Pro Glu Asp Thr Asp Lys Ile Gly Ala
 275 280 285
 Val Leu Phe Thr Val Val Thr Pro Met Ile Asn Pro Phe Ile Tyr Ser
 290 295 300
 Leu Arg Asn Lys Asp Met Lys Gly Ala Leu Arg Lys Leu Ile Asn Arg
 305 310 315 320
 Lys Ile Ser Ser Leu
 325

<210> 1432

<211> 256

<212> PRT

<213> Unknown (H38g349 protein)

<220>

<223> Synthetic construct

<400> 1432

Met Tyr Phe Phe Leu Ser His Leu Ser Phe Leu Asp Thr Cys Tyr Ser
 1 5 10 15
 Asn Val Phe Thr Pro Lys Leu Leu Glu Ile Leu Val Val Glu Asp Arg
 20 25 30
 Thr Ile Ser Phe Lys Gly Cys Met Val Gln Phe Phe Phe Gly Cys Ala
 35 40 45
 Phe Val Ile Thr Glu Met Phe Met Leu Ala Val Met Ala Tyr Asp Leu
 50 55 60
 Phe Met Ala Val Cys Asn Pro Leu Leu Tyr Thr Val Ala Met Ser Pro
 65 70 75 80
 Lys Leu Cys Ala Leu Leu Val Ala Gly Thr Tyr Thr Trp Gly Gly Leu
 85 90 95
 Cys Ser Leu Thr Leu Thr Tyr Ser Leu Leu Val Leu Ser Tyr Cys Gly
 100 105 110
 Ser Asn Ile Ile Asn His Phe Gly Cys Glu Tyr Ser Ala Ile Leu Ser
 115 120 125
 Leu Ser Cys Ser Asp Pro Tyr Phe Asn Gln Met Ala Cys Leu Val Ile
 130 135 140
 Ser Ile Phe Ser Glu Ala Cys Ser Leu Leu Ala Ile Leu Ala Phe Tyr
 145 150 155 160
 Val Phe Ile Val Ala Thr Val Ile Lys Met Leu Ser Thr Gly Gly Pro
 165 170 175
 Gln Lys Ala Ile Ser Thr Cys Ala Ser His Leu Thr Thr Val Ser Ile

			180					185					190		
Phe	His	Gly	Val	Ile	Leu	Leu	Leu	Tyr	Cys	Val	Pro	Asn	Ser	Lys	Ser
		195					200					205			
Ser	Trp	Leu	Leu	Val	Lys	Val	Ala	Thr	Val	Leu	Phe	Thr	Val	Ile	Ile
	210					215					220				
Pro	Met	Leu	Asn	Pro	Leu	Ile	Tyr	Ser	Leu	Arg	Asn	Lys	Asp	Val	Lys
225					230					235					240
Gly	Thr	Val	Arg	Lys	Leu	Ile	Asn	Ser	Gln	Ser	Pro	Phe	His	Ser	Lys
				245					250					255	

<210> 1433

<211> 318

<212> PRT

<213> Unknown (H38g350 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1) ... (318)

<223> Xaa = Any Amino Acid

<400> 1433

Met 1	Ala	Glu	Ser	Gly 5	Thr	Thr	Val	Thr	Glu 10	Phe	Phe	Leu	Arg	Gly 15	Phe
Arg	Leu	Lys	Ala 20	Glu	Leu	Gln	Ile	Gly 25	Leu	Phe	Phe	Val	Phe	Leu	Val
Ile	Phe	Leu 35	Ile	Thr	Met	Gly	Gly 40	Asn	Leu	Gly	Met	Ile	Val	Leu	Met
Leu	Ile 50	Gln	Thr	Asp	Pro	Arg 55	Leu	Gln	Thr	Pro	Met 60	Tyr	Phe	Phe	Leu
Ser 65	His	Leu	Ser	Phe 70	Leu	Asp	Ile	Cys	Tyr	Ser 75	Ser	Val	Ile	Gly	Pro 80
Gln	Leu	Leu	Glu	Thr 85	Leu	Ala	Thr	Asp	Lys 90	Met	Ile	Ile	Thr	Tyr 95	Glu
Arg	Cys	Ala 100	Ser	Gln	Phe	Phe	Phe	Phe 105	Thr	Leu	Cys	Ala	Ser 110	Ile	Glu
Cys	Phe	Leu 115	Leu	Ala	Val	Met	Ala 120	Tyr	Asp	Arg	Tyr	Val	Ala 125	Val	Cys
Asn	Pro 130	Leu	Leu	Tyr	Ala 135	Ile	Val	Met	Thr	Pro	Lys 140	Thr	Arg	Leu	Ala
Leu 145	Leu	Ala	Gly	Ala 150	Tyr	Ser	Gly	Ala	Ile	Val 155	Asn	Ser	Val	Ile	Cys 160
Thr	Gly	Cys	Thr	Phe 165	Ser	Ile	Ser	Phe	Ser 170	Lys	Ser	Asn	His	Val 175	Asp
Phe	Phe	Phe 180	Cys	Asp	Leu	Pro	Pro	Leu 185	Leu	Lys	Leu	Ala	Cys 190	Ser	Glu
Thr	Arg	Pro 195	Arg	Glu	Trp	Val	Ile 200	Tyr	Leu	Ser	Ala	Phe 205	Leu	Val	Ile
Thr	Thr 210	Ser	Ile	Ser	Val	Ile 215	Leu	Thr	Ser	Tyr	Leu	Phe	Ile	Ile	Gln
Ser 225	Val	Leu	Lys	Ile	Arg 230	Thr	Ala	Gly	Gly	Arg 235	Ala	Lys	Thr	Phe	Ser 240
Thr	Cys	Ala	Ser	His 245	Met	Thr	Ala	Leu	Thr 250	Leu	Phe	Phe	Gly	Thr 255	Leu
Ile	Phe	Ile 260	Tyr	Leu	Lys	Gly	Asn 265	Met	Gly	Glu	Ser	Leu	Glu	Glu	Asp
Lys	Ile	Val 275	Ser	Ile	Phe	Tyr	Thr 280	Val	Val	Ile	Pro	Met 285	Leu	Asn	Pro
Met	Ile 290	Tyr	Ser	Leu	Arg	Asn 295	Lys	Asp	Met	Lys	Glu 300	Ala	Leu	Lys	Lys

Val Phe Asn Arg Ile Arg Val Ser Gln Ala Glu Xaa Leu Leu
 305 310 315

<210> 1434

<211> 313

<212> PRT

<213> Unknown (H38g351 protein)

<220>

<223> Synthetic construct

<400> 1434

Met Leu Leu Thr Asp Arg Asn Thr Ser Gly Thr Thr Phe Thr Leu Leu
 1 5 10 15
 Gly Phe Ser Asp Tyr Pro Glu Leu Gln Val Pro Leu Phe Leu Val Phe
 20 25 30
 Leu Ala Ile Tyr Asn Val Thr Val Leu Gly Asn Ile Gly Leu Ile Val
 35 40 45
 Ile Ile Lys Ile Asn Pro Lys Leu His Thr Pro Met Tyr Phe Phe Leu
 50 55 60
 Ser Gln Leu Ser Phe Val Asp Phe Cys Tyr Ser Ser Ile Ile Ala Pro
 65 70 75 80
 Lys Met Leu Val Asn Leu Val Val Lys Asp Arg Thr Ile Ser Phe Leu
 85 90 95
 Gly Cys Val Val Gln Phe Phe Phe Phe Cys Thr Phe Val Val Thr Glu
 100 105 110
 Ser Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys
 115 120 125
 Asn Pro Leu Leu Tyr Thr Val Asp Met Ser Gln Lys Leu Cys Val Leu
 130 135 140
 Leu Val Val Gly Ser Tyr Ala Trp Gly Val Ser Cys Ser Leu Glu Leu
 145 150 155 160
 Thr Cys Ser Ala Leu Lys Leu Cys Phe His Gly Phe Asn Thr Ile Asn
 165 170 175
 His Phe Phe Cys Glu Phe Ser Ser Leu Leu Ser Leu Ser Cys Ser Asp
 180 185 190
 Thr Tyr Ile Asn Gln Trp Leu Leu Phe Phe Leu Ala Thr Phe Asn Glu
 195 200 205
 Ile Ser Thr Leu Leu Ile Val Leu Thr Ser Tyr Ala Phe Ile Val Val
 210 215 220
 Thr Ile Leu Lys Met Arg Ser Val Ser Gly Arg Arg Lys Ala Phe Ser
 225 230 235 240
 Thr Cys Ala Ser His Leu Thr Ala Ile Thr Ile Phe His Gly Thr Ile
 245 250 255
 Leu Phe Leu Tyr Cys Val Pro Asn Ser Lys Asn Ser Arg His Thr Val
 260 265 270
 Lys Val Ala Ser Val Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro
 275 280 285
 Leu Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Asp Thr Val Thr Glu
 290 295 300
 Ile Leu Asp Thr Lys Val Phe Ser Tyr
 305 310

<210> 1435

<211> 312

<212> PRT

<213> Unknown (H38g352 protein)

<220>

<223> Synthetic construct

<400> 1435

```

Met Ala Glu Arg Asn Tyr Thr Val Val Thr Glu Phe Phe Leu Thr Ala
1      5      10      15
Phe Thr Glu His Leu Gln Trp Arg Val Pro Leu Phe Leu Ile Phe Leu
20     25     30
Ser Phe Tyr Leu Ala Thr Met Leu Gly Asn Thr Gly Met Ile Leu Leu
35     40     45
Ile Arg Gly Asp Arg Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser
50     55     60
His Leu Ser Leu Val Asp Ile Cys Tyr Ser Ser Ala Ile Ile Pro Gln
65     70     75     80
Met Leu Ala Val Leu Trp Glu His Gly Thr Thr Ile Ser Gln Ala Arg
85     90     95
Cys Ala Ala Gln Phe Phe Leu Phe Thr Phe Phe Ala Ser Ile Asp Cys
100    105    110
Tyr Leu Leu Ala Ile Met Ala Tyr Asp Arg Tyr Thr Ala Val Cys Gln
115    120    125
Pro Leu Leu Tyr Val Thr Ile Ile Thr Glu Lys Asp Arg Leu Gly Leu
130    135    140
Val Thr Gly Ala Tyr Val Ala Gly Phe Phe Ser Ala Phe Val Arg Thr
145    150    155    160
Val Thr Ala Phe Thr Leu Ser Phe Cys Gly Asn Asn Glu Ile Asn Phe
165    170    175
Ile Phe Cys Asp Leu Pro Pro Leu Leu Lys Leu Ser Cys Gly Asp Ser
180    185    190
Tyr Thr Gln Glu Val Val Ile Ile Val Phe Ala Leu Phe Val Met Pro
195    200    205
Ala Cys Ile Leu Val Ile Leu Val Ser Tyr Leu Phe Ile Ile Val Ala
210    215    220
Ile Leu Gln Ile His Ser Ala Gly Gly Arg Ala Lys Thr Phe Ser Thr
225    230    235    240
Cys Ala Ser His Leu Thr Ala Val Ala Leu Phe Phe Gly Thr Leu Ile
245    250    255
Phe Met Tyr Leu Arg Asp Asn Thr Gly Gln Ser Ser Glu Gly Asp Arg
260    265    270
Val Val Ser Val Leu Tyr Thr Val Val Thr Pro Met Leu Asn Pro Leu
275    280    285
Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Glu Ala Thr Arg Lys Ala
290    295    300
Leu Ser Lys Ser Lys Pro Ala Arg
305    310

```

<210> 1436

<211> 254

<212> PRT

<213> Unknown (H38g353 protein)

<220>

<223> Synthetic construct

<400> 1436

```

Met Tyr Tyr Phe Leu Ser Met Leu Ser Ala Thr Asp Leu Gly Leu Ser
1      5      10      15
Ile Ser Thr Leu Val Thr Met Leu Ser Ile Phe Trp Phe Asn Val Arg
20     25     30
Glu Ile Ser Phe Asn Ala Cys Leu Ser His Met Phe Phe Ile Lys Phe
35     40     45
Phe Thr Val Met Glu Ser Ser Val Leu Leu Ala Met Ala Phe Asp Arg
50     55     60
Phe Val Ala Val Ser Asn Pro Leu Arg Tyr Ala Met Ile Leu Thr Asp
65     70     75     80

```

Ser Arg Ile Ala Gln Ile Gly Val Ala Ser Val Ile Arg Gly Leu Leu
 85 90 95
 Met Leu Thr Pro Met Val Ala Leu Leu Ile Arg Leu Ser Tyr Cys His
 100 105 110
 Ser Gln Val Leu His His Ser Tyr Cys Tyr His Pro Asp Val Met Lys
 115 120 125
 Leu Ser Cys Thr Asp Thr Arg Ile Asn Ser Ala Val Gly Leu Thr Ala
 130 135 140
 Met Phe Ser Thr Val Gly Val Asp Leu Leu Leu Ile Leu Leu Ser Tyr
 145 150 155 160
 Val Leu Ile Ile Arg Thr Val Leu Ser Val Ala Ser Pro Glu Glu Arg
 165 170 175
 Lys Glu Thr Phe Ser Thr Cys Val Ser His Ile Val Ala Phe Ala Ile
 180 185 190
 Tyr Tyr Ile Pro Leu Ile Ser Leu Ser Ile Val His Arg Phe Gly Lys
 195 200 205
 Gln Ala Pro Ala Tyr Val His Thr Met Ile Ala Asn Thr Tyr Leu Leu
 210 215 220
 Ile Ser Pro Leu Met Asn Pro Val Ile Tyr Ser Val Lys Thr Lys Gln
 225 230 235 240
 Ile Arg Arg Ala Val Ile Lys Ile Leu His Ser Lys Glu Thr
 245 250

<210> 1437

<211> 188

<212> PRT

<213> Unknown (H38g354 protein)

<220>

<223> Synthetic construct

<400> 1437

Met Asp Trp Glu Asn Cys Ser Ser Leu Thr Asp Phe Phe Leu Leu Gly
 1 5 10 15
 Ile Thr Asn Asn Pro Glu Met Lys Val Thr Leu Phe Ala Val Phe Leu
 20 25 30
 Ala Val Tyr Ile Ile Asn Phe Ser Ala Asn Leu Gly Met Ile Val Leu
 35 40 45
 Ile Arg Met Asp Tyr Gln Leu His Thr Pro Met Tyr Phe Phe Leu Ser
 50 55 60
 His Leu Ser Phe Cys Asp Leu Cys Tyr Ser Thr Ala Thr Gly Pro Lys
 65 70 75 80
 Met Leu Val Asp Leu Leu Ala Lys Asn Lys Ser Ile Pro Phe Tyr Gly
 85 90 95
 Cys Ala Leu Gln Phe Leu Val Phe Cys Ile Phe Ala Asp Ser Glu Cys
 100 105 110
 Leu Leu Leu Ser Val Met Ala Phe Asp Arg Tyr Lys Ala Ile Ile Asn
 115 120 125
 Pro Leu Leu Tyr Thr Val Asn Met Ser Ser Arg Val Cys Tyr Leu Leu
 130 135 140
 Leu Thr Gly Val Tyr Leu Val Gly Ile Ala Asp Ala Leu Ile His Met
 145 150 155 160
 Thr Leu Ala Phe Arg Leu Cys Phe Cys Gly Ser Asn Glu Ile Asn His
 165 170 175
 Phe Phe Cys Asp Ile Pro Pro Leu Leu Leu Ser
 180 185

<210> 1438

<211> 326

<212> PRT

<213> Unknown (H38g355 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(326)

<223> Xaa = Any Amino Acid

<400> 1438

```

Leu Asn Phe Ile Ile Phe Phe Arg Xaa Thr Ser Tyr Ile Glu Pro Met
 1           5           10           15
Ala Lys Arg Asn Leu Ser Thr Val Thr Glu Phe Ile Leu Val Val Phe
 20           25           30
Thr Asp His Pro Glu Leu Ala Val Pro Leu Phe Leu Val Phe Leu Ser
 35           40           45
Phe Tyr Leu Val Thr Phe Leu Gly Asn Gly Gly Met Ile Ile Leu Ile
 50           55           60
Gln Val Asp Ala Gln Leu His Thr Pro Val Tyr Phe Phe Leu Ser His
 65           70           75           80
Leu Ala Phe Leu Asp Ala Cys Cys Ala Ser Val Ile Thr Pro Gln Ile
 85           90           95
Leu Ala Thr Leu Ala Thr Asp Lys Thr Val Ile Ser Tyr Gly Cys Arg
 100          105          110
Ala Val Gln Phe Ser Phe Phe Thr Ile Cys Ala Gly Thr Glu Cys Tyr
 115          120          125
Leu Leu Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile Ser Asn Pro
 130          135          140
Leu His Cys Asn Met Thr Met Thr Pro Gly Thr Cys Arg Val Phe Leu
 145          150          155          160
Ala Ser Ala Phe Ile Cys Gly Val Ser Gly Ala Ile Leu His Thr Thr
 165          170          175
Cys Thr Phe Thr Leu Ser Phe Cys Cys Asp Asn Gln Ile Asn Phe Phe
 180          185          190
Phe Cys Asp Leu Pro Pro Leu Leu Lys Leu Ala Cys Ser Ser Met Thr
 195          200          205
Gln Thr Glu Ile Val Ile Leu Leu Cys Ala Lys Cys Met Phe Leu Ala
 210          215          220
Asn Val Met Val Ile Leu Ile Cys Tyr Met Leu Ile Ile Arg Ala Ile
 225          230          235          240
Leu Arg Val Lys Ser Ala Gly Gly Xaa Ala Lys Thr Phe Ser Thr Cys
 245          250          255
Thr Ser His Leu Thr Thr Val Val Leu Phe Phe Gly Thr Leu Ala Phe
 260          265          270
Met Tyr Gln Arg Ser Asn Ser Ala Lys Ser Ser Glu Glu Asp Lys Ile
 275          280          285
Val Ser Val Phe Tyr Thr Val Ile Ile Pro Met Leu Asn Pro Leu Ile
 290          295          300
Tyr Ser Leu Arg Asn Lys Asp Val Lys Ala Ala Phe Gly Lys Leu Val
 305          310          315          320
Gly Lys Phe Gln Phe Pro
 325

```

<210> 1439

<211> 328

<212> PRT

<213> Unknown (H38g356 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(328)

<223> Xaa = Any Amino Acid

<400> 1439

```

Met Leu Pro Ser Gln Thr Tyr Val Asn Ile Ser Phe Phe Gln Pro Pro
 1          5          10          15
Ala Leu Leu Met Ile Gly Ile Pro Gly Leu Glu Ala Val His Gly Trp
          20          25          30
Leu Ala Ile Pro Phe Ser Ser Met Tyr Thr Val Ala Leu Pro Gly Asn
          35          40          45
Cys Leu Ile Leu Leu Ala Val Lys Arg Asn Pro Ser Leu His Gln Pro
          50          55          60
Met Cys Tyr Phe Leu Ser Met Leu Ala Leu Pro Lys Ala Gly Leu Thr
65          70          75          80
Leu Ser Thr Leu Pro Ile Thr Leu Ala Val Leu Trp Phe Asp His Arg
          85          90          95
Leu Met Gly Phe Asn Ala Cys Leu Val Gln Met Phe Phe Leu His Ser
          100          105          110
Ser Val Val Glu Ser Ser Val Leu Leu Ala Ile Ser Phe Asp His Phe
          115          120          125
Val Ala Ile Ser Asn Pro Leu His Tyr Ala Ala Val Leu Thr Asn Ser
          130          135          140
Val Ile Ile Arg Ile Gly Leu Ala Ile Val Ala Arg Ser Tyr Leu Val
145          150          155          160
Pro Leu Pro Val Pro Phe Pro Val Lys Ser Leu Asn Phe Cys Pro Gly
          165          170          175
Asp Asn Ile Pro Ser His Ser Phe Cys Phe His Pro Asp Val Met Arg
          180          185          190
Arg Ala Cys Ala Asp Ile Thr Ile Asn Ile Cys Tyr Gly Val Tyr Val
          195          200          205
Val Val Ser Thr Gly Gly Leu Asp Ser Leu Leu Ile Phe Leu Ser Tyr
          210          215          220
Thr Phe Ile Leu His Thr Val Met Gly Leu Ala Ala Pro Arg Glu Arg
225          230          235          240
Ile Trp Ala Leu Asn Thr Cys Val Ser His Ile Pro Ala Val Phe Val
          245          250          255
Phe Phe Ile Pro Gly Ile Thr Val Ser Met Ile His His Phe Gly Arg
          260          265          270
His Leu Pro His Ile Val His Ala Leu Val Thr Tyr Val Tyr Leu Val
          275          280          285
Met Pro Ser Val Leu His Pro Ile Ile Tyr Ser Met Lys Ser Lys Pro
          290          295          300
Ile Arg Glu Ala Ile Leu Arg Met Leu Met Gly Arg Ser Gln Gly Xaa
305          310          315          320
Xaa Asn Tyr Lys Ile Leu Xaa Gly
          325

```

<210> 1440

<211> 311

<212> PRT

<213> Unknown (H38g357 protein)

<220>

<223> Synthetic construct

<400> 1440

```

Met Gly Lys Glu Asn Cys Thr Thr Val Ala Glu Phe Ile Leu Leu Gly
 1          5          10          15
Leu Ser Asp Val Pro Glu Leu Arg Val Cys Leu Phe Leu Leu Phe Leu
          20          25          30
Leu Ile Tyr Gly Val Thr Leu Leu Ala Asn Leu Gly Met Ile Ala Leu

```

```

      35      40      45
Ile Gln Val Ser Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser
  50      55      60
His Leu Ser Ser Val Asp Phe Cys Tyr Ser Ser Ile Ile Val Pro Lys
  65      70      75      80
Met Leu Ala Asn Ile Phe Asn Lys Asp Lys Ala Ile Ser Phe Leu Gly
      85      90      95
Cys Met Val Gln Phe Tyr Leu Phe Cys Thr Cys Val Val Thr Glu Val
      100      105      110
Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys Asn
      115      120      125
Pro Leu Leu Tyr Thr Val Thr Met Ser Trp Lys Val Arg Val Glu Leu
      130      135      140
Ala Ser Cys Cys Tyr Phe Cys Gly Thr Val Cys Ser Leu Ile His Leu
  145      150      155      160
Cys Leu Ala Leu Arg Ile Pro Phe Tyr Arg Ser Asn Val Ile Asn His
      165      170      175
Phe Phe Cys Asp Leu Pro Pro Val Leu Ser Leu Ala Cys Ser Asp Ile
      180      185      190
Thr Val Asn Glu Thr Leu Leu Phe Leu Val Ala Thr Leu Asn Glu Ser
      195      200      205
Val Thr Ile Met Ile Ile Leu Thr Ser Tyr Leu Leu Ile Leu Thr Thr
  210      215      220
Ile Leu Lys Met Gly Ser Ala Glu Gly Arg His Lys Ala Phe Ser Thr
  225      230      235      240
Cys Ala Ser His Leu Thr Ala Ile Thr Val Phe His Gly Thr Val Leu
      245      250      255
Ser Ile Tyr Cys Arg Pro Ser Ser Gly Asn Ser Gly Asp Ala Asp Lys
      260      265      270
Val Ala Thr Val Phe Tyr Thr Val Val Ile Pro Met Leu Asn Ser Val
      275      280      285
Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Glu Ala Leu Arg Lys Val
  290      295      300
Met Gly Ser Lys Ile His Ser
  305      310

```

<210> 1441

<211> 209

<212> PRT

<213> Unknown (H38g358 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(209)

<223> Xaa = Any Amino Acid

<400> 1441

```

Cys His Pro Pro Leu Arg Trp Gly Ser Xaa Glu Pro Ala Glu Glu Glu
  1      5      10      15
Gly Leu Ala Leu Ser Ser Arg Phe Phe Phe Phe Leu Ser Val Leu Asp
      20      25      30
Ala Gln Leu His Asn Leu Ile Ala Leu Gln Met Thr Cys Phe Gln Asp
      35      40      45
Ala Glu Ile Pro Asn Phe Phe Trp Asp Pro Ser Gln Leu Pro His Leu
  50      55      60
Ala Cys Cys Asp Thr Phe Thr Asn Asn Ile Ile Met Tyr Phe Pro Ala
  65      70      75      80
Val Ile Phe Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser Tyr Tyr
      85      90      95

```

Lys Ile Val Ser Ser Ile Leu Ser Val Ser Ser Ser Arg Gly Gln Tyr
 100 105 110
 Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Cys Xaa Phe
 115 120 125
 Tyr Gly Thr Gly Val Gly Gly Tyr Phe Ser Ser Asp Val Ser Ser Ser
 130 135 140
 Pro Arg Lys Ala Ala Val Ala Ser Val Met Tyr Thr Val Ile Thr Pro
 145 150 155 160
 Met Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Arg His Ile Lys Ser
 165 170 175
 Val Leu Arg Arg Pro His Ser Ser Thr Val Gln Ser Pro Cys Leu Leu
 180 185 190
 Asn Cys Ser Ile Pro Phe Val Val Trp Val Asn Lys Gly Ser Lys Val
 195 200 205
 Lys

<210> 1442

<211> 212

<212> PRT

<213> Unknown (H38g359 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(212)

<223> Xaa = Any Amino Acid

<400> 1442

Ile Xaa Leu Lys Leu Ile Phe Gly Asn Pro Arg Xaa Xaa Xaa Ile Phe
 1 5 10 15
 Arg Cys Val Tyr Asp Tyr Leu Trp Asp Cys Gln Pro Leu Leu Tyr Asp
 20 25 30
 Thr Ile Thr Thr Leu Lys Met Ser Gly Arg Ser Trp Xaa Leu His Ile
 35 40 45
 Val Glu Gly Leu Thr Asn Val Ile Gln Cys Ile His Phe Thr Cys Ser
 50 55 60
 Leu Ser Phe Cys Gly Thr Ser Ser Ile Gly Phe Thr Leu Cys Asp Leu
 65 70 75 80
 Pro Leu Leu Leu Thr Leu Asn Cys Gly Asp Ser Phe Leu Gln Gln Leu
 85 90 95
 Leu Ile Phe His Phe Ala Leu Tyr Met Ile Leu Thr Arg Leu Val Leu
 100 105 110
 Ile Leu Phe Ser Asp Leu Phe Ile Ser Lys Ala Ile Xaa Thr Pro Ala
 115 120 125
 Asn Gln Val Ser Arg Gln Arg Phe Leu Asn Leu Phe Leu Pro Leu Pro
 130 135 140
 His Ala Glu Leu Gln Phe Gly Xaa Leu Leu Arg Leu Gln Leu Xaa Ser
 145 150 155 160
 Met Cys Ala Ala Val Gly Lys Ser Leu Thr Gly Glu Arg Ala Val Thr
 165 170 175
 Met Phe Xaa Thr Glu Xaa Thr Pro Gly Xaa Pro Phe Gln Phe Tyr Ser
 180 185 190
 Leu Arg Asn Lys Lys Ala Lys Glu Ala Leu Arg Lys Gly Leu Asn Lys
 195 200 205
 Ala Lys Leu Phe
 210

<210> 1443

<211> 315

<212> PRT

<213> Unknown (H38g360 protein)

<220>

<223> Synthetic construct

<400> 1443

```

Met Ser Ser Cys Asn Phe Thr His Ala Thr Phe Val Leu Ile Gly Ile
 1      5      10      15
Pro Gly Leu Glu Lys Ala His Phe Trp Val Gly Phe Pro Leu Leu Ser
 20      25      30
Met Tyr Val Val Ala Met Phe Gly Asn Cys Ile Val Val Phe Ile Val
 35      40      45
Arg Thr Glu Arg Ser Leu His Ala Pro Met Tyr Leu Phe Leu Cys Met
 50      55      60
Leu Ala Ala Ile Asp Leu Ala Leu Ser Thr Ser Thr Met Pro Lys Ile
 65      70      75      80
Leu Ala Leu Phe Trp Phe Asp Ser Arg Glu Ile Ser Phe Glu Ala Cys
 85      90      95
Leu Thr Gln Met Phe Phe Ile His Ala Leu Ser Ala Ile Glu Ser Thr
100      105      110
Ile Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys His Pro
115      120      125
Leu Arg His Ala Ala Val Leu Asn Asn Thr Val Thr Ala Gln Ile Gly
130      135      140
Ile Val Ala Val Val Arg Gly Ser Leu Phe Phe Phe Pro Leu Pro Leu
145      150      155      160
Leu Ile Lys Arg Leu Ala Phe Cys His Ser Asn Val Leu Ser His Ser
165      170      175
Tyr Cys Val His Gln Asp Val Met Lys Leu Ala Tyr Ala Asp Thr Leu
180      185      190
Pro Asn Val Val Tyr Gly Leu Thr Ala Ile Leu Leu Val Met Gly Val
195      200      205
Asp Val Met Phe Ile Ser Leu Ser Tyr Phe Leu Ile Ile Arg Thr Val
210      215      220
Leu Gln Leu Pro Ser Lys Ser Glu Arg Ala Lys Ala Phe Gly Thr Cys
225      230      235      240
Val Ser His Ile Gly Val Val Leu Ala Phe Tyr Val Pro Leu Ile Gly
245      250      255
Leu Ser Val Val His Arg Phe Gly Asn Ser Leu His Pro Ile Val Arg
260      265      270
Val Val Met Gly Asp Ile Tyr Leu Leu Leu Pro Pro Val Ile Asn Pro
275      280      285
Ile Ile Tyr Gly Ala Lys Thr Lys Gln Ile Arg Thr Arg Val Leu Ala
290      295      300
Met Phe Lys Ile Ser Cys Asp Lys Asp Leu Gln
305      310      315

```

<210> 1444

<211> 278

<212> PRT

<213> Unknown (H38g361 protein)

<220>

<223> Synthetic construct

<400> 1444

```

Met Tyr Ala Leu Ala Thr Leu Gly Asn Leu Thr Ile Val Leu Ile Ile
 1      5      10      15
Arg Val Glu Arg Arg Leu His Glu Pro Met Tyr Leu Phe Leu Ala Met
 20      25      30

```

```

Leu Ser Thr Ile Asp Leu Val Leu Ser Ser Ile Thr Met Pro Lys Met
   35                               40                               45
Ala Ser Leu Phe Leu Met Gly Ile Gln Glu Ile Glu Phe Asn Ile Cys
   50                               55                               60
Leu Ala Gln Met Phe Leu Ile His Ala Leu Ser Ala Val Glu Ser Ala
   65                               70                               75                               80
Val Leu Leu Ala Met Ala Phe Asp Arg Phe Val Ala Ile Cys His Pro
   85                               90                               95
Leu Arg His Ala Ser Val Leu Thr Gly Cys Thr Val Ala Lys Ile Gly
  100                               105                               110
Leu Ser Ala Leu Thr Arg Gly Phe Val Phe Phe Phe Pro Leu Pro Phe
  115                               120                               125
Ile Leu Lys Trp Leu Ser Tyr Cys Gln Thr His Thr Val Thr His Ser
  130                               135                               140
Phe Cys Leu His Gln Asp Ile Met Lys Leu Ser Cys Thr Asp Thr Arg
  145                               150                               155                               160
Val Asn Val Val Tyr Gly Leu Phe Ile Ile Leu Ser Val Met Gly Val
  165                               170                               175
Asp Ser Leu Phe Ile Gly Phe Ser Tyr Ile Leu Ile Leu Trp Ala Val
  180                               185                               190
Leu Glu Leu Ser Ser Arg Arg Ala Ala Leu Lys Ala Phe Asn Thr Cys
  195                               200                               205
Ile Ser His Leu Cys Ala Val Leu Val Phe Tyr Val Pro Leu Ile Gly
  210                               215                               220
Leu Ser Val Val His Arg Leu Gly Gly Pro Thr Ser Leu Leu His Val
  225                               230                               235                               240
Val Met Ala Asn Thr Tyr Leu Leu Leu Pro Pro Val Val Asn Pro Leu
  245                               250                               255
Val Tyr Gly Ala Lys Thr Lys Glu Ile Cys Ser Arg Val Leu Cys Met
  260                               265                               270
Phe Ser Gln Gly Gly Lys
  275

```

<210> 1445

<211> 319

<212> PRT

<213> Unknown (H38g362 protein)

<220>

<223> Synthetic construct

<400> 1445

```

Met Leu Gly Pro Ala Tyr Asn His Thr Met Glu Thr Pro Ala Ser Phe
  1                               5                               10                               15
Leu Leu Val Gly Ile Pro Gly Leu Gln Ser Ser His Leu Trp Leu Ala
  20                               25                               30
Ile Ser Leu Ser Ala Met Tyr Ile Thr Ala Leu Leu Gly Asn Thr Leu
  35                               40                               45
Ile Val Thr Ala Ile Trp Met Asp Ser Thr Arg His Glu Pro Met Tyr
  50                               55                               60
Cys Phe Leu Cys Val Leu Ala Ala Val Asp Ile Val Met Ala Ser Ser
  65                               70                               75                               80
Val Val Pro Lys Met Val Ser Ile Phe Cys Ser Gly Asp Ser Ser Ile
  85                               90                               95
Ser Phe Ser Ala Cys Phe Thr Gln Met Phe Phe Val His Leu Ala Thr
  100                               105                               110
Ala Val Glu Thr Gly Leu Leu Leu Thr Met Ala Phe Asp Arg Tyr Val
  115                               120                               125
Ala Ile Cys Lys Pro Leu His Tyr Lys Arg Ile Leu Thr Pro Gln Val
  130                               135                               140
Met Leu Gly Met Ser Met Ala Val Thr Ile Arg Ala Val Thr Phe Met

```

```

145          150          155          160
Thr Pro Leu Ser Trp Met Met Asn His Leu Pro Phe Cys Gly Ser Asn
          165          170          175
Val Val Val His Ser Tyr Cys Lys His Ile Ala Leu Ala Arg Leu Ala
          180          185          190
Cys Ala Asp Pro Val Pro Ser Ser Leu Tyr Ser Leu Ile Gly Ser Ser
          195          200          205
Leu Met Val Gly Ser Asp Val Ala Phe Ile Ala Ala Ser Tyr Ile Leu
          210          215          220
Ile Leu Arg Ala Val Phe Asp Leu Ser Ser Lys Thr Ala Gln Leu Lys
225          230          235          240
Ala Leu Ser Thr Cys Gly Ser His Val Gly Val Met Ala Leu Tyr Tyr
          245          250          255
Leu Pro Gly Met Ala Ser Ile Tyr Ala Ala Trp Leu Gly Gln Asp Ile
          260          265          270
Val Pro Leu His Thr Gln Val Leu Ala Asp Leu Tyr Val Ile Ile
          275          280          285
Pro Ala Thr Leu Asn Pro Ile Ile Tyr Gly Met Arg Thr Lys Gln Leu
          290          295          300
Leu Glu Gly Ile Trp Ser Tyr Leu Met His Phe Leu Phe Asp His
305          310          315

```

<210> 1446

<211> 322

<212> PRT

<213> Unknown (H38g363 protein)

<220>

<223> Synthetic construct

<400> 1446

```

Met Asn Glu Thr Asn His Ser Trp Val Thr Glu Phe Val Leu Leu Gly
 1          5          10          15
Leu Ser Ser Ser Arg Glu Leu Gln Pro Phe Leu Phe Leu Ile Phe Ser
          20          25          30
Leu Leu Tyr Leu Ala Ile Leu Leu Gly Asn Phe Leu Ile Ile Leu Thr
          35          40          45
Val Thr Ser Asp Ser Arg Leu His Thr Pro Met Tyr Phe Leu Leu Ala
          50          55          60
Asn Leu Ser Phe Ile Asp Val Cys Val Ala Ser Ser Ala Thr Pro Lys
65          70          75          80
Met Ile Ala Asp Phe Leu Val Glu His Lys Thr Ile Ser Phe Asp Ala
          85          90          95
His Leu Ala Gln Ile Phe Phe Val His Leu Phe Thr Gly Ser Glu Met
          100          105          110
Val Leu Leu Val Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys
          115          120          125
Pro Pro His Tyr Met Thr Ile Met Ser Cys Cys Val Cys Val Val Leu
          130          135          140
Val Leu Ile Ser Trp Phe Val Gly Phe Ile His Thr Thr Ser Gln Leu
145          150          155          160
Ala Phe Thr Val Asn Leu Pro Phe Cys Gly Pro Asn Lys Val Asp Ser
          165          170          175
Phe Phe Cys Asp Leu Pro Leu Ala Thr Lys Leu Ala Cys Ile Asp Thr
          180          185          190
Tyr Val Val Ser Leu Leu Ile Val Ala Asp Ser Gly Phe Leu Ser Leu
          195          200          205
Ser Ser Phe Leu Leu Leu Val Val Ser Tyr Thr Val Ile Leu Val Thr
          210          215          220
Val Arg Asn Arg Ser Ser Val Ser Met Val Lys Ala His Ser Thr Leu
225          230          235          240

```

Thr Ala His Ile Thr Val Val Thr Leu Phe Phe Gly Ser Cys Ile Phe
 245 250 255
 Ile Tyr Val Trp Pro Phe Ser Ser Tyr Ser Val Asp Lys Val Leu Ala
 260 265 270
 Val Phe Tyr Thr Ile Phe Thr Ser Ile Leu Asn Pro Val Ile Tyr Met
 275 280 285
 Leu Arg Asn Lys Glu Val Lys Ala Ala Met Ser Lys Leu Lys Ser Arg
 290 295 300
 Tyr Gln Lys Leu Gly Gln Val Ser Val Val Ile Arg Asn Val Leu Phe
 305 310 315 320
 Leu Glu

<210> 1447

<211> 322

<212> PRT

<213> Unknown (H38g364 protein)

<220>

<223> Synthetic construct

<400> 1447

Met Leu Gly Pro Ala Tyr Asn His Thr Met Glu Thr Pro Ala Ser Phe
 1 5 10 15
 Leu Leu Val Gly Ile Pro Gly Leu Gln Ser Ser His Leu Trp Leu Ala
 20 25 30
 Ile Ser Leu Ser Ala Met Tyr Ile Ile Ala Leu Leu Gly Asn Thr Ile
 35 40 45
 Ile Val Thr Ala Ile Trp Met Asp Ser Thr Arg His Glu Pro Met Tyr
 50 55 60
 Cys Phe Leu Cys Val Leu Ala Ala Val Asp Ile Val Met Ala Ser Ser
 65 70 75 80
 Val Val Pro Lys Met Val Ser Ile Phe Cys Ser Gly Asp Ser Ser Ile
 85 90 95
 Ser Phe Ser Ala Cys Phe Thr Gln Met Phe Phe Val His Leu Ala Thr
 100 105 110
 Ala Val Glu Thr Gly Leu Leu Leu Thr Met Ala Phe Asp Arg Tyr Val
 115 120 125
 Ala Ile Cys Lys Pro Leu His Tyr Lys Arg Ile Leu Thr Pro Gln Val
 130 135 140
 Met Leu Gly Met Ser Met Ala Ile Thr Ile Arg Ala Ile Ile Ala Ile
 145 150 155 160
 Thr Pro Leu Ser Trp Met Val Ser His Leu Pro Phe Cys Gly Ser Asn
 165 170 175
 Val Val Val His Ser Tyr Cys Glu His Ile Ala Leu Ala Arg Leu Ala
 180 185 190
 Cys Ala Asp Pro Val Pro Ser Ser Leu Tyr Ser Leu Ile Gly Ser Ser
 195 200 205
 Leu Met Val Gly Ser Asp Val Ala Phe Ile Ala Ala Ser Tyr Ile Leu
 210 215 220
 Ile Leu Lys Ala Val Phe Gly Leu Ser Ser Lys Thr Ala Gln Leu Lys
 225 230 235 240
 Ala Leu Ser Thr Cys Gly Ser His Val Gly Val Met Ala Leu Tyr Tyr
 245 250 255
 Leu Pro Gly Met Ala Ser Ile Tyr Ala Ala Trp Leu Gly Gln Asp Val
 260 265 270
 Val Pro Leu His Thr Gln Val Leu Leu Ala Asp Leu Tyr Val Ile Ile
 275 280 285
 Pro Ala Thr Leu Asn Pro Ile Ile Tyr Gly Met Arg Thr Lys Gln Leu
 290 295 300
 Arg Glu Arg Ile Trp Ser Tyr Leu Met His Val Leu Phe Asp His Ser

305
Asn Leu

310

315

320

<210> 1448
<211> 314
<212> PRT
<213> Unknown (H38g365 protein)

<220>

<223> Synthetic construct

<400> 1448

```

Met Glu Gly Phe Asn Tyr Ser Arg Val Ser Glu Phe Met Leu Leu Gly
 1           5           10           15
Leu Thr Asp Ser Pro Glu Leu Gln Ile Phe Phe Ser Val Val Phe Ser
           20           25           30
Val Phe Tyr Leu Met Thr Met Leu Gly Asn Cys Leu Ile Leu Leu Thr
           35           40           45
Val Leu Ser Thr Ser His Leu His Ser Arg Met Tyr Phe Leu Leu Ser
           50           55           60
Asn Met Ser Ile Asp Met Cys Leu Ser Ser Phe Ala Thr Pro Lys Met
65           70           75           80
Ile Met Asp Phe Phe Ala Leu Arg Lys Thr Ile Ser Phe Glu Gly Cys
           85           90           95
Ile Ser Gln Ile Phe Phe Leu His Leu Phe Asn Gly Thr Glu Ile Val
           100          105          110
Leu Leu Ile Ser Met Ser Phe Asp Arg Tyr Ile Ala Ile Cys Lys Pro
           115          120          125
Leu His Tyr Ser Thr Ile Met Ser Gln Arg Val Cys Val Glu Leu Val
           130          135          140
Ala Val Ser Cys Trp Thr Val Gly Phe Leu His Thr Met Ser Gln Leu
145          150          155          160
Val Phe Ala Leu Tyr Leu Pro Phe Cys Val Pro Asn Val Val Asp Ser
           165          170          175
Phe Phe Cys Asp Leu Pro Leu Val Ile Gln Leu Ala Cys Ile Asp Ile
           180          185          190
Tyr Val Leu Gly Thr Ser Met Ile Ser Thr Ser Gly Val Ile Ala Leu
           195          200          205
Ile Ser Phe Leu Leu Leu Leu Thr Ser Tyr Ile Ile Val Leu Asn Ile
           210          215          220
Val Arg Asp Tyr Ser Ser Thr Gly Ser Ser Lys Ala Leu Ser Thr Cys
225          230          235          240
Thr Ala His Phe Ile Val Val Leu Met Phe Phe Gly Pro Cys Ile Phe
           245          250          255
Ile Tyr Val Trp Pro Ser Thr Asn Phe Leu Val Asp Lys Ile Leu Ser
           260          265          270
Val Phe Tyr Thr Ile Phe Thr Pro Phe Leu Asn Pro Leu Ile Tyr Thr
           275          280          285
Leu Arg Asn Gln Glu Val Lys Thr Ala Met Lys Lys Lys Leu Asn Ile
           290          295          300
Gln Tyr Phe Ser Leu Gly Lys Thr Ala Pro
305          310

```

<210> 1449
<211> 317
<212> PRT
<213> Unknown (H38g366 protein)

<220>

<223> Synthetic construct

<400> 1449

```

Met Leu Thr Phe His Asn Val Cys Ser Val Pro Ser Ser Phe Trp Leu
 1          5          10          15
Thr Gly Ile Pro Gly Leu Glu Ser Leu His Val Trp Leu Ser Ile Pro
          20          25          30
Phe Gly Ser Met Tyr Leu Val Ala Val Val Gly Asn Val Thr Ile Leu
          35          40          45
Ala Val Val Lys Ile Glu Arg Ser Leu His Gln Pro Met Tyr Phe Phe
          50          55          60
Leu Cys Met Leu Ala Ala Ile Asp Leu Val Leu Ser Thr Ser Thr Ile
65          70          75          80
Pro Lys Leu Leu Gly Ile Phe Trp Phe Gly Ala Cys Asp Ile Gly Leu
          85          90          95
Asp Ala Cys Leu Gly Gln Met Phe Leu Ile His Cys Phe Ala Thr Val
          100          105          110
Glu Ser Gly Ile Phe Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile
          115          120          125
Cys Asn Pro Leu Arg His Ser Met Val Leu Thr Tyr Thr Val Val Gly
130          135          140
Arg Leu Gly Leu Val Ser Leu Leu Arg Gly Val Leu Tyr Ile Gly Pro
145          150          155          160
Leu Pro Leu Met Ile Arg Leu Arg Leu Pro Leu Tyr Lys Thr His Val
          165          170          175
Ile Ser His Ser Tyr Cys Glu His Met Ala Val Val Ala Leu Thr Cys
          180          185          190
Gly Asp Ser Arg Val Asn Asn Val Tyr Gly Leu Ser Ile Gly Phe Leu
          195          200          205
Val Leu Ile Leu Asp Ser Val Ala Ile Ala Ala Ser Tyr Val Met Ile
210          215          220
Phe Arg Ala Val Met Gly Leu Ala Thr Pro Glu Ala Arg Leu Lys Thr
225          230          235          240
Leu Gly Thr Cys Ala Ser His Leu Cys Ala Ile Leu Ile Phe Tyr Val
          245          250          255
Pro Ile Ala Val Ser Ser Leu Ile His Arg Phe Gly Gln Cys Val Pro
          260          265          270
Pro Pro Val His Thr Leu Leu Ala Asn Phe Tyr Leu Leu Ile Pro Pro
          275          280          285
Ile Leu Asn Pro Ile Val Tyr Ala Val Arg Thr Lys Gln Ile Arg Glu
          290          295          300
Ser Leu Leu Gln Ile Pro Arg Ile Glu Met Lys Ile Arg
305          310          315

```

<210> 1450

<211> 101

<212> PRT

<213> Unknown (H38g367 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(101)

<223> Xaa = Any Amino Acid

<400> 1450

```

Gln Met Leu Thr Asp Trp Trp Gly Pro Asn Arg Thr Thr Ser Tyr Val
 1          5          10          15
Asn Cys Thr Ile Gln Phe Leu Val Ser Leu Xaa Cys Met Cys His Tyr
          20          25          30
Ile Ile Ser Tyr Asn Tyr Phe Ile Ile Ile Cys His Pro Leu Xaa Tyr

```

```

      35              40              45
Leu Leu Ile Met Asn Leu Tyr Leu Leu Leu Asn Leu Thr Leu Ile Leu
  50              55              60
Glu Gly Xaa Phe Ile His Phe Trp His His Val Tyr Ser Ile Leu Lys
  65              70              75              80
Ile Pro Arg Met Lys Lys Lys Asn Leu Gln Ile Ile Pro Leu Ile Gly
      85              90              95
Cys Cys Leu Ala Glu
      100

```

<210> 1451
 <211> 169
 <212> PRT
 <213> Unknown (H38g368 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(169)
 <223> Xaa = Any Amino Acid

```

<400> 1451
Asn Ser Glu Ser Lys His Phe Leu Leu Leu Lys Leu Cys Ser Met Phe
  1              5              10              15
Ala Val Thr Phe Leu Ser Leu Ile Leu Ser Gly Lys Gly Leu Gln Phe
      20              25              30
Pro Phe Tyr Phe Ser Glu Cys Asn Cys Lys Val Ser Asp Val Phe Thr
      35              40              45
Val Glu Thr Arg Glu Gln Glu Ala Pro Met Lys Thr Thr Gly Phe Tyr
      50              55              60
Gly Gly Ile Met Val Trp Xaa Val Glu Ala Cys Tyr Ser Ser Cys Ile
  65              70              75              80
Ser Leu Gly Ser Asn Pro Asp Tyr Thr Ala Tyr Gly Ala Leu Thr Ala
      85              90              95
Arg Xaa Pro Gln Glu Phe Leu Cys Trp Xaa Asn Arg Phe Ile Ile Met
      100              105              110
Pro Val Asn Leu Lys Met Leu Xaa Val Lys Thr Ile Trp Cys Phe Ser
      115              120              125
Arg Thr Gln Xaa Ser Leu Thr Val Ile Thr Ile Phe Pro Leu Pro Thr
      130              135              140
Phe Asn Lys Xaa Ile Ile Tyr Ile Tyr Xaa Thr Lys Glu Ile Xaa Ser
  145              150              155              160
Cys Phe Ser Glu Thr Thr Gln Phe Tyr
      165

```

<210> 1452
 <211> 279
 <212> PRT
 <213> Unknown (H38g369 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(279)
 <223> Xaa = Any Amino Acid

```

<400> 1452
Leu Pro Pro Leu Phe Phe Arg Val Phe Val Ile Leu Phe Val Ser Leu
  1              5              10              15

```

Leu Phe Val Lys Leu Cys Ile Leu Phe Leu Ile Ile Leu Leu Val Lys
 20 25 30
 Phe Leu Leu Lys Thr Lys Ile Ala Met Thr Tyr Phe Thr Tyr Leu Ser
 35 40 45
 Asn Tyr Lys Leu Lys Ala Xaa Asn Ser Ile Asp Phe His Ile His Met
 50 55 60
 Phe Val Tyr Val Tyr Ile Met Asn Lys Leu Val His Leu Lys Tyr Glu
 65 70 75 80
 Thr Leu Thr Ser Leu Pro Phe Phe Trp Asn Ser Leu Gly Cys Leu Asp
 85 90 95
 Thr Ser Xaa Phe Cys Phe Thr Phe Tyr Val Thr Tyr Ser Ser Leu Ile
 100 105 110
 Val Ile Asn Met Leu Tyr Phe Leu Ala Val Leu Ala Lys Ser Ser Phe
 115 120 125
 Ile Leu Cys Phe Asn Ser Leu Ser Val Asn Cys Asp Thr Phe Cys Val
 130 135 140
 Trp Leu Ser Cys Phe Gly Ile Val Tyr Leu Asp Val His Pro Ile Ala
 145 150 155 160
 His Cys Leu Phe Leu Lys Arg Leu Phe Lys Cys Tyr Val Phe Leu Xaa
 165 170 175
 Ser Leu Val Phe Cys Phe Met His Ala Leu Leu Pro Xaa Thr Leu Lys
 180 185 190
 Asn Thr Cys Phe Asp Val Leu Phe Ile Phe Ile Cys Glu Lys Ser Leu
 195 200 205
 Leu Ala Asn Met Ser Phe Val Thr Ile Val Ser Ser Leu Ile Leu Leu
 210 215 220
 Thr Asn Xaa Glu Ile Ile Ser Phe Ser Ser Val Ile Leu Cys Gly Thr
 225 230 235 240
 Ile His Leu Asn Leu Ser Ser Phe Phe Leu His Arg Phe Phe Ile Phe
 245 250 255
 Phe Phe Cys Leu Lys Ser Ala Asn Ile Tyr Leu Asn Val Asp Leu Leu
 260 265 270
 Ser Ile Ile Leu Thr Leu Val
 275

<210> 1453

<211> 154

<212> PRT

<213> Unknown (H38g370 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(154)

<223> Xaa = Any Amino Acid

<400> 1453

Cys Thr Met Cys Val Trp Leu Leu Ala Xaa Asp Arg Gln Ile His Ile
 1 5 10 15
 His Ser His Ser Asn Lys Pro Lys Gln Val Thr His Pro Met Cys Phe
 20 25 30
 Trp Asp Lys Asp Val His Ser Ser Trp Ala Trp Gly Cys Gly Tyr Arg
 35 40 45
 Lys Gly Asn Lys Phe Phe Leu Ser Tyr Asp Thr Leu Cys Pro Pro Lys
 50 55 60
 Val Ile His Pro Phe Arg Xaa Gln Leu Phe Leu Ser Ser Ser Asp Ile
 65 70 75 80
 Ile Asn Asp Pro His Ile Asp Lys His Asp Ser Thr Leu Ile Thr Leu
 85 90 95
 Xaa Ala Phe Tyr Thr Ile Phe Tyr Lys Pro Thr Met Leu His Leu Phe

```

          100          105          110
Ser Glu Ile Leu Ser Met Ile Tyr Phe Met Gly Thr Lys Lys Asn Glu
          115          120          125
Xaa Lys Pro Arg Lys Lys Asp Cys Glu Ser His Xaa Lys Gly Leu Glu
          130          135          140
Xaa Met Gly Gln Ile Ile Ile Leu Phe Tyr
145          150

```

<210> 1454
 <211> 186
 <212> PRT
 <213> Unknown (H38g371 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(186)
 <223> Xaa = Any Amino Acid

```

<400> 1454
Pro Ala His Pro Arg Ser Pro His His Pro Leu Phe Pro Pro Tyr Ile
1      5      10      15
Tyr Leu Lys Asn Phe Phe Pro Thr Ile Phe Pro Gln Asn Leu Leu Ser
          20      25      30
Leu Leu Phe Thr Thr Val Phe Pro Pro Pro Thr Pro Asn Ile Phe
          35      40      45
Ser Pro Pro Ser Phe Pro His Cys Leu Phe Cys Asn Thr Phe Ser Cys
          50      55      60
Ser Leu Ile Leu Tyr Phe Pro Leu Ala Leu Thr Thr Leu Phe Thr Pro
65      70      75      80
Pro Ser Thr Pro Lys Leu Phe Ser Pro Ser Tyr Arg Ser Ser His Thr
          85      90      95
Ala Val Ser Val Ala Ala Thr Asn Arg Ser Glu Ala Ser Cys Ala Cys
          100     105     110
Arg Ser His Ser Leu Gln His Ala Ala Val Ala Ser Pro Cys Pro Gly
          115     120     125
Pro Leu Ser Arg Glu Arg Ser Ser Pro Ala Arg Arg His Ala Xaa Ala
          130     135     140
Xaa Asn Gly Leu Thr Pro Leu Leu Ala Pro Phe Ile Tyr Xaa Gly Tyr
145     150     155     160
Ala Tyr Glu Val Pro Gly Leu Leu Phe Gln Asp Trp Val Arg Glu Asn
          165     170     175
Ala Glu Ala Tyr Ser Asp Trp Thr Leu Leu
          180     185

```

<210> 1455
 <211> 142
 <212> PRT
 <213> Unknown (H38g372 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(142)
 <223> Xaa = Any Amino Acid

```

<400> 1455
Tyr Ile Glu Met Asp Asn Tyr Phe Leu Thr Xaa Leu Xaa Arg Tyr Leu
1      5      10      15

```

Leu Phe Phe His Phe Ile Ile Ser Thr Gln Tyr Phe Gly Ile Lys Lys
 20 25 30
 Phe Ile Leu Thr Ser Leu Leu Ala Tyr Cys Phe Trp Met Phe Ser Ile
 35 40 45
 Thr Lys Phe Leu Thr Tyr Gly Leu Lys Trp Leu Leu Ile Pro Asp Cys
 50 55 60
 Xaa Ser Trp Tyr Gln His Ala Xaa Phe Asn Pro Xaa Gln Ile Leu Phe
 65 70 75 80
 Leu Gln Asn Ser Xaa Ser Trp Leu Glu Val Tyr Phe Tyr Leu Phe Leu
 85 90 95
 Leu Phe Ala Val Pro Phe Asp Lys Ile Ile Phe Leu Ser Xaa Lys Met
 100 105 110
 Tyr Leu Asn Lys Xaa Ile Ile Ser Val Leu Val Gly Thr Arg Trp Thr
 115 120 125
 Phe Gln Arg Cys Val His Thr Leu Cys Ile Leu Ser Leu Phe
 130 135 140

<210> 1456
 <211> 82
 <212> PRT
 <213> Unknown (H38g373 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(82)
 <223> Xaa = Any Amino Acid

<400> 1456
 Asn Val Phe Arg Xaa Phe Leu Asp Phe Cys Arg Asp Ser Asp Ile His
 1 5 10 15
 Arg Ala Tyr Leu Cys Ile Leu Ser Ser Xaa Leu Arg Phe Ser Val Leu
 20 25 30
 Gly Ile Phe Xaa Gly Arg Ala Met Asn Ile Leu Ile Gly Leu Thr Lys
 35 40 45
 Val Leu Lys Cys Pro Ile Leu Cys Val Val Phe Asn His Thr Cys Ile
 50 55 60
 Leu Ile Thr Thr Leu Ala Val Ile Ala Tyr Arg Phe Arg Gln Ser Gly
 65 70 75 80
 Tyr Ser

<210> 1457
 <211> 207
 <212> PRT
 <213> Unknown (H38g374 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(207)
 <223> Xaa = Any Amino Acid

<400> 1457
 Glu Ile Ile Leu Ile Gly Ile Ser Leu Lys Leu Tyr Leu Val Val Phe
 1 5 10 15
 Thr Ile Ile Lys Ile Lys Xaa His Ser Ile Gly Leu Ser Ser Asn Lys
 20 25 30
 Asn Met Arg Leu Pro Ser Asp Phe Phe Leu Ser Gln Ala Ile Tyr Tyr

35					40					45					
Xaa	Trp	Ala	Leu	Met	Cys	Val	Leu	Glu	Asn	Lys	Thr	Tyr	Ala	Ser	Val
50						55					60				
Arg	Leu	Val	Xaa	Arg	Phe	Gly	Trp	Xaa	Lys	Leu	Ala	Asn	Xaa	Met	Ser
65					70					75					80
Val	Leu	Tyr	Leu	Glu	Ala	Asn	Leu	Gly	Asn	Met	Asp	Asn	Ala	Leu	Leu
				85					90					95	
Lys	Xaa	Leu	Lys	Arg	Asn	Tyr	Phe	Val	Phe	Val	Phe	Thr	Ser	Phe	Leu
			100					105					110		
Phe	Gly	Cys	Ile	Ala	Phe	Lys	Xaa	Lys	Glu	Ile	Phe	Tyr	Pro	Tyr	Thr
		115					120					125			
Ser	Ile	Cys	Ile	Tyr	His	Leu	Leu	Met	Met	Glu	Arg	Lys	Val	Ser	Cys
		130				135					140				
Leu	Thr	Leu	Ile	Cys	Leu	Ala	Xaa	Asp	Leu	Xaa	His	Phe	Xaa	Cys	Ser
145					150					155					160
Leu	Val	Thr	Val	Leu	Ser	Leu	Glu	Cys	Xaa	Gln	Leu	Asp	Ile	Cys	Asn
				165					170					175	
Val	Val	Thr	Tyr	Phe	Asn	Thr	Met	Val	Xaa	Ser	Thr	Thr	Gly	Ser	Asn
			180					185					190		
Ser	Xaa	Thr	Pro	Asn	His	Ser	Val	Leu	Ile	Cys	Asn	Met	Leu	Lys	
		195					200					205			

<210> 1458

<211> 313

<212> PRT

<213> Unknown (H38g375 protein)

<220>

<223> Synthetic construct

<400> 1458

Met	Arg	Asn	Leu	Ser	Gly	Gly	His	Val	Glu	Glu	Phe	Val	Leu	Val	Gly
1				5					10				15		
Phe	Pro	Thr	Thr	Pro	Pro	Leu	Gln	Leu	Leu	Leu	Phe	Val	Leu	Phe	Phe
			20					25					30		
Ala	Ile	Tyr	Leu	Leu	Thr	Leu	Leu	Glu	Asn	Ala	Leu	Ile	Val	Phe	Thr
		35					40					45			
Ile	Trp	Leu	Ala	Pro	Ser	Leu	His	Arg	Pro	Met	Tyr	Phe	Phe	Leu	Gly
	50					55					60				
His	Leu	Ser	Phe	Leu	Glu	Leu	Trp	Tyr	Ile	Asn	Val	Thr	Ile	Pro	Arg
65					70					75					80
Leu	Leu	Ala	Ala	Phe	Leu	Thr	Gln	Asp	Gly	Arg	Val	Ser	Tyr	Val	Gly
				85					90					95	
Cys	Met	Thr	Gln	Leu	Tyr	Phe	Phe	Ile	Ala	Leu	Ala	Cys	Thr	Glu	Cys
			100					105					110		
Val	Leu	Leu	Ala	Val	Met	Ala	Tyr	Asp	Arg	Tyr	Leu	Ala	Ile	Cys	Gly
			115				120					125			
Pro	Leu	Leu	Tyr	Pro	Ser	Leu	Met	Pro	Ser	Ser	Leu	Ala	Thr	Arg	Leu
			130				135					140			
Ala	Ala	Ala	Ser	Trp	Gly	Ser	Gly	Phe	Phe	Ser	Ser	Met	Met	Lys	Leu
145					150					155					160
Leu	Phe	Ile	Ser	Gln	Leu	Ser	Tyr	Cys	Gly	Pro	Asn	Ile	Ile	Asn	His
				165					170					175	
Phe	Phe	Cys	Asp	Ile	Ser	Pro	Leu	Leu	Asn	Leu	Thr	Cys	Ser	Asp	Lys
			180					185					190		
Glu	Gln	Ala	Glu	Leu	Val	Asp	Phe	Leu	Leu	Ala	Leu	Val	Met	Ile	Leu
		195					200					205			
Leu	Pro	Leu	Leu	Ala	Val	Val	Ser	Ser	Tyr	Thr	Ala	Ile	Ile	Ala	Ala
		210					215					220			
Ile	Leu	Arg	Ile	Pro	Thr	Ser	Arg	Gly	Arg	His	Lys	Ala	Phe	Ser	Thr
225					230					235					240

290 295 300
 Arg Arg Leu Arg Ser Arg Thr Val Glu Ser His Asp Leu Leu His Pro
 305 310 315 320
 Phe Ser

<210> 1460
 <211> 186
 <212> PRT
 <213> Unknown (H38g377 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(186)
 <223> Xaa = Any Amino Acid

<400> 1460
 Pro Val Pro Gln His Leu Phe Phe Phe Leu Lys Val Thr Gly His Leu
 1 5 10 15
 Leu Thr Xaa Ile Arg Asn Leu Xaa Phe Val Pro Asp Phe Ser Phe Ser
 20 25 30
 Leu Ala Leu His Ile Tyr Gln Xaa Tyr Xaa Phe Xaa Thr Asn Leu Asn
 35 40 45
 Glu Leu His Leu Cys Pro Ser Leu Ile Ser Pro Pro Ser Leu Ser Val
 50 55 60
 His Xaa Leu Arg Leu His His Val Asn Tyr Tyr His Gly Met Leu Thr
 65 70 75 80
 Glu Leu Leu Leu Pro Met Val Pro Cys His Asn Ser Ser Phe Ile Trp
 85 90 95
 Leu Pro Ile Asn Phe Xaa Lys Phe Ile Cys Ile Cys Tyr Phe Ser Gly
 100 105 110
 Xaa Lys Leu Pro Met His Val Glu Asp Gly Met Gln Thr Ala Leu His
 115 120 125
 Ala Cys Pro Leu Leu Met Gln Leu Leu Leu Ser Ile Pro His Ser Tyr
 130 135 140
 Pro Leu Leu Leu Asp Asn Ser Phe Leu Phe Leu Arg Leu His Pro Arg
 145 150 155 160
 Ser Lys Leu Ser Tyr Phe Leu His Ile Leu Leu Ser Xaa Pro Phe Thr
 165 170 175
 Tyr Val Asn His Leu Leu Pro Phe Leu Leu
 180 185

<210> 1461
 <211> 336
 <212> PRT
 <213> Unknown (H38g378 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(336)
 <223> Xaa = Any Amino Acid

<400> 1461
 Ser Arg Asp Pro Gln Asn Leu Thr Asp Val Ser Ile Phe Leu Leu Leu
 1 5 10 15
 Gly Ser Ser Glu Asp Pro Glu Arg Gln Pro Val Leu Thr Gly Leu Phe
 20 25 30

```

Leu Ser Thr Cys Leu Val Met Ala Leu Gly Asn Leu Leu Ile Ile Leu
  35          40          45
Ala Ile Ser Pro Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu
  50          55          60
Ser Asn Leu Ser Leu Pro Asp Ile Ser Phe Thr Ser Thr Thr Val Pro
  65          70          75          80
Lys Met Thr Val Asp Ile Gln Ser His Ser Arg Val Ile Ser Tyr Ala
          85          90          95
Gly Cys Leu Thr Gln Met Ser Leu Phe Ala Ile Phe Gly Gly Met Glu
          100          105          110
Asp Asn Ile Leu Leu Ser Val Met Ala Tyr Asp Gln Phe Val Ala Lys
          115          120          125
Cys His Pro Leu Tyr His Ser Ala Ile Met Asn Pro Cys Phe Cys Gly
          130          135          140
Phe Leu Leu Leu Leu Ser Phe Phe Ser Ser Leu Ser Leu Leu Asp Ala
          145          150          155          160
Gln Leu Tyr Asn Leu Ile Ala Leu Gln Met Thr Cys Phe Lys Asp Val
          165          170          175
Glu Ile Pro Asn Phe Phe Trp Asp Pro Ser Gln Leu Pro His Leu Ala
          180          185          190
Cys Cys Asp Thr Phe Asn Asn Asn Ile Ile Leu Tyr Phe Pro Asp Ala
          195          200          205
Ile Phe Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser Tyr Asp Lys
          210          215          220
Ile Val Ser Ser Ile Leu Arg Val Ser Ser Ser Gly Gly Lys Tyr Lys
          225          230          235          240
Ala Phe Ser Thr Tyr Gly Ser His Leu Ser Asp Val Ser Xaa Phe Tyr
          245          250          255
Gly Thr Gly Val Gly Gly Tyr Leu Ser Ser Asp Val Ser Ser Ser Pro
          260          265          270
Arg Lys Thr Ala Val Ala Ser Val Met Tyr Ala Val Val Thr Pro Met
          275          280          285
Met Asn Pro Phe Ile Tyr Ser Pro Arg Asn Arg Asp Met Lys Ser Val
          290          295          300
Leu Arg Arg Pro His Gly Ser Thr Phe Xaa Ser Gln Tyr Leu Leu Ile
          305          310          315          320
Cys Ser Ile Pro Phe Ala Val Trp Val Glu Lys Gly Cys Met Met Lys
          325          330          335

```

<210> 1462

<211> 157

<212> PRT

<213> Unknown (H38g379 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(157)

<223> Xaa = Any Amino Acid

<400> 1462

```

Phe Leu Lys Met Arg Leu Lys Glu Leu Met Xaa Asp Arg Thr Ile Met
  1          5          10          15
Asp Tyr Trp Arg Glu Gly Arg His Ile Xaa Gly Met Phe Leu Ala Phe
          20          25          30
Pro Phe Gly Xaa Pro Ile Pro Lys Leu Phe Leu Trp Val Ser Ile Arg
          35          40          45
Asp Met Ala Val Thr Trp Met Asp His Arg His Glu Ser Cys Ser Pro
          50          55          60
Phe Leu Pro Lys Leu Gln Pro Phe Ser Ser Cys His Val Ser Glu Leu

```

65					70					75				80	
Cys	Thr	Cys	Leu	Asp	Thr	Phe	Thr	Lys	Ser	Tyr	Ile	Thr	Xaa	Ile	Arg
				85					90					95	
Gly	Leu	Lys	Gly	Phe	Asn	His	Leu	Cys	Phe	Leu	Leu	His	Tyr	Cys	His
			100					105					110		
Cys	Ala	Arg	Ala	Gln	Val	Ser	Xaa	Asn	Ala	Pro	Trp	Ser	Leu	Ala	Gln
		115					120					125			
Arg	Cys	Gln	Pro	Asn	Met	Leu	Ile	Arg	Xaa	Leu	Phe	Cys	Leu	Lys	Leu
	130					135					140				
Val	Val	His	Asp	Arg	Leu	Xaa	His	Val	Leu	Ser	Leu	Leu			
145					150					155					

<210> 1463

<211> 325

<212> PRT

<213> Unknown (H38g380 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(325)

<223> Xaa = Any Amino Acid

<400> 1463

Met	Lys	Ile	Asn	Gln	Thr	Ile	Leu	Lys	Glu	Phe	Ile	Leu	Val	Gly	Phe
1				5					10					15	
Ser	Val	Tyr	Pro	His	Val	Gln	Thr	Phe	Leu	Phe	Val	Val	Phe	Phe	Cys
			20					25					30		
Leu	Tyr	Leu	Leu	Thr	Leu	Ala	Gly	Asn	Leu	Thr	Ile	Met	Gly	Leu	Thr
		35					40					45			
Xaa	Val	Asp	Arg	Ser	Leu	His	Thr	Pro	Met	Tyr	Leu	Phe	Leu	Ser	Ala
	50					55				60					
Leu	Ser	Phe	Ser	Glu	Thr	Cys	Tyr	Thr	Leu	Thr	Ile	Val	Pro	Lys	Met
65					70				75					80	
Leu	Glu	Asp	Leu	Leu	Ala	Lys	Asp	Arg	Ser	Ile	Ser	Val	Thr	Gly	Cys
			85					90					95		
Ser	Leu	Gln	Met	Cys	Phe	Phe	Leu	Gly	Leu	Gly	Gly	Thr	Asn	Cys	Ile
		100						105					110		
Ile	Leu	Thr	Leu	Met	Gly	Tyr	Asp	Arg	Phe	Leu	Ala	Ile	Cys	Asn	Pro
		115			120							125			
Leu	Arg	Tyr	Pro	Leu	Leu	Met	Thr	Asn	Ile	Val	Cys	Gly	Gln	Leu	Val
	130				135						140				
Ala	Ser	Ala	Cys	Thr	Ala	Gly	Phe	Phe	Ile	Ser	Leu	Thr	Glu	Thr	Ala
145				150					155						160
Leu	Ile	Phe	Arg	Asp	Ser	Phe	Cys	Arg	Pro	Asn	Leu	Val	Lys	His	Phe
			165					170						175	
Phe	Cys	His	Met	Leu	Ala	Val	Ile	Arg	Leu	Ser	Cys	Ile	Asp	Ser	Asn
		180						185					190		
His	Thr	Glu	Phe	Ile	Ile	Thr	Leu	Ile	Ser	Val	Ser	Gly	Leu	Leu	Gly
		195					200					205			
Thr	Leu	Leu	Leu	Ile	Ile	Leu	Thr	Asp	Val	Phe	Ile	Ile	Ser	Thr	Val
	210					215					220				
Leu	Arg	Ile	Pro	Ser	Ala	Glu	Gly	Lys	Gln	Lys	Ala	Phe	Thr	Thr	Cys
225				230						235					240
Ala	Ser	His	Leu	Thr	Val	Val	Ile	Ile	His	Phe	Gly	Phe	Ala	Ser	Ile
			245						250				255		
Val	Tyr	Leu	Lys	Pro	Glu	Ala	Ser	Gly	Asp	Asp	Thr	Leu	Ile	Ala	Val
		260					265						270		
Pro	Tyr	Thr	Val	Ile	Thr	Pro	Phe	Leu	Ser	Pro	Ile	Ile	Phe	Ser	Leu
		275					280						285		

Arg Asn Lys Asp Met Lys Asn Ala Phe Arg Arg Met Met Gly Asn Thr
 290 295 300
 Val Ala Leu Lys Lys Ile Ile Leu Gly Cys Cys Cys Leu Phe Glu Glu
 305 310 315 320
 Gly Leu Asn Val Pro
 325

<210> 1464

<211> 313

<212> PRT

<213> Unknown (H38g381 protein)

<220>

<223> Synthetic construct

<400> 1464

Met Gly Gln Thr Asn Val Thr Ser Trp Arg Asp Phe Val Phe Leu Gly
 1 5 10 15
 Phe Ser Ser Ser Gly Glu Leu Gln Leu Leu Leu Phe Ala Leu Phe Leu
 20 25 30
 Ser Leu Tyr Leu Val Thr Leu Thr Ser Asn Val Phe Ile Ile Ile Ala
 35 40 45
 Ile Arg Leu Asp Ser His Leu His Thr Pro Met Tyr Leu Phe Leu Ser
 50 55 60
 Phe Leu Ser Phe Ser Glu Thr Cys Tyr Thr Leu Gly Ile Ile Pro Arg
 65 70 75 80
 Met Leu Ser Gly Leu Ala Gly Gly Asp Gln Ala Ile Ser Tyr Val Gly
 85 90 95
 Cys Ala Ala Gln Met Phe Phe Ser Ala Ser Trp Ala Cys Thr Asn Cys
 100 105 110
 Phe Leu Leu Ala Ala Met Gly Phe Asp Arg Tyr Val Ala Ile Cys Ala
 115 120 125
 Pro Leu His Tyr Ala Ser His Met Asn Pro Thr Leu Cys Ala Gln Leu
 130 135 140
 Val Ile Thr Ser Phe Leu Thr Gly Tyr Leu Phe Gly Leu Gly Met Thr
 145 150 155 160
 Leu Val Ile Phe His Leu Ser Phe Cys Ser Ser His Glu Ile Gln His
 165 170 175
 Phe Phe Cys Asp Thr Pro Pro Val Leu Ser Leu Ala Cys Gly Asp Thr
 180 185 190
 Gly Pro Ser Glu Leu Arg Ile Phe Ile Leu Ser Leu Leu Val Leu Leu
 195 200 205
 Val Ser Phe Phe Phe Ile Thr Ile Ser Tyr Ala Tyr Ile Leu Ala Ala
 210 215 220
 Ile Leu Arg Ile Pro Ser Ala Glu Gly Gln Lys Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Ala Ser His Leu Thr Val Val Ile Ile His Tyr Gly Cys Ala Ser
 245 250 255
 Phe Val Tyr Leu Arg Pro Lys Ala Ser Tyr Ser Leu Glu Arg Asp Gln
 260 265 270
 Leu Ile Ala Met Thr Tyr Thr Val Val Thr Pro Leu Leu Asn Pro Ile
 275 280 285
 Val Tyr Ser Leu Arg Thr Arg Ala Ile Gln Thr Ala Leu Arg Asn Ala
 290 295 300
 Phe Arg Gly Arg Leu Leu Gly Lys Gly
 305 310

<210> 1465

<211> 289

<212> PRT

<213> Unknown (H38g382 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(289)

<223> Xaa = Any Amino Acid

<400> 1465

```

Leu Leu Phe Phe Ile Leu Leu Leu Leu Ile Tyr Leu Phe Thr Ile Ile
 1           5           10           15
Gly Ser Leu Met Val Phe Phe Ala Ile Lys Leu Asp Phe Cys Leu His
          20           25           30
Ser Ser Leu Tyr Phe Phe Ile Ser Val Leu Ser Phe Leu Glu Ile Trp
          35           40           45
Tyr Thr Thr Ile Thr Ile Pro Lys Met Phe Phe Asn Leu Ala Ser Glu
          50           55           60
Gln Lys Thr Thr Ser Leu Asp Gly Cys Leu Leu Gln Met Tyr Phe Phe
65           70           75           80
Tyr Ser Leu Gly Ile Thr Glu Val Cys Leu Leu Thr Thr Arg Ala Met
          85           90           95
Asp Arg Tyr Leu Ala Ile Cys Asn His Leu Cys Tyr Pro Thr Val Thr
          100          105          110
Thr Pro Xaa Leu Tyr Thr Gln Val Ile Leu Gly Cys Cys Ile Cys Gly
          115          120          125
Phe Phe Thr Leu Leu Pro Glu Ile Ala Trp Ile Ser Thr Leu Pro Phe
          130          135          140
Cys Gly Pro Asn Gln Ile His Asn Ile Phe Cys Asp Leu Asp Pro Ile
145          150          155          160
Leu Asn Leu Ala Cys Val Asp Thr Gly Pro Val Val Leu Ile Lys Val
          165          170          175
Val Asp Ile Val His Ala Val Glu Ile Ile Thr Ala Ile Met Leu Val
          180          185          190
Thr Leu Ala Tyr Val Gln Ile Ile Ala Val Ile Leu Arg Asn Cys Ser
          195          200          205
Ala Asp Gly Cys Gln Lys Ala Phe Ser Thr Tyr Ala Phe His Leu Ala
          210          215          220
Ile Phe Leu Ile Phe Phe Gly Ser Val Ala Leu Met Tyr Leu Leu Phe
225          230          235          240
Ser Ala Lys Tyr Ser Phe Phe Trp Asp Thr Thr Ile Ser Leu Met Phe
          245          250          255
Ala Val Leu Ser Pro Thr Pro Ile Ile Cys Ser Leu Arg Asn Lys Glu
          260          265          270
Ile Lys Glu Ala Ile Lys Lys His Met Cys Gln Ser Met Ile Cys Thr
          275          280          285
His

```

<210> 1466

<211> 318

<212> PRT

<213> Unknown (H38g383 protein)

<220>

<223> Synthetic construct

<400> 1466

```

Met Glu Ser Pro Asn Arg Thr Thr Ile Gln Glu Phe Ile Phe Ser Ala
 1           5           10           15
Phe Pro Tyr Ser Trp Val Lys Ser Val Val Cys Phe Val Pro Leu Leu
          20           25           30

```

```

Phe Ile Tyr Ala Phe Ile Val Val Gly Asn Leu Val Ile Ile Thr Val
  35                               40                               45
Val Gln Leu Asn Thr His Leu His Thr Pro Met Tyr Thr Phe Ile Ser
  50                               55                               60
Ala Leu Ser Phe Leu Glu Ile Trp Tyr Thr Thr Ala Thr Ile Pro Lys
  65                               70                               75                               80
Met Leu Ser Ser Leu Leu Ser Glu Arg Ser Ile Ser Phe Asn Gly Cys
  85                               90                               95
Leu Leu Gln Met Tyr Phe Phe His Ser Thr Gly Ile Cys Glu Val Cys
  100                              105                              110
Leu Leu Thr Val Met Ala Phe Asp His Tyr Leu Ala Ile Cys Ser Pro
  115                              120                              125
Leu His Tyr Pro Ser Ile Met Thr Pro Lys Leu Cys Thr Gln Leu Thr
  130                              135                              140
Leu Ser Cys Trp Val Cys Gly Phe Ile Thr Pro Leu Pro Glu Ile Ala
  145                              150                              155                              160
Trp Ile Ser Thr Leu Pro Phe Cys Gly Ser Asn His Leu Glu His Ile
  165                              170                              175
Phe Cys Asp Phe Leu Pro Val Leu Arg Leu Ala Cys Thr Asp Thr Arg
  180                              185                              190
Ala Ile Val Met Ile Gln Val Val Asp Val Ile His Ala Val Glu Ile
  195                              200                              205
Ile Thr Ala Val Met Leu Ile Phe Met Ser Tyr Asp Gly Ile Val Ala
  210                              215                              220
Val Ile Leu Arg Ile His Ser Ala Gly Gly Arg Arg Thr Ala Phe Ser
  225                              230                              235                              240
Thr Cys Val Ser His Phe Ile Val Phe Ser Leu Phe Phe Gly Ser Val
  245                              250                              255
Thr Leu Met Tyr Leu Arg Phe Ser Ala Thr Tyr Ser Leu Phe Trp Asp
  260                              265                              270
Ile Ala Ile Ala Leu Ala Phe Ala Val Leu Ser Pro Phe Phe Asn Pro
  275                              280                              285
Ile Ile Tyr Ser Leu Arg Asn Lys Glu Ile Lys Glu Ala Ile Lys Lys
  290                              295                              300
His Ile Gly Gln Ala Lys Ile Phe Phe Ser Val Arg Pro Gly
  305                              310                              315

```

<210> 1467

<211> 129

<212> PRT

<213> Unknown (H38g384 protein)

<220>

<223> Synthetic construct

<400> 1467

```

Leu Leu Lys Leu Ser Cys Ser Asp Thr His Leu Asn Glu Val Ile Ile
  1                               5                               10                               15
Leu Ser Glu Gly Ala Leu Val Met Ile Thr Pro Phe Leu Cys Ile Leu
  20                               25                               30
Ala Ser Tyr Met His Ile Thr Cys Thr Val Leu Lys Val Pro Ser Thr
  35                               40                               45
Lys Gly Arg Trp Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ala Val
  50                               55                               60
Val Leu Leu Phe Tyr Ser Thr Ile Ile Ala Val Tyr Phe Asn Pro Leu
  65                               70                               75                               80
Ser Ser His Ser Ala Glu Lys Asp Thr Met Ala Thr Val Leu Tyr Thr
  85                               90                               95
Val Val Thr Pro Met Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Arg
  100                              105                              110
Tyr Leu Lys Gly Ala Leu Lys Lys Val Val Gly Arg Val Val Phe Ser

```

Val 115 120 125

<210> 1468
 <211> 162
 <212> PRT
 <213> Unknown (H38g385 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(162)
 <223> Xaa = Any Amino Acid

<400> 1468
 Leu Leu Ile Ile Pro Ala Ile Ala Thr Asp Thr Arg Leu Ser Val Leu
 1 5 10 15
 Val Arg Phe Phe Leu Ala Asn Leu Ala Phe Val Val Thr Cys Phe Thr
 20 25 30
 Ser Thr Thr Ile Pro Lys Met Leu Ala Cys Lys Glu Ile Pro Cys Val
 35 40 45
 Met Ser Gly Cys Lys Gly Ile Pro Tyr Ala Gly Cys Leu Thr Gln Met
 50 55 60
 Leu Phe Phe Ile Trp Leu Gly Ile His Ser Phe Leu Leu Thr Ala Met
 65 70 75 80
 Ala Asn Glu His Cys Val Ala Ile Cys His Ser Leu Asn Ser Ile Arg
 85 90 95
 Ser Val Thr Pro Xaa Leu Cys Gly Leu Leu Val Val Ala Ser Trp Thr
 100 105 110
 Phe Ala Phe Arg Asn Ala Leu Thr His Pro Val Leu Leu Thr Arg Leu
 115 120 125
 Ser Leu Cys Thr Tyr Glu Trp Val Ser His Val Phe Cys Asn Leu Ser
 130 135 140
 Gln Leu Leu Lys Leu Ala Cys Ser Asp Ala Thr Leu Asn Asn Val Thr
 145 150 155 160
 Val Gln

<210> 1469
 <211> 327
 <212> PRT
 <213> Unknown (H38g386 protein)

<220>
 <223> Synthetic construct

<400> 1469
 Met Leu Thr Pro Asn Asn Ala Cys Ser Val Pro Thr Ser Phe Arg Leu
 1 5 10 15
 Thr Gly Ile Pro Gly Leu Glu Ser Leu His Ile Trp Leu Ser Ile Pro
 20 25 30
 Phe Gly Ser Met Tyr Leu Val Ala Val Leu Gly Asn Ile Thr Ile Leu
 35 40 45
 Ala Val Val Arg Met Glu Tyr Ser Leu His Gln Pro Met Tyr Phe Phe
 50 55 60
 Leu Cys Met Leu Ala Val Ile Asp Leu Val Leu Ser Thr Ser Thr Met
 65 70 75 80
 Pro Lys Leu Leu Ala Ile Phe Trp Phe Gly Ala His Asn Ile Gly Val
 85 90 95

```

Asn Ala Cys Leu Ala Gln Met Phe Phe Ile His Cys Phe Ala Thr Val
      100                      105                      110
Glu Ser Gly Ile Phe Leu Ala Met Ala Phe Asp His Tyr Val Ala Ile
      115                      120                      125
Cys Asp Pro Leu His His Thr Leu Leu Leu Thr His Ala Val Val Gly
      130                      135                      140
Arg Leu Gly Leu Ala Ala Leu Leu Arg Gly Val Ile Tyr Ile Gly Pro
      145                      150                      155                      160
Leu Pro Leu Val Ile Cys Leu Arg Leu Pro Leu Tyr His Thr Gln Ile
      165                      170                      175
Ile Ala His Ser Tyr Cys Glu His Met Ala Val Val Thr Leu Ala Cys
      180                      185                      190
Gly Asp Asp Thr Arg Val Asn Asn Leu Tyr Gly Met Gly Ile Gly Phe
      195                      200                      205
Leu Val Leu Ile Leu Asp Ser Leu Ala Ile Thr Ala Ser Tyr Val Met
      210                      215                      220
Ile Phe Arg Ala Val Met Gly Leu Ala Thr Ser Glu Ala Arg Leu Lys
      225                      230                      235                      240
Thr Leu Gly Thr Cys Gly Ser His Ile Cys Ala Ile Leu Val Phe Tyr
      245                      250                      255
Ile Pro Ile Ala Val Ser Ser Leu Thr His Arg Phe Gly His Arg Val
      260                      265                      270
Pro Pro His Ile His Ile His Ile His Ile His Ile His Ile
      275                      280                      285
Leu Leu Ala Asn Ile Tyr Leu Leu Ile Pro Pro Ile Leu Asn Pro Ile
      290                      295                      300
Val Tyr Ala Val Arg Thr Lys Gln Ile Arg Glu Ala Leu Leu His Ile
      305                      310                      315                      320
Lys Ala Arg Thr Gln Thr Arg
      325

```

<210> 1470

<211> 323

<212> PRT

<213> Unknown (H38g387 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(323)

<223> Xaa = Any Amino Acid

<400> 1470

```

Val Ala Cys Tyr Leu Pro Glu Leu Ser Val Gly Cys Pro Gly Gly Lys
  1          5          10          15
Glu Asn Glu Thr Gly Val Gly Glu Phe Leu Leu Leu Ser Ile Thr Ser
  20          25          30
Asp Ser Glu Lys Gln Gln Ala Leu Phe Trp Leu Phe Leu Cys Met His
  35          40          45
Leu Val Thr Glu Ala Gly Asn Thr Pro Ile Ile Leu Gly Ile Gly Ser
  50          55          60
Asn Pro Arg Leu His Thr Pro Thr Tyr Phe Phe Thr His Leu Ser Phe
  65          70          75          80
Val Asn Ile Cys Phe Ile Thr Asn Leu Ile Pro Lys Leu Leu Val Asn
  85          90          95
His Val Ala Gly Thr Gly Met Ile Thr Ile Ser Ser Pro Gln Cys Leu
  100         105         110
Thr Gln Met Tyr Phe Leu Ile Ser Phe Ala Asn Val Asp Thr Phe Leu
  115         120         125
Leu Ala Ile Met Ala Leu Asp His Tyr Val Ala Ile Cys Ser Ala Leu

```

130	135	140
Arg Tyr Cys Ser Ile Ile Thr Pro Glu Leu Cys Gln Gly Leu Ala Val		
145	150	155
Leu Ala Xaa Ala Gly Ser Ser Leu Ile Ser Leu Val His Thr Val Ile		
	165	170
Met Ser Arg Leu Ala Phe Cys Ser Ser Ala Gln Ile Ser His Phe Tyr		
	180	185
Cys Asp Ala Tyr Leu Leu Met Lys Ile Ala Cys Ser His Thr Val Asn		
	195	200
Gln His Val Phe Leu Gly Ala Val Val Leu Phe Leu Ala Pro Cys Ala		
	210	215
Leu Ile Leu Val Ser Tyr Ile Arg Ile Ala Ala Ala Ile Leu Arg Ile		
225	230	235
Pro Ser Pro Thr Arg Arg Arg Lys Ala Cys Ser Ile Cys Ser Ser His		
	245	250
Leu Ser Leu Val Thr Leu Phe Tyr Gly Thr Val Leu Gly Ile Cys Ile		
	260	265
Xaa Pro Pro Asp Ser Phe Ser Ala Gln Asp Thr Ile Ala Thr Ile Met		
	275	280
Tyr Thr Val Val Thr Ser Met Leu Asn Pro Phe Ile Tyr Ser Leu Met		
	290	295
Asn Lys Glu Val Gln Glu Ala Val Arg Arg Leu Phe Ser Arg Gly Ser		
305	310	315
His Ser Ser		320

<210> 1471

<211> 202

<212> PRT

<213> Unknown (H38g388 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(202)

<223> Xaa = Any Amino Acid

<400> 1471

Leu His Phe Cys Gly Ile Asp Val Thr Ser Tyr Gln Ala Xaa Gln Ile	
1	5
Leu Ala Xaa Gln Pro Tyr Asp Thr Thr Xaa Cys Gly Gln Arg Ile Val	
	20
Gly Ile Met Ala Val Ala Trp Gly Ile Gly Phe Leu His Ser Leu Ser	
	35
Gln Leu Ala Phe Ala Val His Leu Pro Phe Cys Gly Pro Asn Glu Phe	
	50
Asp Ser Phe Tyr Cys Asp Leu Pro Arg Val Ile Lys Leu Ala Cys Thr	
65	70
Asp Thr Tyr Arg Leu Asp Ile Met Val Ile Ala Asn Ser Gly Val Leu	
	85
Thr Val Cys Ser Phe Val Leu Leu Ile Ile Ser Tyr Thr Ile Ile Leu	
	100
Met Thr Ile Gln His Arg Pro Leu Asp Lys Ser Ser Lys Ala Leu Ser	
	115
Thr Leu Thr Ala His Ile Thr Val Val Leu Leu Phe Phe Gly Pro Cys	
	130
Val Phe Ile Tyr Ala Trp Pro Phe Pro Ile Lys Ser Leu Asp Lys Phe	
145	150
Leu Ala Val Phe Tyr Ser Val Ile Thr Pro Leu Leu Asn Pro Ile Ile	
	165
	170
	175

Tyr Thr Leu Arg Asn Lys Asp Met Lys Thr Ala Ile Arg Gln Leu Arg
 180 185 190
 Lys Trp Asp Ala His Ser Ser Val Lys Phe
 195 200

<210> 1472

<211> 311

<212> PRT

<213> Unknown (H38g389 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(311)

<223> Xaa = Any Amino Acid

<400> 1472

Met Leu Thr Phe His Asn Val Cys Ser Val Pro Ser Ser Phe Trp Leu
 1 5 10 15
 Thr Gly Ile Pro Gly Leu Glu Ser Leu His Val Trp Leu Ser Ile Pro
 20 25 30
 Phe Gly Ser Met Tyr Leu Val Ala Val Val Gly Asn Val Thr Ile Leu
 35 40 45
 Ala Val Val Lys Ile Glu Arg Ser Leu His Gln Pro Met Tyr Phe Phe
 50 55 60
 Leu Cys Met Leu Ala Ala Ile Asp Leu Val Leu Ser Thr Ser Thr Ile
 65 70 75 80
 Pro Lys Leu Leu Gly Ile Phe Trp Phe Gly Ala Cys Asp Ile Gly Leu
 85 90 95
 Asp Ala Cys Leu Gly Gln Met Phe Leu Ile His Cys Phe Ala Thr Val
 100 105 110
 Glu Ser Gly Ile Phe Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile
 115 120 125
 Cys Asn Pro Leu Arg His Ser Met Val Leu Thr Tyr Thr Val Val Gly
 130 135 140
 Arg Leu Gly Leu Val Ser Leu Leu Arg Gly Val Leu Tyr Ile Gly Pro
 145 150 155 160
 Leu Pro Leu Met Ile Arg Leu Arg Leu Pro Leu Tyr Lys Thr His Val
 165 170 175
 Ile Ser His Ser Tyr Cys Glu His Met Ala Val Val Ala Leu Thr Cys
 180 185 190
 Gly Asp Ser Lys Val Asn Asn Val Tyr Gly Met Ser Ile Gly Phe Leu
 195 200 205
 Val Leu Ile Met Glu Ser Val Asp Ser Asp Ala Ser Xaa Val Arg Ser
 210 215 220
 Ile Arg Ala Val Met Gly Leu Ala Asn His Glu Asp Arg Ile Lys Thr
 225 230 235 240
 Met Gly Thr Gly Glu Tyr His Ile Cys Ala Ile Met Ile Phe Arg Ile
 245 250 255
 Pro Val Met Tyr Ile Pro Xaa Asp His Arg Asp Gly Gln Cys Val His
 260 265 270
 His Pro Val His Asn Met Met Ala Arg Ile Tyr Ile Ile Ser His Pro
 275 280 285
 Ser Ile Lys Pro Ser Val Xaa Asp Asp Arg Thr Lys Gln Ser Arg Glu
 290 295 300
 Ser Tyr Ile Gln Arg Ala Arg
 305 310

<210> 1473

<211> 315

<212> PRT

<213> Unknown (H38g390 protein)

<220>

<223> Synthetic construct

<400> 1473

```

Met Glu Thr Trp Val Asn Gln Ser Tyr Thr Asp Gly Phe Phe Leu Leu
 1           5           10           15
Gly Ile Phe Ser His Ser Thr Ala Asp Leu Val Leu Phe Ser Val Val
          20           25           30
Met Ala Val Phe Thr Val Ala Leu Cys Gly Asn Val Leu Leu Ile Phe
          35           40           45
Leu Ile Tyr Met Asp Pro His Leu His Thr Pro Met Tyr Phe Phe Leu
          50           55           60
Ser Gln Leu Ser Leu Met Asp Leu Met Leu Val Cys Thr Asn Val Pro
          65           70           75           80
Lys Met Ala Ala Asn Phe Leu Ser Gly Arg Lys Ser Ile Ser Phe Val
          85           90           95
Gly Cys Gly Ile Gln Ile Gly Leu Phe Val Cys Leu Val Gly Ser Glu
          100          105          110
Gly Leu Leu Leu Gly Leu Met Ala Tyr Asp Arg Tyr Val Ala Ile Ser
          115          120          125
His Pro Leu His Tyr Pro Ile Leu Met Asn Gln Arg Val Cys Leu Gln
          130          135          140
Ile Thr Gly Ser Ser Trp Ala Phe Gly Ile Ile Asp Gly Leu Ile Gln
          145          150          155          160
Met Val Val Val Met Asn Phe Pro Tyr Cys Gly Leu Arg Lys Val Asn
          165          170          175
His Phe Phe Cys Glu Met Leu Ser Leu Leu Lys Leu Ala Cys Val Asp
          180          185          190
Thr Ser Leu Phe Glu Lys Val Ile Phe Ala Cys Cys Val Phe Met Leu
          195          200          205
Leu Phe Pro Phe Ser Ile Ile Val Ala Ser Tyr Ala His Ile Leu Gly
          210          215          220
Thr Val Leu Gln Met His Ser Ala Gln Ala Trp Lys Lys Ala Leu Ala
          225          230          235          240
Thr Cys Ser Ser His Leu Thr Ala Val Thr Leu Phe Tyr Gly Ala Ala
          245          250          255
Met Phe Ile Tyr Leu Arg Pro Arg His Tyr Arg Ala Pro Ser His Asp
          260          265          270
Lys Val Ala Ser Ile Phe Tyr Thr Val Leu Thr Pro Met Leu Asn Pro
          275          280          285
Leu Ile Tyr Ser Leu Arg Asn Arg Glu Val Met Gly Ala Leu Arg Lys
          290          295          300
Gly Leu Asp Arg Cys Arg Ile Gly Ser Gln His
          305          310          315

```

<210> 1474

<211> 326

<212> PRT

<213> Unknown (H38g391 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(326)

<223> Xaa = Any Amino Acid

<400> 1474

Met Gly Arg Trp Val Asn Gln Ser Tyr Thr Asp Gly Phe Phe Leu Leu
 1 5 10 15
 Gly Ile Phe Ser His Ser Gln Thr Asp Leu Val Leu Phe Ser Ala Val
 20 25 30
 Met Val Val Phe Thr Val Ala Leu Cys Gly Asn Val Leu Leu Ile Phe
 35 40 45
 Leu Ile Tyr Leu Asp Ala Gly Leu His Thr Pro Met Tyr Phe Phe Leu
 50 55 60
 Ser Gln Leu Ser Leu Met Asp Leu Met Leu Val Cys Asn Ile Val Pro
 65 70 75 80
 Lys Met Ala Ala Asn Phe Leu Ser Gly Arg Lys Ser Ile Ser Phe Val
 85 90 95
 Gly Cys Gly Ile Gln Ile Gly Phe Phe Val Ser Leu Val Gly Ser Glu
 100 105 110
 Gly Leu Leu Leu Gly Leu Met Ala Tyr Asp Arg Tyr Val Ala Val Ser
 115 120 125
 His Pro Leu His Tyr Pro Ile Leu Met Asn Gln Arg Val Cys Leu Gln
 130 135 140
 Ile Thr Gly Ser Ser Trp Ala Phe Gly Ile Ile Asp Gly Val Ile Gln
 145 150 155 160
 Met Val Ala Ala Met Gly Leu Pro Tyr Cys Gly Ser Arg Ser Val Asp
 165 170 175
 His Phe Phe Cys Glu Val Gln Ala Leu Leu Lys Leu Ala Cys Ala Asp
 180 185 190
 Thr Ser Leu Phe Asp Thr Leu Leu Phe Ala Cys Cys Val Phe Met Leu
 195 200 205
 Leu Leu Pro Phe Ser Ile Ile Met Ala Ser Tyr Ala Cys Ile Leu Gly
 210 215 220
 Ala Val Leu Arg Ile Arg Ser Ala Gln Ala Trp Lys Lys Ala Leu Ala
 225 230 235 240
 Thr Cys Ser Ser His Leu Thr Ala Val Thr Leu Phe Tyr Gly Ala Ala
 245 250 255
 Met Phe Met Tyr Leu Arg Pro Arg Arg Tyr Arg Ala Pro Ser His Asp
 260 265 270
 Lys Val Ala Ser Ile Phe Tyr Thr Val Leu Thr Pro Met Leu Asn Pro
 275 280 285
 Leu Ile Tyr Ser Leu Arg Asn Gly Glu Val Met Gly Ala Leu Arg Lys
 290 295 300
 Gly Leu Asp Arg Cys Arg Ile Gly Ser Gln His Xaa Thr Pro Glu Ser
 305 310 315 320
 Gly Ala Cys Cys Ala Pro
 325

<210> 1475

<211> 314

<212> PRT

<213> Unknown (H38g392 protein)

<220>

<223> Synthetic construct

<400> 1475

Met Gly Asp Val Asn Gln Ser Val Ala Ser Asp Phe Ile Leu Val Gly
 1 5 10 15
 Leu Phe Ser His Ser Gly Ser Arg Gln Leu Leu Phe Ser Leu Val Ala
 20 25 30
 Val Met Phe Val Ile Gly Leu Leu Gly Asn Thr Val Leu Leu Phe Leu
 35 40 45
 Ile Arg Val Asp Ser Arg Leu His Thr Pro Met Tyr Phe Leu Leu Ser
 50 55 60
 Gln Leu Ser Leu Phe Asp Ile Gly Cys Pro Met Val Thr Ile Pro Lys

```

65          70          75          80
Met Ala Ser Asp Phe Leu Arg Gly Glu Gly Ala Thr Ser Tyr Gly Gly
      85          90          95
Gly Ala Ala Gln Ile Phe Phe Leu Thr Leu Met Gly Val Ala Glu Gly
      100         105         110
Val Leu Leu Val Leu Met Ser Tyr Asp Arg Tyr Val Ala Val Cys Gln
      115         120         125
Pro Leu Gln Tyr Pro Val Leu Met Arg Arg Gln Val Cys Leu Leu Met
      130         135         140
Met Gly Ser Ser Trp Val Val Gly Val Leu Asn Ala Ser Ile Gln Thr
145          150         155          160
Ser Ile Thr Leu His Phe Pro Tyr Cys Ala Ser Arg Ile Val Asp His
      165         170         175
Phe Phe Cys Glu Val Pro Ala Leu Leu Lys Leu Ser Cys Ala Asp Thr
      180         185         190
Cys Ala Tyr Glu Met Ala Leu Ser Thr Ser Gly Val Leu Ile Leu Met
      195         200         205
Leu Pro Leu Ser Leu Ile Ala Thr Ser Tyr Gly His Val Leu Gln Ala
      210         215         220
Val Leu Ser Met Arg Ser Glu Glu Ala Arg His Lys Ala Val Thr Thr
225          230         235          240
Cys Ser Ser His Ile Thr Val Val Gly Leu Phe Tyr Gly Ala Ala Val
      245         250         255
Phe Met Tyr Met Val Pro Cys Ala Tyr His Ser Pro Gln Gln Asp Asn
      260         265         270
Val Val Ser Leu Phe Tyr Ser Leu Val Thr Pro Thr Leu Asn Pro Leu
      275         280         285
Ile Tyr Ser Leu Arg Asn Pro Glu Val Trp Met Ala Leu Val Lys Val
290          295         300
Leu Ser Arg Ala Gly Leu Arg Gln Met Cys
305          310

```

<210> 1476

<211> 117

<212> PRT

<213> Unknown (H38g393 protein)

<220>

<223> Synthetic construct

<400> 1476

```

Asn Ile Lys Gly Ile Ala Val Pro Met Phe Ile Glu Val Leu Asp Leu
1      5      10      15
Phe Phe Ile Ile Leu Ser Tyr Ile Phe Ile Leu Gln Ala Val Leu Gln
      20      25      30
Leu Ser Ser Gln Glu Ala Arg Tyr Lys Ala Phe Gly Thr Cys Val Ser
      35      40      45
His Ile Gly Ala Ile Leu Ala Phe Tyr Thr Pro Ser Val Ile Ser Ser
      50      55      60
Val Met His Arg Val Ala Arg Cys Ala Ala Pro His Val His Ile Leu
65          70          75          80
Leu Ala Asn Phe Tyr Leu Leu Phe Pro Pro Met Val Asn Pro Ile Ile
      85          90          95
Tyr Gly Val Lys Thr Lys Gln Ile Arg Glu Ser Val Leu Gly Val Phe
      100         105         110
Pro Arg Lys Asp Val
      115

```

<210> 1477

<211> 316

<212> PRT

<213> Unknown (H38g394 protein)

<220>

<223> Synthetic construct

<400> 1477

```

Met Pro Ser Gln Asn Tyr Ser Ile Ile Ser Glu Phe Asn Leu Phe Gly
 1           5           10           15
Phe Ser Ala Phe Pro Gln His Leu Leu Pro Ile Leu Phe Leu Leu Tyr
      20           25           30
Leu Leu Met Phe Leu Phe Thr Leu Leu Gly Asn Leu Leu Ile Met Ala
 35           40           45
Thr Ile Trp Ile Glu His Arg Leu His Thr Pro Met Tyr Leu Phe Leu
 50           55           60
Cys Thr Leu Ser Val Ser Glu Ile Leu Phe Thr Val Ala Ile Thr Pro
 65           70           75           80
Arg Met Leu Ala Asp Leu Leu Ser Thr His His Ser Ile Thr Phe Val
      85           90           95
Ala Cys Ala Asn Gln Met Phe Phe Ser Phe Met Phe Gly Phe Thr His
      100           105           110
Ser Phe Leu Leu Leu Val Met Gly Tyr Asp Arg Tyr Val Ala Ile Cys
 115           120           125
His Pro Leu Arg Tyr Asn Val Leu Met Ser Pro Arg Asp Cys Ala His
 130           135           140
Leu Val Ala Trp Thr Trp Ala Gly Gly Ser Val Met Gly Met Met Val
 145           150           155           160
Thr Thr Ile Val Phe His Leu Thr Phe Cys Gly Ser Asn Val Ile His
      165           170           175
His Phe Phe Cys His Val Leu Ser Leu Leu Lys Leu Ala Cys Glu Asn
 180           185           190
Lys Thr Ser Ser Val Ile Met Gly Val Met Leu Val Cys Val Thr Ala
 195           200           205
Leu Ile Gly Cys Leu Phe Leu Ile Ile Leu Ser Tyr Val Phe Ile Val
 210           215           220
Ala Ala Ile Leu Arg Ile Pro Ser Ala Glu Gly Arg His Lys Thr Phe
 225           230           235           240
Ser Thr Cys Val Ser His Leu Thr Val Val Val Thr His Tyr Ser Phe
      245           250           255
Ala Ser Phe Ile Tyr Leu Lys Pro Lys Gly Leu His Ser Met Tyr Ser
 260           265           270
Asp Ala Leu Met Ala Thr Thr Tyr Thr Val Phe Thr Pro Phe Leu Ser
 275           280           285
Pro Ile Ile Phe Ser Leu Arg Asn Lys Glu Leu Lys Asn Ala Ile Asn
 290           295           300
Lys Asn Phe Tyr Arg Lys Phe Cys Pro Pro Ser Ser
 305           310           315

```

<210> 1478

<211> 330

<212> PRT

<213> Unknown (H38g395 protein)

<220>

<223> Synthetic construct

<400> 1478

```

Met Cys Ser Phe Phe Leu Cys Gln Thr Gly Lys Gln Ala Lys Ile Ser
 1           5           10           15
Met Gly Glu Glu Asn Gln Thr Phe Val Ser Lys Phe Ile Phe Leu Gly
      20           25           30
Leu Ser Gln Asp Leu Gln Thr Gln Ile Leu Leu Phe Ile Leu Phe Leu

```

```

      35      40      45
Ile Ile Tyr Leu Leu Thr Val Leu Gly Asn Gln Leu Ile Ile Ile Leu
  50      55      60
Ile Phe Leu Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Arg
  65      70      75      80
Asn Leu Ser Phe Ala Asp Leu Cys Phe Ser Thr Ser Ile Val Pro Gln
      85      90      95
Val Leu Val His Phe Leu Val Lys Arg Lys Thr Ile Ser Phe Tyr Gly
      100      105      110
Cys Met Thr Gln Ile Ile Val Phe Leu Leu Val Gly Cys Thr Glu Cys
      115      120      125
Ala Leu Leu Ala Val Met Ser Tyr Asp Arg Tyr Val Ala Val Cys Lys
      130      135      140
Pro Leu Tyr Tyr Ser Thr Ile Met Thr Gln Arg Val Cys Leu Trp Leu
      145      150      155      160
Ser Phe Arg Ser Trp Ala Ser Gly Ala Leu Val Ser Leu Val Asp Thr
      165      170      175
Ser Phe Thr Phe His Leu Pro Tyr Trp Gly Gln Asn Ile Ile Asn His
      180      185      190
Tyr Phe Cys Glu Pro Pro Ala Leu Leu Lys Leu Ala Ser Ile Asp Thr
      195      200      205
Tyr Ser Thr Glu Met Ala Ile Phe Ser Met Gly Val Val Ile Leu Leu
      210      215      220
Ala Pro Val Ser Leu Ile Leu Gly Ser Tyr Trp Asn Ile Ile Ser Thr
      225      230      235      240
Val Ile Gln Met Gln Ser Gly Glu Gly Arg Leu Lys Ala Phe Ser Thr
      245      250      255
Cys Gly Ser His Leu Ile Val Val Val Leu Phe Tyr Gly Ser Gly Ile
      260      265      270
Phe Thr Tyr Met Arg Pro Asn Ser Lys Thr Thr Lys Glu Leu Asp Lys
      275      280      285
Met Ile Ser Val Phe Tyr Thr Ala Val Thr Pro Met Leu Asn Pro Ile
      290      295      300
Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Gly Ala Leu Arg Lys Leu
      305      310      315      320
Val Gly Arg Lys Cys Phe Ser His Arg Gln
      325      330

```

<210> 1479

<211> 227

<212> PRT

<213> Unknown (H38g396 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(227)

<223> Xaa = Any Amino Acid

<400> 1479

```

Gly Lys Glu Arg Glu Thr Arg Val Trp Arg Pro Arg Ala Gln Asp Arg
  1      5      10      15
Gly Val Ser Thr Arg His Ala Ala Arg Val Thr Ser Tyr Gln Glu Cys
      20      25      30
Gly Val Arg Gly Gly Gly Val Leu Cys Gly Ala Val Arg Pro Ser Pro
      35      40      45
Leu Asp Ala Gln Leu His Asn Val Ile Ala Tyr Arg Arg Thr Cys Phe
      50      55      60
Lys Asp Val Glu Ile Pro Asn Phe Val Trp Asp Pro Ser Gln Leu Pro
      65      70      75      80

```

Arg Leu Ala Cys Cys Gly Thr Phe Thr Asn Asn Ile Ile Met Tyr Phe
 85 90 95
 Pro Ala Ala Ile Phe Gly Phe Leu Pro Ile Ser Gly Thr Leu Phe Ser
 100 105 110
 Tyr Asp Lys Ile Val Phe Ser Ile Leu Arg Val Ser Ser Ser Gly Gly
 115 120 125
 Lys His Lys Ala Phe Ser Thr Arg Gly Ser His Leu Ser Val Val Cys
 130 135 140
 Xaa Phe Tyr Gly Thr Gly Ile Gly Gly Tyr Leu Ser Ser Asp Val Ser
 145 150 155 160
 Ser Ser Pro Arg Lys Ala Ala Val Ala Ser Val Met Tyr Thr Val Ala
 165 170 175
 Ile Pro Met Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile
 180 185 190
 Lys Ser Val Leu Arg Arg Pro His Gly Ser Thr Val Ser Ser Gln Tyr
 195 200 205
 Leu Leu Ile Cys Ser Ile Pro Phe Val Val Trp Val Lys Lys Gly Ser
 210 215 220
 Lys Val Lys
 225

<210> 1480

<211> 332

<212> PRT

<213> Unknown (H38g397 protein)

<220>

<223> Synthetic construct

<400> 1480

Met Lys Ile Phe Asn Thr Pro Ser Asn Ser Ser Thr Phe Thr Gly Phe
 1 5 10 15
 Ile Leu Leu Gly Phe Pro Cys Pro Arg Glu Gly Gln Ile Leu Leu Val
 20 25 30
 Val Leu Phe Thr Val Val Tyr Leu Leu Thr Leu Met Gly Asn Gly Ser
 35 40 45
 Ile Asn Cys Ala Val His Trp Asp Gln Arg Leu His Ala Pro Met Tyr
 50 55 60
 Ile Leu Leu Ala Asn Phe Ser Phe Leu Glu Ile Trp Tyr Val Thr Ser
 65 70 75 80
 Thr Val Pro Asn Val Leu Ala Asn Phe Leu Ser Asp Thr Lys Ile Ile
 85 90 95
 Ser Phe Ser Gly Cys Phe Leu Gln Phe Tyr Phe Phe Phe Ser Leu Gly
 100 105 110
 Ser Thr Glu Cys Phe Phe Leu Gly Ala Met Ala Phe Asp Leu Tyr Leu
 115 120 125
 Ala Ile Cys Arg Pro Leu Arg Tyr Pro Thr Ile Met Thr Arg Arg Leu
 130 135 140
 Cys Asn Ile Leu Val Gly Ser Cys Trp Val Leu Gly Phe Leu Trp Phe
 145 150 155 160
 Leu Ile Pro Ile Ser Val Ile Ser Gln Met Thr Cys Gly Ser Arg Ile
 165 170 175
 Ile Asp His Phe Pro Cys Asp Pro Gly Pro Leu Leu Ala Leu Thr Cys
 180 185 190
 Ala Arg Ala Pro Leu Leu Glu Leu Thr Ser Ser Thr Leu Ser Ser Leu
 195 200 205
 Leu Leu Phe Ile Pro Phe Leu Phe Ile Val Gly Cys Tyr Ala Leu Val
 210 215 220
 Leu Arg Ala Val Leu Arg Val Pro Ser Ala Ser Gly Arg Arg Lys Ala
 225 230 235 240
 Phe Ser Thr Cys Gly Ser His Leu Ala Val Val Ser Leu Phe Tyr Gly

```

                245                250                255
Ser Met Met Ile Thr Tyr Val Ser Pro Thr Ser Gly His Glu Phe Gly
                260                265                270
Met Gln Lys Thr Val Thr Leu Phe Tyr Ser Val Val Thr Pro Leu Ile
                275                280                285
Asn Pro Val Ile Tyr Ser Leu Arg Asn Lys Glu Met Lys His Ala Met
                290                295                300
Arg Asn Tyr Thr Val Met Phe Tyr Leu Ser Arg Ile His Arg Ala Thr
305                310                315                320
Arg Asp Val Lys Asp Val Phe Tyr Leu Phe Asn Phe
                325                330

```

<210> 1481

<211> 269

<212> PRT

<213> Unknown (H38g398 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(269)

<223> Xaa = Any Amino Acid

<400> 1481

```

Phe Ser Ser Ile Tyr Ala Trp Tyr Ile Ser Asp Leu Tyr Leu Asn Tyr
1          5          10          15
Leu Ser Asn His Leu Ser Ile Phe Lys Leu Val Asp Trp Ile Ile Asn
          20          25          30
Cys Tyr Leu Tyr Tyr Phe Tyr Ser Leu Leu Thr Leu Phe Xaa Gln Phe
          35          40          45
Ile Tyr Thr Cys Glu Met Asn Gln Phe Lys Xaa Xaa Gln Asn Arg Asn
          50          55          60
Asn Leu Thr Thr Phe Xaa Gly Tyr Phe Tyr Ser Gly Ile Cys Gly Arg
65          70          75          80
Arg Asn Cys Thr Met Xaa Leu Ile Thr Ile Phe Ile Leu Lys Tyr Cys
          85          90          95
Xaa His Gly Phe Ile Thr Ile His Ser Val Met Asp Ser Gly Gln His
          100          105          110
Leu Ala Ile Cys His Pro Leu His Tyr Leu Ile Leu Met Thr Asp Glu
          115          120          125
Asn Arg Asp Arg Met Phe Met Gly Pro Leu Thr Ala Phe Pro Tyr Thr
130          135          140
Asp Ala Thr Ser Gln Asn Met His Tyr Val Asn Phe Leu Ile Ile Ile
145          150          155          160
Leu Ser Ile Leu Tyr Ile Pro Gly Pro Tyr Thr Leu Ile Leu Arg Ala
          165          170          175
Met Leu Gln Leu Leu Ser Ala Ala Ser His Gln Asn Ala Phe Ser Ile
          180          185          190
Arg Gly Ser His Leu Ile Val Val Ser Leu Phe Cys Glu Thr Ile Met
          195          200          205
Met Met Cys Val Asn Leu Ile Ser Asp His Leu Val Xaa Met Lys Met
210          215          220
Thr Asn His Asn Ile Ile Met Ile Ser Ser Ile Lys Thr Leu Val Leu
225          230          235          240
Asn Phe Val Asn Tyr Thr Leu Leu Asn Met Asn Leu Lys Leu Tyr Leu
          245          250          255
Gln Phe Phe Phe Tyr Gly Met Ser Ile Ser Gln Ser Ser
          260          265

```

<210> 1482

<211> 311
 <212> PRT
 <213> Unknown (H38g399 protein)

<220>
 <223> Synthetic construct

<400> 1482
 Met Lys Ile Phe Asn Ser Pro Ser Asn Ser Ser Thr Phe Thr Gly Phe
 1 5 10 15
 Ile Leu Leu Gly Phe Pro Cys Pro Arg Glu Gly Gln Ile Leu Leu Phe
 20 25 30
 Val Leu Phe Thr Val Val Tyr Leu Leu Thr Leu Met Gly Asn Gly Ser
 35 40 45
 Ile Ile Cys Ala Val His Trp Asp Gln Arg Leu His Ala Pro Met Tyr
 50 55 60
 Ile Leu Leu Ala Asn Phe Ser Phe Leu Glu Ile Trp Tyr Val Thr Ser
 65 70 75 80
 Thr Val Pro Ser Met Leu Ala Asn Phe Leu Ser Asp Thr Lys Ile Ile
 85 90 95
 Ser Phe Ser Gly Cys Phe Leu Gln Phe Tyr Phe Phe Phe Ser Leu Gly
 100 105 110
 Ser Thr Glu Cys Phe Phe Leu Ala Val Met Ala Phe Asp Arg Tyr Leu
 115 120 125
 Ala Ile Cys Arg Pro Leu Arg Tyr Pro Thr Ile Met Thr Arg Arg Leu
 130 135 140
 Cys Thr Asn Leu Val Val Asn Cys Trp Val Leu Gly Phe Ile Trp Phe
 145 150 155 160
 Leu Ile Pro Ile Val Asn Ile Ser Gln Met Ser Phe Cys Gly Ser Arg
 165 170 175
 Ile Ile Asp His Phe Leu Cys Asp Pro Ala Pro Leu Leu Thr Leu Thr
 180 185 190
 Cys Lys Lys Gly Pro Val Ile Glu Leu Val Phe Ser Val Leu Ser Pro
 195 200 205
 Leu Pro Val Phe Met Leu Phe Leu Phe Ile Val Gly Ser Tyr Ala Leu
 210 215 220
 Val Val Arg Ala Val Leu Arg Val Pro Ser Ala Ala Gly Arg Arg Lys
 225 230 235 240
 Ala Phe Ser Thr Cys Gly Ser His Leu Ala Val Val Ser Leu Phe Tyr
 245 250 255
 Gly Ser Val Leu Val Met Tyr Gly Ser Pro Pro Ser Lys Asn Glu Ala
 260 265 270
 Gly Lys Gln Lys Thr Val Thr Leu Phe Tyr Ser Val Val Thr Pro Leu
 275 280 285
 Leu Asn Pro Val Ile Tyr Ser Leu Arg Asn Lys Asp Met Arg Lys Ala
 290 295 300
 Leu Lys Lys Phe Trp Gly Thr
 305 310

<210> 1483
 <211> 326
 <212> PRT
 <213> Unknown (H38g400 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(326)
 <223> Xaa = Any Amino Acid

<400> 1483

```

Thr Ala Leu Glu Phe Thr Asn Asn Ser Glu Thr Ser Thr Met Thr Glu
1      5      10
Phe Val Leu Leu Gly Phe Pro Gly Cys Gln Glu Met Gln Ser Phe Leu
20      25      30
Phe Ser Leu Phe Phe Val Ile Tyr Val Phe Thr Ile Ile Gly Asn Gly
35      40      45
Thr Ile Val Cys Ala Val Arg Leu Asp Lys Arg Leu His Thr Pro Met
50      55      60
Tyr Ile Leu Leu Gly Asn Phe Ala Phe Leu Glu Ile Arg Xaa Val Thr
65      70      75      80
Ser Thr Val Pro Asn Met Leu Val Asn Phe Leu Ser Glu Thr Lys Thr
85      90      95
Ile Ser Phe Val Gly Cys Phe Leu Gln Phe Tyr Phe Phe Thr Ser Leu
100     105     110
Gly Thr Ile Glu Ala Tyr Phe Leu Cys Ile Met Ala Tyr Asp Arg Tyr
115     120     125
Leu Ala Ile Cys Arg Pro Leu His Tyr Pro Thr Ile Met Thr Pro Gln
130     135     140
Leu Cys Tyr Ile Leu Met Ser Phe Cys Trp Val Phe Gly Phe Leu Ser
145     150     155     160
Tyr Ser Val Ser Thr Val Gln Leu Ser Gln Leu Pro Phe Cys Gly Pro
165     170     175
Asn Ile Ile Asn His Phe Leu Cys Asp Met Asp Pro Leu Met Ala Leu
180     185     190
Ser Cys Ala Ser Ala Pro Ile Thr Glu Ile Ile Phe Tyr Ile Leu Ser
195     200     205
Ser Leu Ile Ile Ile Leu Thr Leu Leu Tyr Ile Cys Gly Ser Tyr Met
210     215     220
Leu Leu Leu Ile Ala Val Leu Lys Val Pro Ser Ala Ala Gly Gln Gln
225     230     235     240
Lys Ala Phe Ser Thr Cys Gly Ser His Leu Thr Val Val Cys Leu Phe
245     250     255
Phe Gly Ala Leu Leu Ala Met Tyr Val Ser Pro Thr Thr Asp Asn Pro
260     265     270
Ala Ala Ile Xaa Lys Ile Ile Thr Leu Phe Tyr Ser Val Val Thr Pro
275     280     285
Phe Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Glu Met Lys Ala
290     295     300
Ala Leu Lys Lys Val Leu Arg Ile Glu Xaa Glu Xaa Ser His Leu His
305     310     315     320
Glu Thr Lys Gln Thr Ile
325

```

<210> 1484

<211> 315

<212> PRT

<213> Unknown (H38g401 protein)

<220>

<223> Synthetic construct

<400> 1484

```

Met Glu Ser Gly Asn Gln Ser Thr Val Thr Glu Phe Ile Phe Thr Gly
1      5      10      15
Phe Pro Gln Leu Gln Asp Gly Ser Leu Leu Tyr Phe Phe Pro Leu Leu
20      25      30
Phe Ile Tyr Thr Phe Ile Ile Ile Asp Asn Leu Leu Ile Phe Ser Ala
35      40      45
Val Arg Leu Asp Thr His Leu His Asn Pro Met Tyr Asn Phe Ile Ser
50      55      60

```

Ile Phe Ser Phe Leu Glu Ile Trp Tyr Thr Thr Ala Thr Ile Pro Lys
 65 70 75 80
 Met Leu Ser Asn Leu Ile Ser Glu Lys Lys Ala Ile Ser Met Thr Gly
 85 90 95
 Cys Ile Leu Gln Met Tyr Phe Phe His Ser Leu Glu Asn Ser Glu Gly
 100 105 110
 Ile Leu Leu Thr Thr Met Ala Ile Asp Arg Tyr Val Ala Ile Cys Asn
 115 120 125
 Pro Leu Arg Tyr Gln Met Ile Met Thr Pro Arg Leu Cys Ala Gln Leu
 130 135 140
 Ser Ala Gly Ser Cys Leu Phe Gly Phe Leu Ile Leu Leu Pro Glu Ile
 145 150 155 160
 Val Met Ile Ser Thr Leu Pro Phe Cys Gly Pro Asn Gln Ile His Gln
 165 170 175
 Ile Phe Cys Asp Leu Val Pro Val Leu Ser Leu Ala Cys Thr Asp Thr
 180 185 190
 Ser Met Ile Leu Ile Glu Asp Val Ile His Ala Val Thr Ile Ile Ile
 195 200 205
 Thr Phe Leu Ile Ile Ala Leu Ser Tyr Val Arg Ile Val Thr Val Ile
 210 215 220
 Leu Arg Ile Pro Ser Ser Glu Gly Arg Gln Lys Ala Phe Ser Thr Cys
 225 230 235 240
 Ala Gly His Leu Met Val Phe Leu Ile Phe Phe Gly Ser Val Ser Leu
 245 250 255
 Met Tyr Leu Arg Phe Ser Asp Thr Tyr Pro Pro Val Leu Asp Thr Ala
 260 265 270
 Ile Ala Leu Met Phe Thr Val Leu Ala Pro Phe Phe Asn Pro Ile Ile
 275 280 285
 Tyr Ser Leu Arg Asn Lys Asp Met Asn Asn Ala Ile Lys Lys Leu Phe
 290 295 300
 Cys Leu Gln Lys Val Leu Asn Lys Pro Gly Gly
 305 310 315

<210> 1485

<211> 307

<212> PRT

<213> Unknown (H38g402 protein)

<220>

<223> Synthetic construct

<400> 1485

Met His Phe Val Thr Glu Phe Val Leu Leu Gly Phe His Gly Gln Arg
 1 5 10 15
 Glu Met Gln Ser Cys Phe Phe Ser Phe Ile Leu Val Leu Tyr Leu Leu
 20 25 30
 Thr Leu Leu Gly Asn Gly Ala Ile Val Cys Ala Val Lys Leu Asp Arg
 35 40 45
 Arg Leu His Thr Pro Met Tyr Ile Leu Leu Gly Asn Phe Ala Phe Leu
 50 55 60
 Glu Ile Trp Tyr Ile Ser Ser Thr Val Pro Asn Met Leu Val Asn Ile
 65 70 75 80
 Leu Ser Glu Ile Lys Thr Ile Ser Phe Ser Gly Cys Phe Leu Gln Phe
 85 90 95
 Tyr Phe Phe Phe Ser Leu Gly Thr Thr Glu Cys Phe Phe Leu Ser Val
 100 105 110
 Met Ala Tyr Asp Arg Tyr Leu Ala Ile Cys Arg Pro Leu His Tyr Pro
 115 120 125
 Ser Ile Met Thr Gly Lys Phe Cys Ile Ile Leu Val Cys Val Cys Trp
 130 135 140
 Val Gly Gly Phe Leu Cys Tyr Pro Val Pro Ile Val Leu Ile Ser Gln

```

145          150          155          160
Leu Pro Phe Cys Gly Pro Asn Ile Ile Asp His Leu Val Cys Asp Pro
          165          170          175
Gly Pro Leu Phe Ala Leu Ala Cys Ile Ser Ala Pro Ser Thr Glu Leu
          180          185          190
Ile Cys Tyr Thr Phe Asn Ser Met Ile Ile Phe Gly Pro Phe Leu Ser
          195          200          205
Ile Leu Gly Ser Tyr Thr Leu Val Ile Arg Ala Val Leu Cys Ile Pro
          210          215          220
Ser Gly Ala Gly Arg Thr Lys Ala Phe Ser Thr Cys Gly Ser His Leu
225          230          235          240
Met Val Val Ser Leu Phe Tyr Gly Thr Leu Met Val Met Tyr Val Ser
          245          250          255
Pro Thr Ser Gly Asn Pro Ala Gly Met Gln Lys Ile Ile Thr Leu Val
          260          265          270
Tyr Thr Ala Met Thr Pro Phe Leu Asn Pro Leu Ile Tyr Ser Leu Arg
          275          280          285
Asn Lys Asp Met Lys Asp Ala Leu Lys Arg Val Leu Gly Leu Thr Val
          290          295          300
Ser Gln Asn
305

```

<210> 1486

<211> 256

<212> PRT

<213> Unknown (H38g403 protein)

<220>

<223> Synthetic construct

<400> 1486

```

Met Tyr Asn Phe Ile Ser Ile Phe Ser Phe Leu Glu Ile Trp Tyr Thr
 1          5          10          15
Thr Ala Thr Ile Pro Lys Met Leu Ser Ile Leu Ile Ser Arg Gln Arg
          20          25          30
Thr Ile Ser Met Val Gly Cys Leu Leu Gln Met Tyr Phe Phe His Ser
          35          40          45
Leu Gly Asn Ser Glu Gly Ile Leu Leu Thr Thr Met Ala Ile Asp Arg
          50          55          60
Tyr Val Ala Ile Cys Asn Pro Leu Arg Tyr Pro Thr Ile Met Thr Pro
65          70          75          80
Gly Leu Cys Val Gln Leu Ser Val Gly Ser Cys Ile Phe Gly Phe Leu
          85          90          95
Val Leu Leu Pro Glu Ile Ala Trp Ile Ser Thr Leu Pro Phe Cys Gly
          100          105          110
Pro Asn Gln Ile His Gln Ile Phe Cys Asp Phe Glu Pro Val Leu Arg
          115          120          125
Leu Ala Cys Thr Asp Thr Ser Met Ile Leu Ile Glu Asp Val Ile His
          130          135          140
Ala Val Ala Ile Val Phe Ser Val Leu Ile Ile Ala Leu Ser Tyr Ile
145          150          155          160
Arg Ile Ile Thr Val Ile Leu Arg Ile Pro Ser Val Glu Gly Arg Gln
          165          170          175
Lys Ala Phe Ser Thr Cys Ala Ala His Leu Ser Val Phe Leu Met Phe
          180          185          190
Tyr Gly Ser Val Ser Leu Met Tyr Leu Arg Phe Ser Ala Thr Phe Pro
          195          200          205
Pro Ile Leu Asp Thr Ala Val Ala Leu Met Phe Ala Val Leu Ala Pro
          210          215          220
Phe Phe Asn Pro Ile Ile Tyr Ser Phe Arg Asn Lys Asp Met Lys Ile
225          230          235          240

```

Ala Ile Lys Lys Leu Phe Cys Pro Gln Lys Met Val Asn Leu Ser Val
 245 250 255

<210> 1487

<211> 320

<212> PRT

<213> Unknown (H38g404 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(320)

<223> Xaa = Any Amino Acid

<400> 1487

Ser Leu Gly Ser Met Asn Asn Ser Gln Ile Ser Thr Val Thr Gln Phe
 1 5 10 15
 Val Leu Leu Gly Phe Pro Gly Pro Trp Lys Ile Gln Ile Ile Phe Phe
 20 25 30
 Ser Met Ile Leu Leu Val Tyr Ile Phe Thr Leu Thr Gly Asn Met Ala
 35 40 45
 Ile Ile Cys Ala Val Arg Trp Asp His Arg Leu His Thr Pro Met Tyr
 50 55 60
 Val Leu Leu Ala Asn Phe Ser Phe Leu Glu Ile Trp Tyr Val Thr Cys
 65 70 75 80
 Thr Val Pro Asn Met Leu Val Asn Phe Phe Ser Lys Thr Lys Thr Ile
 85 90 95
 Ser Phe Ser Gly Cys Phe Thr Gln Phe His Phe Phe Phe Ser Leu Gly
 100 105 110
 Thr Thr Glu Cys Phe Phe Leu Cys Val Met Ala Tyr Asp Arg Tyr Leu
 115 120 125
 Ala Ile Cys His Pro Leu His Tyr Pro Ser Ile Met Thr Gly Gln Leu
 130 135 140
 Cys Gly Ile Leu Val Ser Leu Cys Trp Leu Ile Gly Phe Leu Gly His
 145 150 155 160
 Ser Ile Ser Ile Phe Phe Ile Phe Gln Leu Pro Phe Cys Gly Pro Asn
 165 170 175
 Ile Ile Asp His Phe Leu Cys Asp Val Asp Pro Leu Met Ala Leu Ser
 180 185 190
 Ser Ala Pro Thr His Ile Ile Gly His Val Phe His Ser Val Ser Ser
 195 200 205
 Leu Phe Ile Asn Leu Thr Met Val Tyr Ile Leu Gly Ser Tyr Thr Leu
 210 215 220
 Val Leu Arg Thr Val Leu Xaa Val Pro Ser Ser Ala Gly Trp Gln Lys
 225 230 235 240
 Ala Ile Ser Thr Cys Gly Ser His Leu Val Val Val Ser Leu Phe Tyr
 245 250 255
 Gly Ala Ile Met Leu Met Tyr Val Ser Pro Thr Pro Gly Asn Ser Val
 260 265 270
 Ala Met His Lys Leu Ile Thr Leu Ile Tyr Ser Val Val Thr Pro Val
 275 280 285
 Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp Met Lys Tyr Ala
 290 295 300
 Leu His His Val Phe Cys Gly Met Arg Ile Ile Gln Arg Ser Xaa Ile
 305 310 315 320

<210> 1488

<211> 319

<212> PRT

<213> Unknown (H38g405 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(319)

<223> Xaa = Any Amino Acid

<400> 1488

```

Met Asp Pro Glu Asn Gln Thr Met Val Thr Glu Phe Tyr Phe Ser Asp
 1           5           10           15
Phe Pro Gln Ser Lys Asn Gly Ser Leu Leu Phe Phe Ile Pro Met Leu
          20           25           30
Phe Ile Tyr Ile Phe Ile Leu Val Gly Asn Phe Met Ile Phe Phe Ala
          35           40           45
Val Gln Pro Asp Pro His Leu His Asn Pro Met Tyr Ser Phe Ile Ser
          50           55           60
Val Phe Ser Phe Leu Glu Ile Trp Tyr Thr Thr Val Thr Ile Pro Lys
65           70           75           80
Met Leu Ser Asn Leu Leu Ser Glu Gln Lys Thr Ile Ser Phe Ile Gly
          85           90           95
Cys Leu Leu Gln Met Tyr Phe Phe His Ser Leu Gly Val Thr Glu Ala
          100          105          110
Leu Val Leu Thr Val Met Ala Ile Asp Arg Cys Val Ala Ile Cys Asn
          115          120          125
Pro Leu Arg Tyr Ala Ile Thr Met Ser Pro Xaa Leu Cys Ile Gln Leu
          130          135          140
Ser Thr Gly Ser Cys Ile Phe Gly Phe Leu Met Leu Leu Pro Glu Ile
145          150          155          160
Val Cys Ile Ser Thr Leu Pro Phe Cys Gly Ala Asn Gln Ile His Gln
          165          170          175
Leu Phe Cys Asp Phe Glu Pro Val Leu Gln Leu Ala Cys Thr Asp Thr
          180          185          190
Tyr Ile Ile Leu Val Glu Asp Val Ile Arg Ala Ile Ser Ile Leu Thr
          195          200          205
Ser Val Ser Val Ile Thr Leu Phe Tyr Leu Arg Ile Ile Thr Val Ile
          210          215          220
Leu Arg Ile Pro Ser Gly Glu Ser Arg Gln Lys Ala Phe Phe Thr Cys
225          230          235          240
Ala Ala His Ile Ala Ile Phe Leu Leu Phe Phe Gly Ser Val Ser Leu
          245          250          255
Met Tyr Leu Arg Phe Ser Val Thr Phe Pro Pro Leu Leu Asp Lys Ala
          260          265          270
Ile Ala Leu Met Phe Ala Val Leu Ala Leu Leu Phe Asn Pro Val Ile
          275          280          285
Tyr Ser Leu Arg Asn Lys Asp Met Lys Asn Ala Thr Lys Lys Ile Leu
          290          295          300
Cys Ser Gln Lys Met Phe Asn Ala Ser Gly Ser Xaa Trp Ser Ser
305          310          315

```

<210> 1489

<211> 317

<212> PRT

<213> Unknown (H38g406 protein)

<220>

<223> Synthetic construct

<400> 1489

```

Met Thr Gln Leu Thr Ala Ser Gly Asn Gln Thr Met Val Thr Glu Phe
 1           5           10           15

```

Leu Phe Ser Met Phe Pro His Ala His Arg Gly Gly Leu Leu Phe Phe
 20 25 30
 Ile Pro Leu Leu Leu Ile Tyr Gly Phe Ile Leu Thr Gly Asn Leu Ile
 35 40 45
 Met Phe Ile Val Ile Gln Val Gly Met Ala Leu His Thr Pro Leu Tyr
 50 55 60
 Phe Phe Ile Ser Val Leu Ser Phe Leu Glu Ile Cys Tyr Thr Thr Thr
 65 70 75 80
 Thr Ile Pro Lys Met Leu Ser Cys Leu Ile Ser Glu Gln Lys Ser Ile
 85 90 95
 Ser Val Ala Gly Cys Leu Leu Gln Met Tyr Phe Phe His Ser Leu Gly
 100 105 110
 Ile Thr Glu Ser Cys Val Leu Thr Ala Met Ala Ile Asp Arg Tyr Ile
 115 120 125
 Ala Ile Cys Asn Pro Leu Arg Tyr Pro Thr Ile Met Ile Pro Lys Leu
 130 135 140
 Cys Ile Gln Leu Thr Val Gly Ser Cys Phe Cys Gly Phe Leu Leu Val
 145 150 155 160
 Leu Pro Glu Ile Ala Trp Ile Ser Thr Leu Pro Phe Cys Gly Ser Asn
 165 170 175
 Gln Ile His Gln Ile Phe Cys Asp Phe Thr Pro Val Leu Ser Leu Ala
 180 185 190
 Cys Thr Asp Thr Phe Leu Val Val Ile Val Asp Ala Ile His Ala Ala
 195 200 205
 Glu Ile Val Ala Ser Phe Leu Val Ile Ala Leu Ser Tyr Ile Arg Ile
 210 215 220
 Ile Ile Val Ile Leu Gly Met His Ser Ala Glu Gly His His Lys Ala
 225 230 235 240
 Phe Ser Thr Cys Ala Ala His Leu Ala Val Phe Leu Leu Phe Phe Gly
 245 250 255
 Ser Val Ala Val Met Tyr Leu Arg Phe Ser Ala Thr Tyr Ser Val Phe
 260 265 270
 Trp Asp Thr Ala Ile Ala Val Thr Phe Val Ile Leu Ala Pro Phe Phe
 275 280 285
 Asn Pro Ile Ile Tyr Ser Leu Lys Asn Lys Asp Met Lys Glu Ala Ile
 290 295 300
 Gly Arg Leu Phe His Tyr Gln Lys Arg Ala Gly Trp Ala
 305 310 315

<210> 1490

<211> 277

<212> PRT

<213> Unknown (H38g407 protein)

<220>

<223> Synthetic construct

<400> 1490

Met Ala Leu Ile Gly Asn Leu Ser Met Ile Leu Leu Ile Phe Leu Asp
 1 5 10 15
 Thr His Leu His Thr Pro Met Tyr Phe Leu Leu Ser Gln Leu Ser Leu
 20 25 30
 Ile Asp Leu Asn Tyr Ile Ser Thr Ile Val Pro Lys Met Ala Ser Asp
 35 40 45
 Phe Leu Ser Gly Asn Lys Ser Ile Ser Phe Thr Gly Cys Gly Ile Gln
 50 55 60
 Ser Phe Phe Phe Ser Ala Leu Gly Gly Ala Glu Ala Leu Leu Leu Ala
 65 70 75 80
 Ser Met Ala Tyr Asp Arg Tyr Ile Ala Ile Cys Phe Pro Leu His Tyr
 85 90 95
 Pro Ile Arg Met Ser Lys Arg Met Cys Val Leu Met Ile Thr Gly Ser

```

      100      105      110
Trp Ile Ile Gly Ser Ile Asn Ala Cys Ala His Thr Val Tyr Val Leu
      115      120      125
His Ile Pro Tyr Cys Gln Ser Arg Ala Ile Asn His Phe Phe Cys Asp
      130      135      140
Val Pro Ala Met Val Thr Leu Ala Cys Met Asp Thr Trp Val Tyr Glu
      145      150      155      160
Gly Thr Val Phe Leu Ser Thr Thr Ile Phe Leu Val Phe Pro Phe Ile
      165      170      175
Ala Ile Ser Cys Ser Tyr Gly Arg Val Leu Leu Ala Val Tyr His Met
      180      185      190
Lys Ser Ala Glu Gly Arg Lys Lys Ala Tyr Leu Thr Cys Ser Thr His
      195      200      205
Leu Thr Val Val Thr Phe Tyr Tyr Ala Pro Phe Val Tyr Thr Tyr Leu
      210      215      220
Arg Pro Arg Ser Leu Arg Ser Pro Thr Glu Asp Lys Val Leu Ala Val
      225      230      235      240
Phe Tyr Thr Ile Leu Thr Pro Met Leu Asn Pro Ile Ile Tyr Ser Leu
      245      250      255
Arg Asn Lys Glu Val Met Gly Ala Leu Thr Arg Val Ser Gln Arg Ile
      260      265      270
Cys Ser Val Lys Met
      275

```

<210> 1491

<211> 241

<212> PRT

<213> Unknown (H38g408 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(241)

<223> Xaa = Any Amino Acid

<400> 1491

```

Met Asp Arg Val Asn Asn Ser Ala Val Ser Lys Phe Val Leu Ile Gly
  1          5          10          15
Leu Ser Ser Ser Trp Glu Met His Leu Phe Leu Phe Trp Phe Phe Ser
      20      25      30
Val Phe Tyr Met Gly Ile Ile Leu Glu Asn Leu Phe Ile Val Phe Thr
      35      40      45
Val Ile Ile Asp Ser His Leu Asn Ser Pro Val Tyr Cys Leu Leu Ala
      50      55      60
Asn Ile Tyr Leu Leu Asp Leu Val Phe Ser Tyr Ser Ser Asp Phe Phe
      65      70      75      80
Thr Asn Cys Ser Ile Ile Ser Phe Pro Arg Cys Met Ile Gln Ile Phe
      85      90      95
Phe Ile Cys Val Met Arg Lys Ile Glu Met Val Leu Leu Ile Thr Met
      100      105      110
Ala Xaa Ser Arg Tyr Thr Ala Ile Cys Lys Pro Pro His Tyr Leu Thr
      115      120      125
Thr Met Asn Pro Lys Met Cys Val Ser Leu Leu Glu Ala Ser Trp Ile
      130      135      140
Val Arg Ile Ile His Ala Val Ser Gln Phe Val Phe Ala Ile Asn Leu
      145      150      155      160
Pro Phe Cys Gly Pro Asn Arg Val Gly Ser Phe His Cys Asp Phe Pro
      165      170      175
Tyr Val Met Lys Leu Ala Cys Val Asp Thr Tyr Lys Leu Glu Val Val
      180      185      190

```

Val Thr Ala Asn Ser Gly Leu Ile Ser Ile Ala Thr Cys Phe Leu Leu
 195 200 205
 Ile Ile Ser Tyr Ile Phe Ile Ser Val Thr Val Xaa Asn Pro Ser Ser
 210 215 220
 Gly Asp Leu Ser Lys Ala Phe Val Ser Cys Ser Asp His Ile Thr Val
 225 230 235 240
 Gly

<210> 1492

<211> 312

<212> PRT

<213> Unknown (H38g409 protein)

<220>

<223> Synthetic construct

<400> 1492

Met Asp Thr Gly Asn Trp Ser Gln Val Ala Glu Phe Ile Ile Leu Gly
 1 5 10 15
 Phe Pro His Leu Gln Gly Val Gln Ile Tyr Leu Phe Leu Leu Leu
 20 25 30
 Leu Ile Tyr Leu Met Thr Val Leu Gly Asn Leu Leu Ile Phe Leu Val
 35 40 45
 Val Cys Leu Asp Ser Arg Leu His Thr Pro Met Tyr His Phe Val Ser
 50 55 60
 Ile Leu Ser Phe Ser Glu Leu Gly Tyr Thr Ala Ala Thr Ile Pro Lys
 65 70 75 80
 Met Leu Ala Asn Leu Phe Ser Glu Lys Lys Thr Ile Ser Phe Ser Gly
 85 90 95
 Cys Leu Leu Gln Ile Tyr Phe Phe His Ser Leu Gly Ala Thr Glu Cys
 100 105 110
 Tyr Leu Leu Thr Ala Met Ala Tyr Asp Arg Tyr Leu Ala Ile Cys Arg
 115 120 125
 Pro Leu His Tyr Pro Thr Leu Met Thr Pro Thr Leu Cys Ala Glu Ile
 130 135 140
 Ala Ile Gly Cys Trp Leu Gly Gly Leu Ala Gly Pro Val Val Glu Ile
 145 150 155 160
 Ser Leu Ile Ser Arg Leu Pro Phe Cys Gly Pro Asn Arg Ile Gln His
 165 170 175
 Val Phe Cys Asp Phe Pro Pro Val Leu Ser Leu Ala Cys Thr Asp Thr
 180 185 190
 Ser Thr Asn Val Leu Val Asp Phe Val Ile Asn Ser Cys Lys Ile Leu
 195 200 205
 Ala Thr Phe Leu Leu Ile Leu Cys Ser Tyr Val Gln Ile Ile Cys Thr
 210 215 220
 Val Leu Arg Ile Pro Ser Ala Ala Gly Lys Arg Lys Ala Ile Ser Thr
 225 230 235 240
 Cys Ala Ser His Leu Thr Val Val Leu Ile Phe Tyr Gly Ser Ile Leu
 245 250 255
 Ser Met Tyr Val Arg Leu Lys Lys Ser Tyr Ser Leu Asp Tyr Asp Gln
 260 265 270
 Ala Leu Ala Val Val Tyr Ser Val Leu Thr Pro Phe Leu Asn Pro Phe
 275 280 285
 Ile Tyr Ser Leu His Asn Lys Glu Ile Lys Glu Ala Val Arg Arg Gln
 290 295 300
 Leu Lys Arg Ile Gly Ile Leu Ala
 305 310

<210> 1493

<211> 212

<212> PRT

<213> Unknown (H38g410 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(212)

<223> Xaa = Any Amino Acid

<400> 1493

```

Glu Phe Leu Phe Tyr Asn Tyr Asn Gln Thr Ser Thr Asp Phe Ile Leu
 1           5           10           15
Leu Gly Leu Phe Pro Gln Ser Arg Ile Gly Leu Phe Val Phe Thr Leu
          20           25           30
Ile Phe Leu Ile Phe Leu Met Ala Leu Ile Gly Asn Leu Ser Met Ile
      35           40           45
Leu Leu Ile Phe Leu Asp Ile His Leu His Thr Pro Met Tyr Phe Leu
      50           55           60
Leu Ser Gln Leu Ser Leu Ile Asp Leu Asn Tyr Ile Ser Thr Ile Val
      65           70           75           80
Pro Lys Met Val Tyr Asp Phe Leu Tyr Gly Asn Lys Ser Ile Ser Phe
          85           90           95
Thr Gly Cys Gly Ile Gln Ser Phe Phe Leu Thr Leu Ala Val Ala
          100          105          110
Glu Gly Leu Leu Leu Thr Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile
          115          120          125
Cys Phe Pro Leu His Tyr Pro Ile Arg Ile Ser Lys Arg Val Cys Val
          130          135          140
Met Met Ile Thr Gly Ser Trp Met Ile Ser Ser Ile Asn Ser Cys Ala
          145          150          155          160
His Thr Val Tyr Ala Leu Cys Ile Pro Tyr Cys Lys Ser Arg Ala Ile
          165          170          175
Asn His Phe Phe Cys Glu Gly Ser Ser Glu Arg Tyr Leu Gly Cys Met
          180          185          190
Gln Ala Trp Arg Trp Ala Ala Val Glu Thr Ala Xaa Leu Val Lys Pro
          195          200          205
Trp Ala Gly Pro
          210

```

<210> 1494

<211> 263

<212> PRT

<213> Unknown (H38g411 protein)

<220>

<223> Synthetic construct

<400> 1494

```

Met Leu Gly Asn Tyr Ser Ser Ala Thr Glu Phe Phe Leu Leu Gly Phe
 1           5           10           15
Pro Gly Ser Gln Glu Val Cys Arg Ile Leu Phe Ala Thr Phe Phe Leu
          20           25           30
Leu Tyr Ala Val Thr Val Met Gly Asn Val Val Ile Ile Thr Val
          35           40           45
Cys Val Asp Lys Cys Leu Gln Ser Pro Ile Tyr Phe Phe Leu Gly His
          50           55           60
Leu Cys Val Leu Glu Ile Leu Ile Thr Ser Thr Ala Val Pro Phe Met
          65           70           75           80
Leu Trp Gly Leu Leu Pro Ser Thr Gln Ile Met Ser Leu Thr Ala
          85           90           95

```

Cys Ala Ala Gln Leu Tyr Leu Tyr Leu Ser Leu Gly Thr Leu Glu Leu
 100 105 110
 Ala Leu Met Gly Val Met Ala Val Asp Arg Tyr Val Ala Val Cys Asn
 115 120 125
 Pro Leu Arg Tyr Asn Ile Ile Met Asn Ser Ser Thr Phe Ile Trp Val
 130 135 140
 Ile Ile Val Ser Trp Val Leu Gly Phe Leu Ser Glu Ile Trp Pro Val
 145 150 155 160
 Tyr Ala Thr Phe Gln Leu Thr Phe Cys Lys Ser Ser Val Leu Asp His
 165 170 175
 Phe Tyr Cys Asp Arg Gly Gln Leu Leu Lys Val Ser Cys Glu Asp Thr
 180 185 190
 Leu Phe Arg Glu Phe Ile Leu Phe Leu Met Ala Val Phe Ile Ile Ile
 195 200 205
 Gly Ser Leu Ile Pro Thr Ile Val Ser Tyr Thr Tyr Ile Ile Ser Thr
 210 215 220
 Asn Leu Lys Ile Pro Ser Ala Ser Gly Trp Arg Lys Ser Phe Ser Thr
 225 230 235 240
 Cys Ala Ser His Phe Thr Tyr Val Val Ile Gly Tyr Gly Ser Cys Leu
 245 250 255
 Phe Leu Tyr Val Lys Pro Lys
 260

<210> 1495

<211> 317

<212> PRT

<213> Unknown (H38g412 protein)

<220>

<223> Synthetic construct

<400> 1495

Met Asp Gln Tyr Asn His Ser Ser Leu Ala Glu Phe Val Phe Leu Gly
 1 5 10 15
 Phe Ala Ser Val Gly Tyr Val Arg Gly Trp Leu Phe Val Leu Leu Leu
 20 25 30
 Leu Ala Tyr Leu Phe Thr Ile Cys Gly Asn Met Leu Ile Phe Ser Val
 35 40 45
 Ile Arg Leu Asp Ala Ala Leu His Thr Pro Met Tyr His Phe Val Ser
 50 55 60
 Val Leu Ser Phe Leu Glu Leu Trp Tyr Thr Ala Thr Thr Ile Pro Lys
 65 70 75 80
 Met Leu Ser Asn Ile Leu Ser Glu Lys Lys Thr Ile Ser Phe Ala Gly
 85 90 95
 Cys Leu Leu Gln Thr Tyr Phe Phe His Ser Leu Gly Ala Ser Glu Cys
 100 105 110
 Tyr Leu Leu Thr Ala Met Ala Tyr Asp Arg Tyr Leu Ala Ile Cys Arg
 115 120 125
 Pro Leu His Tyr Pro Ile Ile Met Thr Thr Thr Leu Cys Ala Lys Met
 130 135 140
 Ala Ala Ala Cys Trp Thr Cys Gly Phe Leu Cys Pro Ile Ser Glu Val
 145 150 155 160
 Ile Leu Ala Ser Gln Leu Pro Phe Cys Ala Tyr Asn Glu Ile Gln His
 165 170 175
 Ile Phe Cys Asp Phe Pro Pro Leu Leu Ser Leu Ala Cys Lys Asp Thr
 180 185 190
 Ser Ala Asn Ile Leu Val Asp Phe Ala Ile Asn Ala Phe Ile Ile Leu
 195 200 205
 Ile Thr Phe Phe Phe Ile Met Ile Ser Tyr Ala Arg Ile Ile Gly Ala
 210 215 220
 Val Leu Lys Ile Lys Thr Ala Ser Gly Arg Lys Lys Ala Phe Ser Thr

225 230 235 240
 Cys Ala Ser His Leu Ala Val Val Leu Ile Phe Phe Gly Ser Ile Ile
 245 250 255
 Phe Met Tyr Val Arg Leu Lys Lys Ser Tyr Ser Leu Thr Leu Asp Arg
 260 265 270
 Thr Leu Ala Ile Val Tyr Ser Val Leu Thr Pro Met Val Asn Pro Ile
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Glu Ile Ile Lys Ala Ile Lys Arg Thr
 290 295 300
 Ile Phe Gln Lys Gly Asp Lys Ala Ser Leu Ala His Leu
 305 310 315

<210> 1496

<211> 315

<212> PRT

<213> Unknown (H38g413 protein)

<220>

<223> Synthetic construct

<400> 1496

Met Gln Gly Leu Asn His Thr Ser Val Ser Glu Phe Ile Leu Val Gly
 1 5 10 15
 Phe Ser Ala Phe Pro His Leu Gln Leu Met Leu Phe Leu Leu Phe Leu
 20 25 30
 Leu Met Tyr Leu Phe Thr Leu Leu Gly Asn Leu Leu Ile Met Ala Thr
 35 40 45
 Val Trp Ser Glu Arg Ser Leu His Met Pro Met Tyr Leu Phe Leu Cys
 50 55 60
 Ala Leu Ser Ile Thr Glu Ile Leu Tyr Thr Val Ala Ile Ile Pro Arg
 65 70 75 80
 Met Leu Ala Asp Leu Leu Ser Thr Gln Arg Ser Ile Ala Phe Leu Ala
 85 90 95
 Cys Ala Ser Gln Met Phe Phe Ser Phe Ser Phe Gly Phe Thr His Ser
 100 105 110
 Phe Leu Leu Thr Val Met Gly Tyr Asp Arg Tyr Val Ala Ile Cys His
 115 120 125
 Pro Leu Arg Tyr Asn Val Leu Met Ser Leu Arg Gly Cys Thr Cys Arg
 130 135 140
 Val Gly Cys Ser Trp Ala Gly Gly Leu Val Met Gly Met Val Val Thr
 145 150 155 160
 Ser Ala Ile Phe His Leu Ala Phe Cys Gly His Lys Glu Ile His His
 165 170 175
 Phe Phe Cys His Val Pro Pro Leu Leu Lys Leu Ala Cys Gly Asp Asp
 180 185 190
 Val Leu Val Val Ala Lys Gly Val Gly Leu Val Cys Ile Thr Ala Leu
 195 200 205
 Leu Gly Cys Phe Leu Leu Ile Leu Leu Ser Tyr Ala Phe Ile Val Ala
 210 215 220
 Ala Ile Leu Lys Ile Pro Ser Ala Glu Gly Arg Asn Lys Ala Phe Ser
 225 230 235 240
 Thr Cys Ala Ser His Leu Thr Val Val Val Val His Tyr Gly Phe Ala
 245 250 255
 Ser Val Ile Tyr Leu Lys Pro Lys Gly Pro Gln Ser Pro Glu Gly Asp
 260 265 270
 Thr Leu Met Gly Ile Thr Tyr Thr Val Leu Thr Pro Phe Leu Ser Pro
 275 280 285
 Ile Ile Phe Ser Leu Arg Asn Lys Glu Leu Lys Val Ala Met Lys Lys
 290 295 300
 Thr Cys Phe Thr Lys Leu Phe Pro Gln Asn Cys
 305 310 315

<210> 1497
 <211> 319
 <212> PRT
 <213> Unknown (H38g414 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(319)
 <223> Xaa = Any Amino Acid

<400> 1497
 His Thr Glu Pro Arg His Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu
 1 5 10 15
 Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Gly Leu Ser
 20 25 30
 Pro Ser Met Tyr Leu Val Thr Val Leu Arg Asn Leu Leu Val Ile Leu
 35 40 45
 Ala Val Ser Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu
 50 55 60
 Ser Asn Pro Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Thr Val Pro
 65 70 75 80
 Lys Met Thr Val Asp Met Gln Ser His Ile Arg Val Ile Ser Tyr Ala
 85 90 95
 Ser Cys Leu Thr Arg Met Ser Phe Leu Val Leu Phe Ala Cys Ile Glu
 100 105 110
 Asp Met Leu Leu Thr Val Met Ala Xaa Asp Cys Phe Val Ala Ile Cys
 115 120 125
 Arg Pro Leu His Tyr Ala Val Ile Val Asn Pro His Leu Cys Val Phe
 130 135 140
 Leu Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His
 145 150 155 160
 Ser Xaa Ile Leu Gln Phe Thr Phe Phe Lys Asn Val Glu Ile Ser His
 165 170 175
 Phe Val Cys Glu Pro Ser Gln Leu Leu Asn Leu Ala Cys Ser Asp Ser
 180 185 190
 Val Ile Asn Ser Ile Phe Met Tyr Phe Asn Ser Thr Met Phe Gly Phe
 195 200 205
 Leu Pro Ile Ser Gly Ile Leu Leu Ser Tyr Tyr Lys Ile Val Pro Ser
 210 215 220
 Ile Leu Arg Ile Ser Ser Asp Gly Lys Tyr Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Gly Ser His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Gly Ile
 245 250 255
 Gly Met Tyr Leu Thr Ser Ala Val Ala Pro Pro Pro Arg Asn Gly Val
 260 265 270
 Val Ala Ser Val Met Tyr Ala Val Val Thr Pro Met Leu Asn Pro Phe
 275 280 285
 Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu Trp Arg Leu
 290 295 300
 Arg Ser Arg Thr Val Glu Ser His Asp Leu Phe His Pro Phe Ser
 305 310 315

<210> 1498
 <211> 157
 <212> PRT
 <213> Unknown (H38g415 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(157)

<223> Xaa = Any Amino Acid

<400> 1498

```

Val Ser Pro Leu Trp Glu Cys Val Ser Xaa Gln Arg Ser Pro His Phe
 1          5          10          15
Leu Cys Ser Gly Asp Ser Val Phe Cys Leu Val His Ser Val Gly Cys
          20          25          30
Cys Thr Leu Leu Leu Ser Gln Ser Leu Arg Leu Leu Ser Val Phe Leu
          35          40          45
Leu Ser Ser Cys Ala Ala Ser Trp Lys Lys Val His Ser Met Asn Leu
          50          55          60
Tyr Thr Pro Phe Cys Leu Ser Lys Trp Xaa Asn His Val Asn Asn Ala
65          70          75          80
Phe Asn Leu Pro Ser Trp Lys Lys Ser Lys Ser Val Val Thr Met Phe
          85          90          95
Xaa Gly Pro Ala Met Ile Thr Tyr Leu Arg Ser Asp Ser Xaa Tyr Asn
          100          105          110
Pro Thr Val Gly Lys Gln Leu Val Leu Phe Tyr Ser Ile Val Ser Ala
          115          120          125
Phe Ile Lys Pro Ile Ile Ser Ser Leu Arg Asn Lys Asp Val Lys Gly
          130          135          140
Ala Ser Trp Lys Val Leu Arg Val Lys Gly Thr Ala Gln
145          150          155

```

<210> 1499

<211> 287

<212> PRT

<213> Unknown (H38g416 protein)

<220>

<223> Synthetic construct

<400> 1499

```

Met Glu Asn Tyr Asn Gln Thr Ser Thr Asp Phe Ile Leu Leu Gly Leu
 1          5          10          15
Phe Pro Pro Ser Arg Ile Asp Leu Phe Phe Phe Ile Leu Phe Val Leu
          20          25          30
Ile Phe Leu Met Ala Leu Ile Gly Asn Leu Ser Met Ile Leu Leu Ile
          35          40          45
Phe Leu Asp Thr His Leu His Thr Pro Met Tyr Phe Leu Leu Ser Gln
          50          55          60
Leu Ser Leu Ile Asp Leu Asn Tyr Ile Ser Thr Ile Val Pro Lys Met
65          70          75          80
Ala Ser Asp Phe Leu Tyr Gly Asn Lys Ser Ile Ser Phe Ile Gly Cys
          85          90          95
Gly Ile Gln Ser Phe Phe Phe Met Thr Phe Ala Gly Ala Glu Ala Leu
          100          105          110
Leu Leu Thr Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro
          115          120          125
Leu His Tyr Pro Ile Arg Met Ser Lys Arg Met Tyr Val Leu Met Ile
          130          135          140
Thr Gly Ser Trp Met Ile Gly Ser Ile Asn Ser Cys Ala His Thr Val
145          150          155          160
Tyr Ala Phe Arg Ile Pro Tyr Cys Lys Ser Arg Ala Ile Asn His Phe
          165          170          175
Phe Cys Asp Val Pro Ala Met Leu Thr Leu Ala Cys Thr Asp Thr Trp
          180          185          190

```

Val Tyr Glu Tyr Thr Val Phe Leu Ser Ser Thr Ile Phe Leu Val Phe
 195 200 205
 Pro Phe Thr Gly Ile Ala Cys Ser Tyr Gly Trp Val Leu Leu Ala Val
 210 215 220
 Tyr Arg Met His Ser Ala Glu Gly Arg Lys Lys Ala Tyr Ser Thr Cys
 225 230 235 240
 Ser Thr His Leu Thr Val Val Thr Phe Tyr Tyr Ala Pro Leu Arg Tyr
 245 250 255
 Thr Tyr Leu Cys Pro Arg Ser Leu Phe Ile Ser Thr Glu Asp Lys Val
 260 265 270
 Gly Gly Gly Gly Tyr Thr Ile Leu Thr Ser Met Leu Asn Pro Ile
 275 280 285

<210> 1500

<211> 310

<212> PRT

<213> Unknown (H38g417 protein)

<220>

<223> Synthetic construct

<400> 1500

Met Asp Lys Glu Asn Ser Ser Met Val Thr Glu Phe Ile Phe Met Gly
 1 5 10 15
 Ile Thr Gln Asp Pro Gln Met Glu Ile Ile Phe Phe Val Val Phe Leu
 20 25 30
 Ile Val Tyr Leu Val Asn Val Val Gly Asn Ile Gly Met Ile Ile Leu
 35 40 45
 Ile Thr Thr Asp Thr Gln Leu His Thr Pro Met Tyr Phe Phe Leu Cys
 50 55 60
 Asn Leu Ser Phe Val Asp Leu Gly Tyr Ser Ser Ala Ile Ala Pro Arg
 65 70 75 80
 Met Leu Ala Asp Phe Leu Thr Asn His Lys Val Ile Ser Phe Ser Ser
 85 90 95
 Cys Ala Thr Gln Phe Ala Phe Phe Val Gly Phe Val Asp Ala Glu Cys
 100 105 110
 Tyr Val Leu Ala Ala Met Ala Tyr Gly Arg Phe Val Ala Ile Cys Arg
 115 120 125
 Pro Leu His Tyr Ser Thr Phe Met Ser Lys Gln Val Cys Leu Ala Leu
 130 135 140
 Met Leu Gly Ser Tyr Leu Ala Gly Leu Val Ser Leu Val Ala His Thr
 145 150 155 160
 Thr Leu Thr Phe Ser Leu Ser Tyr Cys Gly Ser Asn Ile Ile Asn His
 165 170 175
 Phe Phe Cys Glu Ile Pro Pro Leu Leu Ala Leu Ser Cys Ser Asp Thr
 180 185 190
 Tyr Ile Ser Glu Ile Leu Leu Phe Ser Leu Cys Gly Phe Ile Glu Phe
 195 200 205
 Ser Thr Ile Leu Ile Ile Phe Ile Ser Tyr Thr Phe Ile Leu Val Ala
 210 215 220
 Ile Ile Arg Met Arg Ser Ala Glu Gly Arg Leu Lys Ala Phe Ser Thr
 225 230 235 240
 Cys Gly Ser His Leu Thr Gly Ile Thr Leu Phe Tyr Gly Thr Val Met
 245 250 255
 Phe Met Tyr Leu Arg Pro Thr Ser Ser Tyr Ser Leu Asp Gln Asp Lys
 260 265 270
 Trp Ala Ser Val Phe Tyr Thr Val Ile Ile Pro Met Leu Asn Pro Leu
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Ala Ala Phe Lys Lys Leu
 290 295 300
 Ile Gly Lys Lys Ser Gln

305

310

<210> 1501

<211> 335

<212> PRT

<213> Unknown (H38g418 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(335)

<223> Xaa = Any Amino Acid

<400> 1501

Ser	Thr	Asp	Pro	Gln	Asn	Leu	Ile	Asp	Val	Ser	Ile	Phe	Leu	Leu	Leu
1				5					10					15	
Gly	Thr	Ser	Glu	Asp	Pro	Glu	Arg	Gln	Leu	Val	Leu	Ala	Gly	Leu	Phe
			20					25					30		
Leu	Ser	Met	Cys	Leu	Val	Thr	Val	Leu	Gly	Asn	Leu	Leu	Ile	Ile	Leu
		35					40					45			
Ala	Val	Ser	Pro	Asp	Ser	His	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu
	50					55				60					
Ser	Asn	Leu	Ser	Leu	Pro	Asp	Ile	Gly	Phe	Thr	Ser	Thr	Thr	Val	Pro
65					70					75					80
Lys	Met	Ile	Val	Asp	Ile	Arg	Ser	His	Ser	Arg	Val	Ile	Ser	Tyr	Ala
				85					90					95	
Gly	Cys	Leu	Thr	Gln	Thr	Ser	Leu	Phe	Ala	Ile	Phe	Gly	Gly	Met	Glu
			100					105					110		
Glu	Asn	Met	Leu	Leu	Ser	Val	Met	Ala	Tyr	Asp	Gln	Phe	Val	Ala	Ile
		115					120					125			
Cys	His	Pro	Leu	Tyr	His	Ser	Ala	Val	Met	Asn	Pro	Cys	Phe	Cys	Gly
	130					135					140				
Phe	Leu	Val	Leu	Leu	Thr	Phe	Phe	Phe	Leu	Ser	Leu	Leu	Asp	Ala	Gln
145					150					155					160
Leu	His	Asn	Leu	Ile	Ala	Leu	Gln	Met	Thr	Cys	Phe	Lys	Asp	Val	Glu
				165					170					175	
Ile	Pro	Asn	Phe	Phe	Trp	Asp	Pro	Ser	Pro	Leu	Pro	His	Leu	Ala	Cys
		180						185					190		
Cys	Asp	Thr	Phe	Thr	Asn	Asn	Ile	Ile	Met	Tyr	Phe	Pro	Ala	Ala	Ile
	195						200					205			
Phe	Gly	Phe	Leu	Pro	Ile	Ser	Gly	Thr	Leu	Phe	Ser	Tyr	Tyr	Lys	Ile
	210					215					220				
Val	Ser	Ser	Ile	Leu	Arg	Val	Ser	Ser	Ser	Gly	Gly	Lys	Tyr	Lys	Ala
225					230					235					240
Phe	Ser	Thr	Cys	Gly	Ser	His	Leu	Ser	Val	Val	Cys	Xaa	Phe	Tyr	Gly
			245						250					255	
Thr	Gly	Ile	Gly	Gly	Tyr	Leu	Ser	Ser	Asp	Val	Ser	Ser	Ser	Pro	Arg
			260					265					270		
Lys	Ala	Ala	Val	Ala	Ser	Val	Met	Tyr	Thr	Val	Val	Thr	Pro	Met	Leu
	275						280					285			
Asn	Pro	Phe	Ile	Tyr	Ser	Leu	Arg	Asn	Arg	Asp	Ile	Lys	Ser	Val	Leu
	290					295					300				
Arg	Trp	Leu	His	Gly	Ser	Ser	Val	Xaa	Ser	Gln	His	Leu	Leu	Ile	Cys
305					310					315					320
Cys	Ile	Pro	Phe	Val	Val	Trp	Val	Lys	Lys	Gly	Ser	Arg	Val	Lys	
				325					330					335	

<210> 1502

<211> 303

<212> PRT

<213> Unknown (H38g419 protein)

<220>

<223> Synthetic construct

<400> 1502

```

Met Asp His Val Ser His Asn Trp Thr Gln Ser Phe Ile Leu Ala Gly
 1           5           10          15
Phe Thr Thr Thr Gly Thr Leu Gln Pro Leu Ala Phe Leu Gly Thr Leu
      20           25          30
Cys Ile Tyr Leu Leu Thr Leu Ala Gly Asn Ile Leu Ile Ile Val Leu
      35           40          45
Val Gln Leu Asp Ser Gly Leu Phe Thr Pro Met Tyr Leu Phe Ile Ser
      50           55          60
Val Leu Ser Phe Val Glu Val Trp Tyr Val Ser Thr Thr Val Pro Met
      65           70          75          80
Leu Leu His Thr Leu Leu Gln Gly Cys Ser Pro Val Ser Ser Ala Val
      85           90          95
Cys Phe Ile Gln Thr Met Phe Phe His Ser Leu Gly Met Thr Glu Cys
      100          105         110
Tyr Leu Leu Gly Val Met Ala Leu Asp Ser Tyr Leu Ile Ile Cys His
      115          120         125
Pro Leu His Tyr His Ala Leu Met Ser Arg Gln Val Gln Leu Arg Leu
      130          135         140
Ala Gly Ala Ser Trp Val Ala Gly Phe Ser Ala Ala Leu Val Pro Ala
      145          150         155         160
Thr Leu Thr Ala Thr Leu Pro Phe Cys Leu Lys Glu Val Ala His Tyr
      165          170         175
Phe Cys Asp Leu Ala Pro Leu Met Arg Leu Ala Cys Val Asp Thr Ser
      180          185         190
Trp His Ala Arg Ala His Gly Thr Val Ile Gly Val Ala Thr Gly Cys
      195          200         205
Asn Phe Val Leu Ile Leu Gly Leu Tyr Gly Gly Ile Leu Asn Ala Val
      210          215         220
Leu Lys Leu Pro Ser Ala Ala Ser Ser Ala Lys Ala Phe Ser Thr Cys
      225          230         235         240
Ser Ser His Val Thr Val Val Ala Leu Phe Tyr Ala Ser Ala Phe Thr
      245          250         255
Val Tyr Val Gly Ser Pro Gly Ser Arg Pro Glu Ser Thr Asp Lys Leu
      260          265         270
Val Ala Leu Val Tyr Ala Leu Ile Thr Pro Phe Leu Asn Pro Ile Ile
      275          280         285
Tyr Ser Leu Arg Asn Lys Glu Val Lys Lys Ala Leu Arg Arg Val
      290          295         300

```

<210> 1503

<211> 336

<212> PRT

<213> Unknown (H38g420 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(336)

<223> Xaa = Any Amino Acid

<400> 1503

```

Pro Thr Lys Arg Glu Asn His Thr Val Ile Arg Glu Phe Val Phe Gln
 1           5           10          15
Gly Phe Ser Ser Phe His Glu His Lys Leu Thr Leu Phe Val Val Phe

```

<400> 1504															
Met	Ser	Ile	Thr	Lys	Ala	Trp	Asn	Ser	Ser	Ser	Val	Thr	Met	Phe	Ile
1				5					10					15	
Leu	Leu	Gly	Phe	Thr	Asp	His	Pro	Glu	Leu	Gln	Ala	Leu	Leu	Phe	Val
			20					25					30		
Thr	Phe	Leu	Gly	Ile	Tyr	Leu	Thr	Leu	Ala	Trp	Asn	Leu	Ala	Leu	
		35				40					45				
Ile	Phe	Leu	Ile	Arg	Gly	Asp	Thr	His	Leu	His	Thr	Pro	Met	Tyr	Phe
	50				55						60				
Phe	Leu	Ser	Asn	Leu	Ser	Phe	Ile	Asp	Ile	Cys	Tyr	Ser	Ser	Ala	Val
65				70						75				80	
Ala	Pro	Asn	Met	Leu	Thr	Asp	Phe	Phe	Trp	Glu	Gln	Lys	Thr	Ile	Ser
				85					90					95	

Phe Val Gly Cys Ala Ala Gln Phe Phe Phe Phe Val Gly Met Gly Leu
 100 105 110
 Ser Glu Cys Leu Leu Leu Thr Ala Met Ala Tyr Asp Arg Tyr Ala Ala
 115 120 125
 Ile Ser Ser Pro Leu Leu Tyr Pro Thr Ile Met Thr Gln Gly Leu Cys
 130 135 140
 Thr Arg Met Val Val Gly Ala Tyr Val Gly Gly Phe Leu Ser Ser Leu
 145 150 155 160
 Ile Gln Ala Ser Ser Ile Phe Arg Leu His Phe Cys Gly Pro Asn Ile
 165 170 175
 Ile Asn His Phe Phe Cys Asp Leu Pro Pro Val Leu Ala Leu Ser Cys
 180 185 190
 Ser Asp Thr Phe Leu Ser Gln Val Val Asn Phe Leu Val Val Val Thr
 195 200 205
 Val Gly Gly Thr Ser Phe Leu Gln Leu Leu Ile Ser Tyr Gly Tyr Ile
 210 215 220
 Val Ser Ala Val Leu Lys Ile Pro Ser Ala Glu Gly Arg Trp Lys Ala
 225 230 235 240
 Cys Asn Thr Cys Ala Ser His Leu Met Val Val Thr Leu Leu Phe Gly
 245 250 255
 Thr Ala Leu Phe Val Tyr Leu Arg Pro Ser Ser Ser Tyr Leu Leu Gly
 260 265 270
 Arg Asp Lys Val Val Ser Val Phe Tyr Ser Leu Val Ile Pro Met Leu
 275 280 285
 Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Glu Ile Lys Asp Ala Leu
 290 295 300
 Trp Lys Val Leu Glu Arg Lys Lys Val Phe Ser
 305 310 315

<210> 1505

<211> 317

<212> PRT

<213> Unknown (H38g422 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(317)

<223> Xaa = Any Amino Acid

<400> 1505

Met Pro Xaa Lys Met Glu Ser Ile Asn Thr Asn Phe Thr Val Thr Glu
 1 5 10 15
 Phe Val Phe Leu Gly Leu Ser Ser Glu Pro Lys Ile Gln Leu Ile Leu
 20 25 30
 Phe Ile Met Phe Leu Phe Tyr Leu Ser Thr Val Ala Gly Asn Val Ile
 35 40 45
 Ile Ile Thr Ile Ile Xaa Met Glu Pro Leu Leu Gln Thr Pro Met Tyr
 50 55 60
 Phe Phe Leu Thr Asn Leu Ser Phe Leu Asp Ile Cys Tyr Thr Ser Thr
 65 70 75 80
 Asn Val Pro Gln Met Leu Ser Asn Met Ala Gly Lys Lys Asn Thr Ile
 85 90 95
 Ser Phe Ser Ser Cys Ala Thr Gln Met Tyr Phe Ser Leu Ser Phe Gly
 100 105 110
 Ser Asp Cys Val Leu Leu Gly Val Met Ala Tyr Asp Arg Tyr Val Ala
 115 120 125
 Ile Cys His Pro Leu His Tyr Thr Phe Ile Met Asp Gln Asn Thr Cys
 130 135 140
 Ile Gln Leu Ala Val Ile Ser Trp Ser Ser Ser Phe Leu Ser Ser Met

```

145          150          155          160
Val Ile Asn Val Leu Thr Leu Ser Leu Pro Tyr Cys Gly Pro Asn Ile
          165          170          175
Leu Asn His Phe Phe Cys Glu Val Leu Ser Val Leu Arg Leu Ala Cys
          180          185          190
Thr Asn Thr Ser Phe Thr Glu Leu Val Val Phe Ile Phe Ser Ile Ile
          195          200          205
Ile Val Phe Ile Pro Phe Leu Leu Ile Val Val Ser Tyr Val Arg Ile
          210          215          220
Leu Gln Ser Val Leu Arg Met Arg Ser Ala Ser Gly Arg Tyr Gln Ala
225          230          235          240
Leu Ser Thr Cys Thr Ser His Leu Thr Val Val Thr Leu Phe Tyr Gly
          245          250          255
Thr Ala Ile Phe Met Asp Met Arg Pro Gln Ser Arg Ser Ser Trp Ala
          260          265          270
Gly Gly Lys Ile Ile Ala Val Phe Tyr Thr Val Val Thr Pro Met Leu
          275          280          285
Asn Pro Leu Ile Tyr Ser Leu Arg Asn Gln Asp Val Lys Gly Ala Arg
          290          295          300
Arg Arg Ala Ile Ala Lys Gln Arg Met Xaa Gln Leu Leu
305          310          315

```

<210> 1506

<211> 340

<212> PRT

<213> Unknown (H38g423 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(340)

<223> Xaa = Any Amino Acid

<400> 1506

```

Met Pro Lys Leu Asn Ser Thr Phe Val Thr Glu Phe Leu Phe Glu Gly
1          5          10          15
Phe Ser Ser Phe Arg Arg Gln His Lys Leu Val Phe Phe Val Val Phe
          20          25          30
Leu Thr Leu Tyr Leu Leu Thr Leu Ser Gly Asn Val Ile Ile Met Thr
          35          40          45
Ile Ile Arg Leu Asp His His Leu His Thr Pro Met Tyr Phe Phe Leu
          50          55          60
Cys Met Leu Ser Ile Ser Glu Thr Cys Tyr Thr Val Ala Ile Ile Pro
65          70          75          80
His Met Leu Ser Gly Leu Leu Asn Pro His Gln Pro Ile Ala Thr Gln
          85          90          95
Ser Cys Ala Thr Gln Leu Phe Phe Tyr Leu Thr Phe Gly Ile Asn Asn
          100          105          110
Cys Phe Leu Leu Thr Val Met Gly Tyr Asp Arg Tyr Val Ala Ile Cys
          115          120          125
Asn Pro Leu Arg Tyr Ser Val Ile Met Gly Lys Arg Ala Cys Ile Gln
          130          135          140
Leu Ala Ser Gly Ser Leu Gly Ile Gly Leu Gly Met Ala Ile Val Gln
145          150          155          160
Val Thr Ser Val Phe Gly Leu Pro Phe Cys Asp Ala Phe Val Ile Ser
          165          170          175
His Phe Phe Cys Asp Val Arg His Leu Leu Lys Leu Ala Cys Thr Asp
          180          185          190
Thr Thr Val Asn Glu Ile Ile Asn Phe Val Val Ser Val Cys Val Leu
          195          200          205

```

Val Leu Pro Met Gly Leu Val Phe Ile Ser Tyr Val Leu Ile Ile Ser
 210 215 220
 Thr Ile Leu Lys Ile Ala Ser Ala Glu Gly Gln Lys Lys Ala Phe Ala
 225 230 235 240
 Thr Cys Ala Ser His Leu Thr Val Val Ile Ile His Tyr Gly Cys Ala
 245 250 255
 Ser Ile Ile Tyr Leu Lys Pro Lys Ser Gln Ser Ser Leu Gly Gln Asp
 260 265 270
 Arg Leu Ile Ser Val Thr Tyr Thr Ile Thr Pro Leu Leu Asn Pro Val
 275 280 285
 Val Tyr Ser Leu Lys Asn Lys Glu Val Lys Asp Ala Leu His Arg Ala
 290 295 300
 Val Gly Gln Lys Thr Leu Ser Pro Xaa Xaa Arg Glu Val Val Lys Ala
 305 310 315 320
 Phe Pro Phe Val Tyr Lys Tyr Val Leu Ile Phe Asn Ala Leu Ser Ile
 325 330 335
 Met Pro Leu Cys
 340

<210> 1507

<211> 313

<212> PRT

<213> Unknown (H38g424 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(313)

<223> Xaa = Any Amino Acid

<400> 1507

Met Asp Ile Gly Leu Ser Ile Ala Asn Ser Ser Gly Phe Gln Leu Ser
 1 5 10 15
 Glu Phe Ile Leu Ile Gly Phe Pro Gly Ile His Glu Trp Gln His Trp
 20 25 30
 Leu Ser Leu Pro Leu Ala Leu Gly Ala Asn Leu Leu Ile Ile Ile Thr
 35 40 45
 Ile Gln His Glu Thr Met Leu His Glu Pro Met Tyr His Leu Leu Gly
 50 55 60
 Ile Leu Ala Val Val Asp Ile Gly Leu Ala Thr Thr Ile Met Pro Lys
 65 70 75 80
 Ile Leu Ala Ile Phe Trp Phe Asp Ala Lys Ala Ile Ser Leu Pro Glu
 85 90 95
 Cys Phe Ala Gln Ile Tyr Ala Ile His Ser Phe Met Cys Met Glu Ser
 100 105 110
 Gly Ile Phe Leu Cys Met Ala Val Asp Arg Tyr Met Ala Ile Cys Tyr
 115 120 125
 Pro Leu Gln Tyr Thr Ser Ile Val Thr Glu Ala Phe Val Ile Lys Ala
 130 135 140
 Thr Leu Ser Val Val Leu Arg Asn Gly Leu Leu Thr Ile Pro Val Pro
 145 150 155 160
 Val Leu Ala Ala Gln Arg His Tyr Cys Ser Arg Asn Glu Ile Asp Gln
 165 170 175
 Cys Leu Cys Ser Asn Leu Gly Val Thr Ser Leu Ala Cys Asp Asp Thr
 180 185 190
 Thr Ile Asn Arg Phe Tyr Gln Leu Ala Leu Val Trp Val Val Val Gly
 195 200 205
 Ser Asp Met Gly Leu Val Phe Ala Ser Tyr Ser Leu Ile Ile His Ser
 210 215 220
 Val Leu Lys Leu Asn Ser Ala Lys Ala Thr Ser Lys Ala Leu Asn Thr

```

225          230          235          240
Cys Ser Ser His Leu Ile Leu Ile Leu Phe Phe Tyr Thr Ala Ile Ile
          245          250          255
Val Val Ser Val Thr Asn Leu Ala Gly Arg Arg Ala Pro Arg Ile Pro
          260          265          270
Val Leu Leu Asn Val Leu His Ile Val Ile Pro Ser Ala Leu Asn Pro
          275          280          285
Ile Val Tyr Ala Leu Arg Thr Xaa Glu Leu Arg Ala Gly Phe Gln Lys
          290          295          300
Leu Leu Gly Leu Gly Glu Tyr Val Ser
305          310

```

<210> 1508

<211> 315

<212> PRT

<213> Unknown (H38g425 protein)

<220>

<223> Synthetic construct

<400> 1508

```

Met Phe Ser Pro Asn His Thr Ile Val Thr Glu Phe Ile Leu Leu Gly
 1          5          10          15
Leu Thr Asp Asp Pro Val Leu Glu Lys Ile Leu Phe Gly Val Phe Leu
          20          25          30
Ala Ile Tyr Leu Ile Thr Leu Ala Gly Asn Leu Cys Met Ile Leu Leu
          35          40          45
Ile Arg Thr Asn Ser His Leu Gln Thr Pro Met Tyr Phe Phe Leu Gly
          50          55          60
His Leu Ser Phe Val Asp Ile Cys Tyr Ser Ser Asn Val Thr Pro Asn
65          70          75          80
Met Leu His Asn Phe Leu Ser Glu Gln Lys Thr Ile Ser Tyr Ala Gly
          85          90          95
Cys Phe Thr Gln Cys Leu Leu Phe Ile Ala Leu Val Ile Thr Glu Phe
          100          105          110
Tyr Ile Leu Ala Ser Met Ala Leu Asp Arg Tyr Val Ala Ile Cys Ser
          115          120          125
Pro Leu His Tyr Ser Ser Arg Met Ser Lys Asn Ile Cys Val Cys Leu
          130          135          140
Val Thr Ile Pro Tyr Met Tyr Gly Phe Leu Ser Gly Phe Ser Gln Ser
145          150          155          160
Leu Leu Thr Phe His Leu Ser Phe Cys Gly Ser Leu Glu Ile Asn His
          165          170          175
Phe Tyr Cys Ala Asp Pro Pro Leu Ile Met Leu Ala Cys Ser Asp Thr
          180          185          190
Arg Val Lys Lys Met Ala Met Phe Val Val Ala Gly Phe Asn Leu Ser
          195          200          205
Ser Ser Leu Phe Ile Ile Leu Leu Ser Tyr Leu Phe Ile Phe Ala Ala
          210          215          220
Ile Phe Arg Ile Arg Ser Ala Glu Gly Arg His Lys Ala Phe Ser Thr
225          230          235          240
Cys Ala Ser His Leu Thr Ile Val Thr Leu Phe Tyr Gly Thr Leu Phe
          245          250          255
Cys Met Tyr Val Arg Pro Pro Ser Glu Lys Ser Val Glu Glu Ser Lys
          260          265          270
Ile Thr Ala Val Phe Tyr Thr Phe Leu Ser Pro Met Leu Asn Pro Leu
          275          280          285
Ile Tyr Ser Leu Arg Asn Thr Asp Val Ile Leu Ala Met Gln Gln Met
          290          295          300
Ile Arg Gly Lys Ser Phe His Lys Ile Ala Val
305          310          315

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<210> 1509
 <211> 257
 <212> PRT
 <213> Unknown (H38g426 protein)

<220>
 <223> Synthetic construct

<400> 1509
 Met Phe Leu Leu Leu Ala Ile Leu Ala Ala Thr Asp Leu Gly Leu Ala
 1 5 10 15
 Thr Ser Ile Ala Pro Gly Leu Leu Ala Val Leu Trp Leu Gly Pro Arg
 20 25 30
 Ser Val Pro Tyr Ala Val Cys Leu Val Gln Met Phe Phe Val His Ala
 35 40 45
 Leu Thr Ala Met Glu Ser Gly Val Leu Leu Ala Met Ala Cys Asp Arg
 50 55 60
 Ala Ala Ala Ile Gly Arg Pro Leu His Tyr Pro Val Leu Val Thr Lys
 65 70 75 80
 Ala Cys Val Gly Tyr Ala Ala Leu Ala Leu Ala Leu Lys Ala Val Ala
 85 90 95
 Ile Val Val Pro Phe Pro Leu Leu Val Ala Lys Phe Glu His Phe Gln
 100 105 110
 Ala Lys Thr Ile Gly His Thr Tyr Cys Ala His Met Ala Val Val Glu
 115 120 125
 Leu Val Val Gly Asn Thr Gln Ala Thr Asn Leu Tyr Gly Leu Ala Leu
 130 135 140
 Ser Leu Ala Ile Ser Gly Met Asp Ile Leu Gly Ile Thr Gly Ser Tyr
 145 150 155 160
 Gly Leu Ile Ala His Ala Val Leu Gln Leu Pro Thr Arg Glu Ala His
 165 170 175
 Ala Lys Ala Phe Gly Thr Cys Ser Ser His Ile Cys Val Ile Leu Ala
 180 185 190
 Phe Tyr Ile Pro Gly Leu Phe Ser Tyr Leu Ala His Arg Phe Gly His
 195 200 205
 His Thr Val Pro Lys Pro Val His Ile Leu Leu Ser Asn Ile Tyr Leu
 210 215 220
 Leu Leu Pro Pro Ala Leu Asn Pro Leu Ile Tyr Gly Ala Arg Thr Lys
 225 230 235 240
 Gln Ile Arg Asp Arg Leu Leu Glu Thr Phe Thr Phe Arg Lys Ser Pro
 245 250 255
 Leu

<210> 1510
 <211> 358
 <212> PRT
 <213> Unknown (H38g427 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(358)
 <223> Xaa = Any Amino Acid

<400> 1510
 Val Ser Met Ser Phe Leu Ile Arg Ser Asp Ser Thr Leu His Thr Pro
 1 5 10 15
 Met Cys Leu Phe Leu Ser His Leu Ser Phe Val Asp Leu Tyr Tyr Ala

<400> 1511
Met Phe Gly Ala Asn Leu Thr Thr Phe His Pro Thr Leu Phe Ile Leu
1 5 10 15
Leu Gly Ile Pro Gly Leu Glu Gln Tyr His Ile Trp Leu Ser Ile Pro
20 25 30

Phe Tyr Leu Met Tyr Ile Thr Ala Val Leu Gly Asn Gly Ala Leu Ile
 35 40 45
 Leu Val Val Leu Ser Glu His Thr Leu His Val Phe Leu Ser Met Leu
 50 55 60
 Ala Gly Thr Asp Ile Leu Leu Ser Thr Thr Thr Val Pro Lys Ala Leu
 65 70 75 80
 Ala Ile Phe Trp Val His Ala Gly Glu Ile Ala Phe Asp Ala Cys Ile
 85 90 95
 Thr Gln Met Phe Phe Ile His Val Ala Phe Val Ala Glu Ser Gly Ile
 100 105 110
 Leu Leu Ala Met Ala Phe Asp Ser Tyr Val Ala Ile Cys Thr Pro Leu
 115 120 125
 Arg Tyr Thr Thr Ile Leu Thr Ser Met Val Asn Gly Lys Met Thr Leu
 130 135 140
 Thr Ile Trp Gly Gln Ser Ile Gly Thr Ile Phe Pro Val Ile Phe Leu
 145 150 155 160
 Leu Lys Arg Leu Pro Tyr Cys Gln Thr Asn Ile Ile Pro His Ser Tyr
 165 170 175
 Cys Glu His Ile Gly Val Ala Gln Leu Ala Cys Ala Asp Ile Thr Val
 180 185 190
 Asn Ile Trp Tyr Gly Phe Ser Val Pro Met Ala Ser Val Leu Val Asp
 195 200 205
 Val Ala Phe Ile Gly Phe Ser Tyr Thr Leu Ile Leu Gln Ala Val Phe
 210 215 220
 Arg Leu Pro Ser Gln Glu Ser Gln His Lys Ala Leu Asn Thr Cys Gly
 225 230 235 240
 Ser His Ile Gly Val Val Leu Leu Phe Phe Ile Pro Ser Phe Phe Thr
 245 250 255
 Phe Leu Thr His Arg Phe Gly Lys Asn Ile Pro His His Val His Ile
 260 265 270
 Leu Leu Ala Asn Leu Tyr Leu Leu Val Pro Pro Met Leu Asn Pro Ile
 275 280 285
 Ile Tyr Gly Glu Lys Thr Lys Gln Ile Arg Asp Ser Met Ala His Met
 290 295 300
 Leu Ser Val Val Gly Lys Ser Xaa Asp
 305 310

<210> 1512

<211> 314

<212> PRT

<213> Unknown (H38g429 protein)

<220>

<223> Synthetic construct

<400> 1512

Met Lys Met Lys Ile Asp Pro Lys Cys Asn Gly Thr Glu Val Thr Glu
 1 5 10 15
 Phe Ile Leu Leu Gly Leu Thr Ser Gln Pro Glu Leu Gln Pro Met Leu
 20 25 30
 Phe Val Val Phe Leu Leu Ile Tyr Leu Ile Thr Leu Thr Gly Lys Phe
 35 40 45
 Gly Met Ile Phe Leu Ile Arg Phe Thr Pro Gln Leu Gln Thr His Met
 50 55 60
 Tyr Phe Phe Leu Thr His Leu Ala Cys Val Asp Ile Phe Tyr Ser Thr
 65 70 75 80
 Asn Val Ser Pro Gln Met Leu Val Asn Phe Leu Ser Glu Lys Lys Thr
 85 90 95
 Ile Ser Tyr Ala Gly Cys Leu Ala Gln Cys Phe Val Phe Val Thr Leu
 100 105 110
 Leu Leu Thr Glu Tyr Tyr Met Leu Gly Ala Met Ala Tyr Asp Cys Tyr

115	120	125
Met Ala Ile Cys Asn Pro	Leu His Tyr Ser Ser	Lys Met Ser Arg Ala
130	135	140
Val Cys Ile Cys Leu Val	Thr Phe Pro Tyr Phe	Trp Gly Ser Met Val
145	150	155
Gly Thr Met Gln Val Ile	Leu Thr Ser Arg Leu	Ser Phe Phe Gly Pro
165	170	175
Asn Thr Ile Asn His Phe	Tyr Cys Thr Asp Pro	Pro Leu Leu Met Leu
180	185	190
Thr Ser Ser Asp Thr Tyr	Ile Lys Gln Thr Ala	Leu Phe Val Ser Ala
195	200	205
Gly Ile Asn Leu Thr Val	Ser Leu Leu Ile Ile	Leu Ile Ser Tyr Ile
210	215	220
Phe Ile Phe Ile Thr Ile	Met Arg Ile Arg Ser	Ser Glu Gly Gln Leu
225	230	235
Lys Ala Phe Ser Thr Cys	Gly Ser His Leu Thr	Ala Val Thr Met Phe
245	250	255
Tyr Gly Ser Leu Phe Cys	Met Tyr Leu Arg Pro	Thr Asn Glu Leu Ser
260	265	270
Val Glu Gln Gly Lys Met	Gly Val Val Phe Cys	Ile Phe Val Ser Pro
275	280	285
Met Leu Asn Pro Phe Ile	Tyr Arg Leu Arg Asn	Lys Asp Val Lys Gln
290	295	300
Ala Leu Lys Arg Val Phe	Met Arg Asn Leu	
305	310	

<210> 1513

<211> 320

<212> PRT

<213> Unknown (H38g430 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(320)

<223> Xaa = Any Amino Acid

<400> 1513

Met Ser Leu Leu Phe Xaa	Asp Xaa Asp Met Arg	Asn Phe Thr Pro Leu
1	5	10
Ser Gly Phe Ile Ile Leu	Gly Phe Thr Asp His	Pro Glu Leu Gln Cys
20	25	30
Leu Leu Phe Val Leu Phe	Leu Leu Ile Tyr Met	Phe Thr Val Val Gly
35	40	45
Asn Leu Gly Met Ile Leu	Leu Ile Lys Ile Asp	Ser His Leu His Thr
50	55	60
Pro Met Tyr Phe Phe Leu	Ser Asn Leu Cys Leu	Val Asp Phe Cys Tyr
65	70	75
Ser Ser Val Ile Ala Pro	Asn Met Leu Ile Asn	Phe Trp Val Glu Asn
85	90	95
Pro Val Ile Ser Phe Asn	Glu Cys Ala Thr Gln	Phe Phe Phe Gly
100	105	110
Ser Phe Ala Gly Ile Glu	Gly Phe Leu Leu Ala	Val Met Ala Tyr Asp
115	120	125
Cys Tyr Val Ala Ile Cys	Lys Pro Leu Leu Tyr	Thr Val Leu Met Ser
130	135	140
Pro His Leu Ser Ala Leu	Leu Val Leu Ala Thr	Tyr Leu Leu Gly Phe
145	150	155
Val Asn Ala Ala Ile His	Thr Gly Phe Thr Phe	Gln Leu Ser Phe Cys
165	170	175

His Ser Asn Ile Ile Asn Tyr Phe Phe Cys Asp Ile Pro Pro Leu Leu
 180 185 190
 Lys Leu Cys Ser Asp Thr His Ile Asn Glu Val Val Ile Phe Ala Phe
 195 200 205
 Ala Ser Phe Asn Glu Leu Ser Cys Leu Leu Leu Ile Leu Val Ser Cys
 210 215 220
 Leu Tyr Ile Leu Ala Ala Ile Leu Lys Ile His Ser Ala Glu Gly Arg
 225 230 235 240
 His Lys Ala Phe Ser Thr Cys Ala Ser His Leu Ala Val Val Thr Ile
 245 250 255
 Phe Phe Gly Thr Ile Leu Phe Met Tyr Leu Leu Arg Pro Ser Ser Ser
 260 265 270
 Tyr Ser Met Asp Gln Asp Lys Val Val Ser Val Phe Tyr Thr Val Val
 275 280 285
 Ile Pro Met Leu Asn Pro Phe Ile Tyr Ser Leu Arg Asn Lys Glu Val
 290 295 300
 Lys Ala Ser Leu Ser Lys Met Phe Lys Thr Val Ser Tyr Ile Ser Thr
 305 310 315 320

<210> 1514

<211> 299

<212> PRT

<213> Unknown (H38g431 protein)

<220>

<223> Synthetic construct

<400> 1514

Met Gly Leu Pro Gly Ile His Glu Trp Gln His Trp Leu Ser Leu Pro
 1 5 10 15
 Leu Thr Leu Leu Tyr Leu Leu Ala Leu Gly Ala Asn Leu Leu Ile Ile
 20 25 30
 Ile Thr Ile Gln His Glu Thr Val Leu His Glu Pro Met Tyr His Leu
 35 40 45
 Leu Gly Ile Leu Ala Val Val Asp Ile Gly Leu Ala Thr Thr Ile Met
 50 55 60
 Pro Lys Ile Leu Ala Ile Phe Trp Phe Asp Ala Lys Ala Ile Ser Leu
 65 70 75 80
 Pro Met Cys Phe Ala Gln Ile Tyr Ala Ile His Cys Phe Phe Cys Ile
 85 90 95
 Glu Ser Gly Ile Phe Leu Cys Met Ala Val Asp Arg Tyr Ile Ala Ile
 100 105 110
 Cys Arg Pro Leu Gln Tyr Pro Ser Ile Val Thr Lys Ala Phe Val Phe
 115 120 125
 Lys Ala Thr Gly Phe Ile Met Leu Arg Asn Gly Leu Leu Thr Ile Pro
 130 135 140
 Val Pro Ile Leu Ala Ala Gln Arg His Tyr Cys Ser Arg Asn Glu Ile
 145 150 155 160
 Glu His Cys Leu Cys Ser Asn Leu Gly Val Ile Ser Leu Ala Cys Asp
 165 170 175
 Asp Ile Thr Val Asn Lys Phe Tyr Gln Leu Met Leu Ala Trp Val Leu
 180 185 190
 Val Gly Ser Asp Met Ala Leu Val Phe Ser Ser Tyr Ala Val Ile Leu
 195 200 205
 His Ser Val Leu Arg Leu Asn Ser Ala Glu Ala Met Ser Lys Ala Leu
 210 215 220
 Ser Thr Cys Ser Ser His Leu Ile Leu Ile Leu Phe His Thr Gly Ile
 225 230 235 240
 Ile Val Leu Ser Val Thr His Leu Ala Glu Lys Lys Ile Pro Leu Ile
 245 250 255
 Pro Val Phe Leu Asn Val Leu His Asn Val Ile Pro Pro Ala Leu Asn

260 265 270
 Pro Leu Ala Cys Ala Leu Arg Met His Lys Leu Arg Leu Gly Phe Gln
 275 280 285
 Arg Leu Leu Gly Leu Gly Gln Asp Val Ser Lys
 290 295

<210> 1515
 <211> 317
 <212> PRT
 <213> Unknown (H38g432 protein)

<220>
 <223> Synthetic construct

<400> 1515
 Met Met Arg Leu Met Lys Glu Val Arg Gly Arg Asn Gln Thr Glu Val
 1 5 10 15
 Thr Glu Phe Leu Leu Gly Leu Ser Asp Asn Pro Asp Leu Gln Gly
 20 25 30
 Val Leu Phe Ala Leu Phe Leu Leu Ile Tyr Met Ala Asn Met Val Gly
 35 40 45
 Asn Leu Gly Met Ile Val Leu Ile Lys Ile Asp Leu Cys Leu His Thr
 50 55 60
 Pro Met Tyr Phe Phe Leu Ser Ser Leu Ser Phe Val Asp Ala Ser Tyr
 65 70 75 80
 Ser Ser Ser Val Thr Pro Lys Met Leu Val Asn Leu Met Ala Glu Asn
 85 90 95
 Lys Ala Ile Ser Phe His Gly Cys Ala Ala Gln Phe Tyr Phe Phe Gly
 100 105 110
 Ser Phe Leu Gly Thr Glu Cys Phe Leu Leu Ala Met Met Ala Tyr Asp
 115 120 125
 Arg Tyr Ala Ala Ile Trp Asn Pro Leu Leu Tyr Pro Val Leu Val Ser
 130 135 140
 Gly Arg Ile Cys Phe Leu Leu Ile Ala Thr Ser Phe Leu Ala Gly Cys
 145 150 155 160
 Gly Asn Ala Ala Ile His Thr Gly Met Thr Phe Arg Leu Ser Phe Cys
 165 170 175
 Gly Ser Asn Arg Ile Asn His Phe Tyr Cys Asp Thr Pro Pro Leu Leu
 180 185 190
 Lys Leu Ser Cys Ser Asp Thr His Phe Asn Gly Ile Val Ile Met Ala
 195 200 205
 Phe Ser Ser Phe Ile Val Ile Ser Cys Val Met Ile Val Leu Ile Ser
 210 215 220
 Tyr Leu Cys Ile Phe Ile Ala Val Leu Lys Met Pro Ser Leu Glu Gly
 225 230 235 240
 Arg His Lys Ala Phe Ser Thr Cys Ala Ser Tyr Leu Met Ala Val Thr
 245 250 255
 Ile Phe Phe Gly Thr Ile Leu Phe Met Tyr Leu Arg Pro Thr Ser Ser
 260 265 270
 Tyr Ser Met Glu Gln Asp Lys Val Val Ser Val Phe Tyr Thr Val Ile
 275 280 285
 Ile Pro Val Leu Asn Pro Leu Ile Tyr Ser Leu Lys Asn Lys Asp Val
 290 295 300
 Lys Lys Ala Leu Lys Lys Ile Leu Trp Lys His Ile Leu
 305 310 315

<210> 1516
 <211> 317
 <212> PRT
 <213> Unknown (H38g433 protein)

<220>

<223> Synthetic construct

<400> 1516

```

Met Ser His Thr Asn Val Thr Ile Phe His Pro Ala Val Phe Val Leu
 1           5           10           15
Pro Gly Ile Pro Gly Leu Glu Ala Tyr His Ile Trp Leu Ser Ile Pro
          20           25           30
Leu Cys Leu Ile Tyr Ile Thr Ala Val Leu Gly Asn Ser Ile Leu Ile
          35           40           45
Val Val Ile Val Met Glu Arg Asn Leu His Val Pro Met Tyr Phe Phe
          50           55           60
Leu Ser Met Leu Ala Val Met Asp Ile Leu Leu Ser Thr Thr Thr Val
65           70           75           80
Pro Lys Ala Leu Ala Ile Phe Trp Leu Gln Ala His Asn Ile Ala Phe
          85           90           95
Asp Ala Cys Val Thr Gln Gly Phe Phe Val His Met Met Phe Val Gly
          100          105          110
Glu Ser Ala Ile Leu Leu Ala Met Ala Phe Asp Arg Phe Val Ala Ile
          115          120          125
Cys Ala Pro Leu Arg Tyr Thr Thr Val Leu Thr Trp Pro Val Val Gly
          130          135          140
Arg Ile Ala Leu Ala Val Ile Thr Arg Ser Phe Cys Ile Ile Phe Pro
145           150           155           160
Val Ile Phe Leu Leu Lys Arg Leu Pro Phe Cys Leu Thr Asn Ile Val
          165          170          175
Pro His Ser Tyr Cys Glu His Ile Gly Val Ala Arg Leu Ala Cys Ala
          180          185          190
Asp Ile Thr Val Asn Ile Trp Tyr Gly Phe Ser Val Pro Ile Val Met
          195          200          205
Val Ile Leu Asp Val Ile Leu Ile Ala Val Ser Tyr Ser Leu Ile Leu
          210          215          220
Arg Ala Val Phe Arg Leu Pro Ser Gln Asp Ala Arg His Lys Ala Leu
225           230           235           240
Ser Thr Cys Gly Ser His Leu Cys Val Ile Leu Met Phe Tyr Val Pro
          245          250          255
Ser Phe Phe Thr Leu Leu Thr His His Phe Gly Arg Asn Ile Pro Gln
          260          265          270
His Val His Ile Leu Leu Ala Asn Leu Tyr Val Ala Val Pro Pro Met
          275          280          285
Leu Asn Pro Ile Val Tyr Gly Val Lys Thr Lys Gln Ile Arg Glu Gly
          290          295          300
Val Ala His Arg Phe Phe Asp Ile Lys Thr Trp Cys Cys
305           310           315

```

<210> 1517

<211> 305

<212> PRT

<213> Unknown (H38g434 protein)

<220>

<223> Synthetic construct

<400> 1517

```

Met Gln Arg Ser Asn His Thr Val Thr Glu Phe Ile Leu Leu Gly Phe
 1           5           10           15
Thr Thr Asp Pro Gly Met Gln Leu Gly Leu Phe Val Val Phe Leu Gly
          20           25           30
Val Tyr Ser Leu Thr Val Val Gly Asn Ser Thr Leu Ile Val Leu Ile
          35           40           45
Cys Asn Asp Ser Cys Leu His Thr Pro Met Tyr Phe Val Ala Gly Asn

```

```

      50      55      60
Leu Ser Phe Leu Asp Leu Trp Tyr Ser Ser Val Tyr Thr Pro Lys Ile
65      70      75      80
Leu Val Thr Cys Ile Ser Glu Asp Lys Ser Ile Ser Phe Ala Gly Cys
      85      90      95
Leu Cys Gln Phe Phe Phe Ser Ala Gly Leu Ala Tyr Ser Glu Cys Tyr
      100      105      110
Leu Leu Ala Ala Val Ala Tyr Asp Arg Tyr Val Ala Ile Ser Lys Pro
      115      120      125
Leu Leu Tyr Ala Gln Ala Met Ser Ile Lys Leu Cys Ala Leu Leu Val
      130      135      140
Ala Val Ser Tyr Cys Gly Gly Phe Ile Asn Ser Ser Ile Ile Thr Lys
145      150      155      160
Lys Thr Phe Ser Phe Asn Phe Cys Arg Glu Asn Ile Ile Asp Asp Phe
      165      170      175
Phe Cys Asp Leu Leu Pro Leu Val Glu Leu Ala Cys Gly Glu Lys Gly
      180      185      190
Gly Tyr Lys Ile Met Met Tyr Phe Leu Leu Ala Ser Asn Val Ile Cys
      195      200      205
Pro Ala Val Leu Ile Leu Ala Ser Tyr Leu Phe Ile Ile Thr Ser Val
      210      215      220
Leu Arg Ile Ser Ser Ser Lys Gly Tyr Leu Lys Ala Phe Ser Thr Cys
225      230      235      240
Ser Ser His Leu Thr Ser Val Thr Leu Tyr Tyr Gly Ser Ile Leu Tyr
      245      250      255
Ile Tyr Ala Leu Pro Arg Ser Ser Tyr Ser Phe Asp Met Asp Lys Ile
      260      265      270
Val Ser Thr Phe Tyr Thr Val Val Phe Pro Met Leu Asn Leu Met Ile
      275      280      285
Tyr Ser Leu Arg Asn Lys Asp Val Lys Glu Ala Leu Lys Lys Leu Leu
      290      295      300
Pro
305

```

<210> 1518

<211> 314

<212> PRT

<213> Unknown (H38g435 protein)

<220>

<223> Synthetic construct

<400> 1518

```

Met Leu Pro Ser Asn Ile Thr Ser Thr His Pro Ala Val Phe Leu Leu
1      5      10      15
Val Gly Ile Pro Gly Leu Glu His Leu His Ala Trp Ile Ser Ile Pro
      20      25      30
Phe Cys Phe Ala Tyr Thr Leu Ala Leu Leu Gly Asn Cys Thr Leu Leu
      35      40      45
Phe Ile Ile Arg Ala Asp Ala Ala Leu His Glu Pro Met Tyr Leu Phe
      50      55      60
Leu Ala Met Leu Ala Thr Ile Asp Leu Val Leu Ser Ser Thr Thr Leu
65      70      75      80
Pro Lys Met Leu Ala Ile Phe Trp Phe Arg Asp Gln Glu Ile Asn Phe
      85      90      95
Phe Ala Cys Leu Val Gln Met Phe Phe Leu His Ser Phe Ser Ile Met
      100      105      110
Glu Ser Ala Val Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile
      115      120      125
Cys Lys Pro Leu His Tyr Thr Val Leu Thr Gly Ser Leu Ile Thr
130      135      140

```

Lys Ile Gly Met Ala Ala Val Ala Arg Ala Val Thr Leu Met Thr Pro
 145 150 155 160
 Leu Pro Phe Leu Leu Arg Arg Phe His Tyr Cys Arg Gly Pro Val Ile
 165 170 175
 Ala His Cys Tyr Cys Glu His Met Ala Val Val Arg Leu Ala Cys Gly
 180 185 190
 Asp Thr Ser Phe Asn Asn Ile Tyr Gly Ile Ala Val Ala Met Phe Ser
 195 200 205
 Val Val Leu Asp Leu Leu Phe Val Ile Leu Ser Tyr Val Phe Ile Leu
 210 215 220
 Gln Ala Val Leu Gln Leu Ala Ser Gln Glu Ala Arg Tyr Lys Ala Phe
 225 230 235 240
 Gly Thr Cys Val Ser His Ile Gly Ala Ile Leu Ser Thr Tyr Thr Pro
 245 250 255
 Val Val Ile Ser Ser Val Met His Arg Val Ala Arg His Ala Ala Pro
 260 265 270
 Arg Val His Ile Leu Leu Ala Ile Phe Tyr Leu Leu Phe Pro Pro Met
 275 280 285
 Val Asn Pro Ile Ile Tyr Gly Val Lys Thr Lys Gln Ile Arg Glu Tyr
 290 295 300
 Val Leu Ser Leu Phe Gln Arg Lys Asn Met
 305 310

<210> 1519

<211> 312

<212> PRT

<213> Unknown (H38g436 protein)

<220>

<223> Synthetic construct

<400> 1519

Met Leu Lys Lys Asn His Thr Ala Val Thr Glu Phe Val Leu Leu Gly
 1 5 10 15
 Leu Thr Asp Arg Ala Glu Leu Gln Ser Leu Leu Phe Val Val Phe Leu
 20 25 30
 Val Ile Tyr Leu Ile Thr Val Ile Gly Asn Val Ser Met Ile Leu Leu
 35 40 45
 Ile Arg Ser Asp Ser Thr Leu His Thr Pro Met Tyr Phe Phe Leu Ser
 50 55 60
 His Leu Ser Phe Val Asp Leu Cys Tyr Thr Thr Asn Val Thr Pro Gln
 65 70 75 80
 Met Leu Val Asn Phe Leu Ser Lys Arg Lys Thr Ile Ser Phe Ile Gly
 85 90 95
 Cys Phe Ile Gln Phe His Phe Phe Ile Ala Leu Val Ile Thr Asp Tyr
 100 105 110
 Tyr Met Leu Thr Val Met Ala Tyr Asp Arg Tyr Met Ala Ile Cys Lys
 115 120 125
 Pro Leu Leu Tyr Gly Ser Lys Met Thr Arg Cys Val Cys Leu Cys Leu
 130 135 140
 Ala Ala Ala Pro Tyr Ile Tyr Gly Phe Ala Asn Gly Leu Ser Gln Thr
 145 150 155 160
 Thr Leu Met Leu Arg Leu Ser Phe Cys Gly Pro Asn Asp Ile Asn His
 165 170 175
 Phe Tyr Cys Ala Asp Pro Pro Leu Leu Val Leu Ala Cys Ser Asp Thr
 180 185 190
 Tyr Val Lys Glu Thr Ala Met Leu Val Val Ala Gly Ser Asn Leu Ile
 195 200 205
 Cys Ser Leu Thr Val Ile Leu Ile Ser Tyr Thr Phe Ile Phe Thr Ala
 210 215 220
 Ile Leu Arg Ile His Thr Ala Glu Gly Arg Arg Lys Ala Phe Ser Thr

225 230 235 240
 Cys Gly Ser His Val Thr Ala Val Thr Val Phe Tyr Gly Thr Leu Phe
 245 250 255
 Cys Met Tyr Leu Arg Pro Pro Ser Glu Thr Ser Ile Gln Gln Gly Lys
 260 265 270
 Ile Val Ala Val Phe Tyr Ile Phe Val Ser Pro Met Leu Asn Pro Leu
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Arg Ser Ile Arg Lys Val
 290 295 300
 Ile Gln Lys Lys Leu Phe Ala Lys
 305 310

<210> 1520

<211> 314

<212> PRT

<213> Unknown (H38g437 protein)

<220>

<223> Synthetic construct

<400> 1520

Met Ser Ala Ser Asn Ile Thr Leu Thr His Pro Thr Ala Phe Leu Leu
 1 5 10 15
 Val Gly Ile Pro Gly Leu Glu His Leu His Ile Trp Ile Ser Ile Pro
 20 25 30
 Phe Cys Leu Ala Tyr Thr Leu Ala Leu Leu Gly Asn Cys Thr Leu Leu
 35 40 45
 Leu Ile Ile Gln Ala Asp Ala Ala Leu His Glu Pro Met Tyr Leu Phe
 50 55 60
 Leu Ala Met Leu Ala Ala Ile Asp Leu Val Leu Ser Ser Ser Ala Leu
 65 70 75 80
 Pro Lys Met Leu Ala Ile Phe Trp Phe Arg Asp Arg Glu Ile Asn Phe
 85 90 95
 Phe Ala Cys Leu Ala Gln Met Phe Phe Leu His Ser Phe Ser Ile Met
 100 105 110
 Glu Ser Ala Val Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile
 115 120 125
 Cys Lys Pro Leu His Tyr Thr Lys Val Leu Thr Gly Ser Leu Ile Thr
 130 135 140
 Lys Ile Gly Met Ala Ala Val Ala Arg Ala Val Thr Leu Met Thr Pro
 145 150 155 160
 Leu Pro Phe Leu Leu Arg Cys Phe His Tyr Cys Arg Gly Pro Val Ile
 165 170 175
 Ala His Cys Tyr Cys Glu His Met Ala Val Val Arg Leu Ala Cys Gly
 180 185 190
 Asp Thr Ser Phe Asn Asn Ile Tyr Gly Ile Ala Val Ala Met Phe Ile
 195 200 205
 Val Val Leu Asp Leu Leu Leu Val Ile Leu Ser Tyr Ile Phe Ile Leu
 210 215 220
 Gln Ala Val Leu Leu Leu Ala Ser Gln Glu Ala Arg Tyr Lys Ala Phe
 225 230 235 240
 Gly Thr Cys Val Ser His Ile Gly Ala Ile Leu Ala Phe Tyr Thr Thr
 245 250 255
 Val Val Ile Ser Ser Val Met His Arg Val Ala Arg His Ala Ala Pro
 260 265 270
 His Val His Ile Leu Leu Ala Asn Phe Tyr Leu Leu Phe Pro Pro Met
 275 280 285
 Val Asn Pro Ile Ile Tyr Gly Val Lys Thr Lys Gln Ile Arg Glu Ser
 290 295 300
 Ile Leu Gly Val Phe Pro Arg Lys Asp Met
 305 310

<210> 1521
 <211> 313
 <212> PRT
 <213> Unknown (H38g438 protein)

<220>
 <223> Synthetic construct

<400> 1521
 Met Ser Ala Ser Ser Ile Thr Ser Thr His Pro Thr Ser Phe Leu Leu
 1 5 10 15
 Met Gly Ile Pro Gly Leu Glu His Leu His Ile Trp Ile Ser Ile Pro
 20 25 30
 Phe Ser Ala Tyr Thr Leu Ala Leu Leu Gly Asn Cys Thr Leu Leu Leu
 35 40 45
 Ile Ile Gln Ala Asp Ala Ala Leu His Glu Pro Ile Tyr Leu Phe Leu
 50 55 60
 Ala Met Leu Ala Ala Ile Asp Leu Val Leu Ser Ser Ser Ala Leu Pro
 65 70 75 80
 Lys Met Leu Ala Ile Phe Trp Phe Arg Asp Arg Glu Ile Asn Phe Phe
 85 90 95
 Ala Cys Leu Val Gln Met Phe Phe Leu His Ser Phe Ser Ile Met Glu
 100 105 110
 Ser Ala Val Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys
 115 120 125
 Lys Pro Leu His Tyr Thr Thr Val Leu Thr Gly Ser Leu Ile Thr Lys
 130 135 140
 Ile Gly Met Ala Ala Val Ala Arg Ala Val Thr Leu Met Thr Pro Leu
 145 150 155 160
 Pro Phe Leu Leu Arg Cys Phe His Tyr Cys Arg Gly Pro Val Ile Ala
 165 170 175
 Arg Cys Tyr Cys Glu His Met Ala Val Val Arg Leu Ala Cys Gly Asn
 180 185 190
 Thr Ser Phe Asn Asn Ile Tyr Gly Ile Ala Val Ala Met Phe Ile Gly
 195 200 205
 Val Leu Asp Leu Phe Phe Ile Ile Leu Ser Tyr Ile Phe Ile Leu Gln
 210 215 220
 Ala Val Leu Gln Leu Ser Ser Gln Glu Ala Arg Tyr Lys Ala Phe Gly
 225 230 235 240
 Thr Cys Val Ser His Ile Gly Ala Ile Leu Ala Phe Tyr Thr Pro Ser
 245 250 255
 Val Ile Ser Ser Val Met His Arg Val Ala Arg Cys Ala Ala Pro His
 260 265 270
 Val His Ile Leu Leu Ala Asn Phe Tyr Leu Leu Phe Pro Pro Met Val
 275 280 285
 Asn Pro Ile Ile Tyr Gly Val Lys Thr Lys Gln Ile Arg Glu Ser Val
 290 295 300
 Leu Gly Val Phe Pro Arg Lys Asp Val
 305 310

<210> 1522
 <211> 318
 <212> PRT
 <213> Unknown (H38g439 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(318)

<223> Xaa = Any Amino Acid

<400> 1522

```

Met Thr Thr His Asn Ser Thr Gly Ser Ser His Ser Leu Phe Ile Leu
 1           5           10           15
Leu Ser Ile Pro Gly Leu Glu Asp Gln His Thr Trp Met Ser Leu Pro
 20           25           30
Phe Phe Ile Ser Tyr Leu Val Ala Phe Leu Gly Asn Ser Leu Ile Ile
 35           40           45
Phe Ile Ile Ile Thr Glu Cys Ser Leu His Glu Pro Met Tyr Leu Phe
 50           55           60
Leu Cys Met Leu Ala Val Ala Asp Leu Ile Leu Ser Thr Thr Thr Val
 65           70           75           80
Pro Lys Ala Leu Ala Ile Phe Trp Phe Tyr Ala Gly Ala Ile Ser Leu
 85           90           95
Gly Gly Cys Val Thr Gln Ile Phe Phe Ile His Ala Thr Phe Ile Glu
 100          105          110
Glu Ser Gly Ile Leu Leu Ala Met Ala Leu Asp Arg Tyr Val Ala Ile
 115          120          125
Cys Asp Pro Leu His Tyr Thr Thr Val Leu Ser Arg Ala Lys Ile Thr
 130          135          140
Lys Ile Gly Leu Ala Val Val Leu Arg Ser Phe Cys Val Ile Met Pro
 145          150          155          160
Asp Val Phe Leu Val Lys Arg Leu Pro Phe Cys His Ser Asn Leu Leu
 165          170          175
Pro His Thr Tyr Cys Glu His Met Ala Val Ala Lys Phe Ala Cys Ala
 180          185          190
Asp Ile His Val Asn Val Trp Tyr Gly Leu Ser Val Leu Leu Tyr Thr
 195          200          205
Val Val Leu Asp Ala Leu Leu Ile Leu Val Ser Xaa Ser Phe Ile Leu
 210          215          220
Tyr Thr Gly Phe His Leu Pro Ser Pro Gly Ala Arg Gln Lys Ala Leu
 225          230          235          240
Gly Thr Cys Gly Ser His Leu Arg Val Ile Ser Met Phe Tyr Leu Pro
 245          250          255
Gly Ile Phe Thr Ile Ile Thr Gln Arg Phe Gly His His Val Pro Leu
 260          265          270
His Thr His Ile Leu Leu Gly Asn Val Trp Val Leu Ala Pro Pro Met
 275          280          285
Leu Asn Pro Ile Ile Tyr Gly Ile Asn Thr Arg Gln Ile Gln Glu Cys
 290          295          300
Val Leu Ser Leu Leu Ser Ser Gln Arg Lys Xaa Cys Xaa Ile
 305          310          315

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<210> 1523

<211> 313

<212> PRT

<213> Unknown (H38g440 protein)

<220>

<223> Synthetic construct

<400> 1523

```

Met Asn Trp Val Asn Asp Ser Ile Ile Gln Glu Phe Ile Leu Leu Gly
 1           5           10           15
Phe Ser Asp Arg Pro Trp Leu Glu Phe Pro Leu Leu Val Val Phe Leu
 20           25           30
Ile Ser Tyr Thr Val Thr Ile Phe Gly Asn Leu Thr Ile Ile Leu Val
 35           40           45
Ser Arg Leu Asp Thr Lys Leu His Thr Pro Met Tyr Phe Phe Leu Thr
 50           55           60

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Asn Leu Ser Leu Leu Asp Leu Cys Tyr Thr Thr Cys Thr Val Pro Gln
65          70          75          80
Met Leu Val Asn Leu Cys Ser Ile Arg Lys Val Ile Ser Tyr Arg Gly
          85          90          95
Cys Val Ala Gln Leu Phe Ile Phe Leu Ala Leu Gly Ala Thr Glu Tyr
          100          105          110
Leu Leu Leu Ala Val Met Ser Phe Asp Arg Phe Val Ala Ile Cys Arg
          115          120          125
Pro Leu His Tyr Ser Val Ile Met His Gln Arg Leu Cys Leu Gln Leu
          130          135          140
Ala Ala Ala Ser Trp Val Thr Gly Phe Ser Asn Ser Val Trp Leu Ser
145          150          155          160
Thr Leu Thr Leu Gln Leu Pro Leu Cys Asp Pro Tyr Val Ile Asp His
          165          170          175
Phe Leu Cys Glu Val Pro Ala Leu Leu Lys Leu Ser Cys Val Glu Thr
          180          185          190
Thr Ala Asn Glu Ala Glu Leu Phe Leu Val Ser Glu Leu Phe His Leu
          195          200          205
Ile Pro Leu Thr Leu Ile Leu Ile Ser Tyr Ala Phe Ile Val Arg Ala
          210          215          220
Val Leu Arg Ile Gln Ser Ala Glu Gly Arg Gln Lys Ala Phe Gly Thr
225          230          235          240
Cys Gly Ser His Leu Ile Val Val Ser Leu Phe Tyr Ser Thr Ala Val
          245          250          255
Ser Val Tyr Leu Gln Pro Pro Ser Pro Ser Ser Lys Asp Gln Gly Lys
          260          265          270
Met Val Ser Leu Phe Tyr Gly Ile Ile Ala Pro Met Leu Asn Pro Leu
          275          280          285
Ile Tyr Thr Leu Arg Asn Lys Glu Val Lys Glu Gly Phe Lys Arg Leu
          290          295          300
Val Ala Arg Val Phe Leu Ile Lys Lys
305          310

```

<210> 1524

<211> 333

<212> PRT

<213> Unknown (H38g441 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(333)

<223> Xaa = Any Amino Acid

<400> 1524

```

Met Glu Lys Ser Asn Val Ser Ser Val Tyr Gly Phe Ile Leu Val Gly
1          5          10          15
Phe Ser Asp Arg Pro Lys Leu Glu Met Val Leu Phe Thr Val Asn Phe
          20          25          30
Ile Leu Tyr Ser Val Ala Val Leu Gly Asn Ser Thr Ile Ile Leu Val
          35          40          45
Cys Ile Leu Asp Ser Gln Leu His Thr Pro Met Tyr Phe Phe Leu Ala
          50          55          60
Asn Leu Ser Phe Leu Asp Leu Cys Phe Ser Thr Ser Cys Ile Pro Gln
65          70          75          80
Met Leu Val Asn Leu Trp Gly Pro Asp Lys Thr Ile Ser Cys Ala Gly
          85          90          95
Cys Val Val Gln Leu Phe Ser Phe Leu Ser Val Arg Gly Ile Glu Cys
          100          105          110
Ile Leu Leu Ala Val Met Ala Tyr Asp Ser Tyr Ala Ala Val Cys Lys

```

```

      115      120      125
Pro Leu Arg Tyr Leu Val Ile Met His Leu Gln Leu Cys Leu Gly Leu
  130      135      140
Met Ala Ala Ala Trp Gly Ser Gly Leu Val Asn Ala Val Val Met Ser
  145      150      155      160
Pro Leu Thr Met Thr Leu Ser Arg Ser Gly Arg Arg Arg Val Asn His
      165      170      175
Phe Leu Cys Glu Met Pro Ala Leu Ile Lys Met Ala Cys Leu Asp Val
      180      185      190
Arg Ala Val Glu Met Leu Ala Phe Ala Phe Ala Val Leu Ile Val Leu
      195      200      205
Leu Pro Leu Thr Leu Ile Leu Val Ser Tyr Gly Tyr Ile Ala Ala Ala
      210      215      220
Val Leu Ser Ile Lys Ser Ala Ala Arg Gln Trp Lys Ala Phe His Thr
  225      230      235      240
Cys Ser Ser His Leu Thr Val Val Ser Leu Phe Tyr Gly Ser Ile Ile
      245      250      255
Tyr Met Tyr Met Gln Pro Gly Asn Ser Ser Ser Gln Asp Gln Gly Lys
      260      265      270
Phe Leu Thr Leu Phe Tyr Asn Leu Val Thr Pro Met Leu Asn Leu Leu
      275      280      285
Ile Tyr Thr Leu Arg Asn Lys Glu Val Lys Gly Ala Leu Lys Lys Val
      290      295      300
Leu Gly Arg Gln Xaa Xaa Thr Gly Glu Ile Xaa Xaa Val Val Lys Ser
  305      310      315      320
Xaa Ala Lys Tyr Leu Phe Gln Tyr Thr Phe Ile Leu Cys
      325      330

```

<210> 1525

<211> 317

<212> PRT

<213> Unknown (H38g442 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(317)

<223> Xaa = Any Amino Acid

<400> 1525

```

Gln Val Val His Thr Gly Phe Ser Pro Xaa Leu Tyr Val Phe Thr Leu
  1      5      10      15
Leu Gly Asn Gly Ser Ile Leu Gly Leu Ile Trp Leu Asp Ser Arg Leu
      20      25      30
His Thr Pro Met Tyr Phe Phe Leu Ser His Leu Ala Ile Ile Asp Ile
      35      40      45
Ser Tyr Ala Ser Asn Asn Val Pro Lys Met Leu Thr Asn Leu Gly Leu
      50      55      60
Asn Lys Arg Lys Thr Ile Ser Phe Val Pro Cys Thr Met Gln Thr Phe
  65      70      75      80
Leu Tyr Met Ala Phe Ala His Thr Glu Cys Leu Ile Leu Val Met Met
      85      90      95
Ser Tyr Asp Arg Tyr Met Ala Val Cys His Pro Leu Gln Tyr Ser Val
      100      105      110
Ile Met Arg Trp Gly Val Cys Thr Val Leu Ala Val Thr Ser Trp Ala
      115      120      125
Cys Gly Ser Leu Leu Ala Leu Val His Val Val Leu Ile Leu Arg Leu
      130      135      140
Pro Phe Cys Gly Pro His Glu Ile Asn His Phe Phe Cys Glu Ile Leu
  145      150      155      160

```

Ser Val Leu Lys Leu Ala Cys Ala Asp Thr Trp Leu Asn Gln Val Val
 165 170 175
 Ile Phe Ala Ser Ser Val Phe Ile Leu Val Gly Ala Leu Cys Leu Val
 180 185 190
 Leu Val Ser Tyr Ser Arg Ile Leu Ala Ala Ile Leu Arg Asn Gln Ser
 195 200 205
 Gly Glu Gly Arg Arg Lys Gly Phe Ser Thr Cys Tyr Ser His Leu Cys
 210 215 220
 Met Val Gly Leu Phe Phe Gly Ser Ala Ile Val Thr Tyr Met Ala Pro
 225 230 235 240
 Lys Ser Arg His Pro Glu Glu Gln Gln Lys Val Leu Ser Leu Phe Tyr
 245 250 255
 Ser Leu Phe Asn Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn
 260 265 270
 Ala Glu Val Lys Gly Ala Leu Arg Ser Ala Leu Arg Lys Glu Arg Leu
 275 280 285
 Thr Xaa Asp Ile Ser Lys Gly Thr Met Gly Arg Glu Pro Cys Ser Leu
 290 295 300
 Gln Asn Ile Glu Val Gly Phe Phe Phe Cys Leu Leu Leu
 305 310 315

<210> 1526

<211> 239

<212> PRT

<213> Unknown (H38g443 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(239)

<223> Xaa = Any Amino Acid

<400> 1526

Gln Met Leu Thr Asp Trp Trp Gly Pro Asn Arg Thr Thr Ser Tyr Val
 1 5 10 15
 Asn Cys Thr Ile Gln Phe Leu Val Ser Leu Xaa Cys Met Cys His Tyr
 20 25 30
 Ile Ile Ser Tyr Asn Tyr Phe Ile Ile Ile Cys His Pro Leu Xaa Tyr
 35 40 45
 Leu Leu Ile Met Asn Leu Tyr Leu Leu Leu Asn Leu Thr Leu Met Thr
 50 55 60
 Trp Ser Asp Asn Ser Phe Ile Phe Val Ile Met Tyr Thr Leu Ile Leu
 65 70 75 80
 Lys Phe Pro Ser Met Lys Lys Lys Asn Leu Gln Asp Asn Ser Leu His
 85 90 95
 Val Leu Leu Ala Met Leu Lys Thr Val Phe Leu Asp Ala Thr Ile Glu
 100 105 110
 Glu Met Ser Val Phe Val Leu Asn Asn Val Asn Val Leu Ile Cys Leu
 115 120 125
 Ile Ser Asn Phe Thr Cys Tyr Gly Tyr Ile Ala Gly Ala Leu Arg Met
 130 135 140
 Asn Thr Ser Asn Xaa Ile Arg Ser Lys Leu Arg Asn Gln Tyr His His
 145 150 155 160
 His His His Arg Cys His Phe Ile Ile Asp Ser Ile Phe Tyr Gly Ile
 165 170 175
 Ile Val Xaa Met Leu Leu Gln Asp Gly Asn Asn Ser Ser Gln Asp Gln
 180 185 190
 Glu Arg Phe Phe Ile Leu Phe Tyr Thr Ile Leu Thr Pro Ser Leu Lys
 195 200 205
 Leu Leu Val Tyr Leu Leu Arg Asn Lys Asp Ile Lys Asp Ile Ser Arg

210 215 220
 Arg Ile Leu Arg Phe Gly Arg Glu Ser Ser Lys Met Lys Gly Asn
 225 230 235

<210> 1527
 <211> 255
 <212> PRT
 <213> Unknown (H38g444 protein)

<220>
 <223> Synthetic construct

<400> 1527
 Met Tyr Phe Leu Leu Ser Gln Leu Ser Leu Ile Asp Leu Asn Tyr Ile
 1 5 10 15
 Ser Thr Ile Val Pro Lys Met Ala Ser Asp Phe Leu His Gly Asn Lys
 20 25 30
 Ser Ile Ser Phe Thr Gly Cys Gly Ile His Ser Phe Phe Phe Thr Thr
 35 40 45
 Leu Ala Val Val Glu Ala Leu Leu Leu Ile Ser Met Ala Tyr Val Arg
 50 55 60
 Cys Ile Ala Ile Cys Phe Pro Leu His Tyr Leu Met Arg Met Ser Lys
 65 70 75 80
 Arg Val Cys Val Leu Met Ile Thr Gly Ser Trp Ile Ile Gly Ser Ile
 85 90 95
 Asn Ala Cys Ala His Thr Val Tyr Ile Leu His Ile Pro Tyr Cys Pro
 100 105 110
 Ser Arg Val Ile Asn His Phe Phe Cys Asp Val Pro Ala Met Val Thr
 115 120 125
 Leu Ala Cys Met Asp Thr Trp Val Tyr Glu Gly Thr Val Leu Leu Ser
 130 135 140
 Ala Thr Ile Phe Leu Val Phe Pro Phe Ile Ala Ile Ser Cys Ser Tyr
 145 150 155 160
 Gly Arg Val Leu Leu Ala Val Tyr His Met Lys Ser Ala Glu Gly Lys
 165 170 175
 Lys Lys Ala Tyr Leu Thr Cys Ser Thr His Leu Thr Val Val Thr Phe
 180 185 190
 Tyr Tyr Ala Pro Phe Ala Tyr Thr Tyr Leu Arg Pro Arg Ser Leu Arg
 195 200 205
 Ser Pro Thr Glu Asp Lys Val Leu Ala Val Phe Tyr Thr Ile Leu Thr
 210 215 220
 Pro Met Leu Asn Pro Ile Ile Tyr Ser Leu Arg Asn Lys Glu Val Met
 225 230 235 240
 Gly Ala Leu Thr Arg Val Ile Gln Lys Ile Phe Ser Val Lys Ile
 245 250 255

<210> 1528
 <211> 320
 <212> PRT
 <213> Unknown (H38g445 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(320)
 <223> Xaa = Any Amino Acid

<400> 1528
 Leu Ser Xaa Pro Thr Arg Ala Ala Gln Lys Gln Phe Ile Leu Leu Gly
 1 5 10 15

Phe Ser Gly Arg Pro Arg Leu Glu His Val Leu Phe Val Phe Val Leu
 20 25 30
 Ile Phe Tyr Leu Val Thr Leu Val Gly Asn Ile Ile Ile Ile Leu Ile
 35 40 45
 Ser His Leu Asp Pro Cys Leu His Met Pro Met Tyr Phe Phe Leu Thr
 50 55 60
 Asn Leu Ser Phe Leu Asp Leu Cys Phe Thr Thr Ser Ser Ile Pro Gln
 65 70 75 80
 Leu Leu Phe Asn Leu Gly Ser Pro Gly Lys Thr Ile Ser His Thr Gly
 85 90 95
 Cys Ala Ile Gln Leu Phe Met Phe Leu Gly Leu Gly Gly Thr Glu Cys
 100 105 110
 Ile Leu Leu Ala Ala Val Ala Tyr Asp Arg Phe Ile Ala Ile Cys Lys
 115 120 125
 Pro Leu His Tyr Ser Val Ile Met His Pro Gln Leu Cys Trp Lys Leu
 130 135 140
 Val Ser Val Ala Arg Gly Cys Trp Thr Pro Gln Phe Ser Ser Tyr Val
 145 150 155 160
 Ser Trp Thr Met Lys Leu Pro Arg Cys Gly Arg Cys Lys Leu Lys His
 165 170 175
 Phe Leu Cys Glu Met Pro Ala Leu Ile Lys Ile Thr Cys Val Asp Thr
 180 185 190
 Val Ala Met Glu Ser Thr Val Phe Thr Leu Ser Val Val Ile Val Leu
 195 200 205
 Met Pro Leu Cys Leu Ile Leu Ile Ser Tyr Ser Tyr Ile Ala Leu Ala
 210 215 220
 Val Leu Arg Ile Lys Ser Ala Ala Gly Arg Arg Lys Ala Phe Asn Met
 225 230 235 240
 Cys Gly Ser His Leu Thr Val Val Ser Leu Phe Tyr Gly Asn Ile Ile
 245 250 255
 Tyr Met Tyr Met Gln Pro Xaa Asn Asn Ser Ser Gln Asp Gln Gly Lys
 260 265 270
 Phe Leu Thr Leu Phe Tyr Asn Leu Met Thr Pro Met Leu Asn Pro Val
 275 280 285
 Ile Tyr Thr Leu Arg Asn Lys Asp Val Lys Gly Ala Leu Lys Arg Leu
 290 295 300
 Val Ser Arg Lys His Ser Asp Ser Asp Cys Ser Xaa Asp Cys Phe Phe
 305 310 315 320

<210> 1529

<211> 126

<212> PRT

<213> Unknown (H38g446 protein)

<220>

<223> Synthetic construct

<400> 1529

Met Glu Asn Tyr Asn Gln Thr Ser Thr Ala Phe Ile Leu Leu Gly Leu
 1 5 10 15
 Ser Pro Pro Pro Lys Ile Gly His Phe Ile Phe Ile Leu Ile Asn Phe
 20 25 30
 Val Phe Leu Met Ala Leu Ile Gly Asn Leu Ser Met Ile Leu Leu Ile
 35 40 45
 Phe Leu Asp Ile His Leu His Thr Pro Met Tyr Phe Leu Leu Ser Gln
 50 55 60
 Leu Ser Leu Ile Asp Leu Asn Tyr Ile Ser Thr Ile Val Pro Lys Met
 65 70 75 80
 Val Tyr Asp Phe Ser Cys His Gly Asn Lys Ser Ile Ser Phe Thr Gly
 85 90 95
 Cys Gly Ile Gln Ser Phe Phe Phe Leu Thr Leu Ala Gly Ala Glu Ala

	100		105		110								
Leu	Leu	Leu	Thr	Ser	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Ile
	115						120					125	

<210> 1530
 <211> 326
 <212> PRT
 <213> Unknown (H38g447 protein)

<220>
 <223> Synthetic construct

<400> 1530

Met	Glu	Arg	Ala	Asn	Asp	Ser	Thr	Phe	Ser	Gly	Phe	Ile	Leu	Leu	Gly
1				5				10					15		
Phe	Ser	Asn	Arg	Pro	Gln	Leu	Glu	Thr	Ala	Leu	Phe	Val	Val	Ile	Leu
		20					25					30			
Ile	Ile	Tyr	Phe	Leu	Ser	Phe	Leu	Gly	Asn	Gly	Thr	Ile	Ile	Leu	Leu
	35					40					45				
Ser	Ile	Val	Asp	Pro	Arg	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Ser
	50					55				60					
Asn	Leu	Ser	Phe	Met	Asp	Leu	Cys	Leu	Thr	Thr	Cys	Thr	Val	Pro	Gln
65				70					75					80	
Thr	Leu	Val	Asn	Phe	Lys	Gly	Lys	Asp	Lys	Thr	Ile	Thr	Tyr	Gly	Gly
			85					90						95	
Cys	Val	Thr	Gln	Leu	Phe	Ile	Ala	Leu	Gly	Leu	Gly	Gly	Ser	Glu	Cys
			100				105						110		
Val	Leu	Leu	Ser	Ala	Met	Ala	Tyr	Asp	Arg	Tyr	Ala	Ala	Val	Cys	Arg
		115				120						125			
Pro	Leu	His	Tyr	Met	Val	Ser	Met	His	Pro	Gln	Leu	Cys	Leu	Gln	Leu
	130					135					140				
Val	Val	Thr	Thr	Trp	Leu	Thr	Gly	Phe	Gly	Asn	Ser	Val	Ile	Gln	Thr
145				150					155					160	
Ala	Leu	Thr	Met	Thr	Leu	Pro	Leu	Cys	Asp	Lys	Asn	Gln	Val	Asp	His
			165					170						175	
Phe	Phe	Cys	Glu	Val	Pro	Val	Met	Leu	Lys	Leu	Ser	Cys	Thr	Asn	Thr
		180					185						190		
Ser	Ile	Asn	Glu	Ala	Glu	Ile	Phe	Ala	Val	Ser	Val	Phe	Phe	Leu	Val
	195					200						205			
Val	Pro	Leu	Ser	Leu	Ile	Leu	Ala	Ser	Tyr	Gly	His	Ile	Thr	His	Ala
	210				215						220				
Val	Leu	Lys	Ile	Lys	Ser	Ala	Gln	Gly	Arg	Gln	Lys	Ala	Phe	Gly	Thr
225				230					235					240	
Cys	Gly	Ser	His	Leu	Leu	Val	Val	Ile	Ile	Phe	Phe	Gly	Thr	Leu	Ile
			245					250						255	
Ser	Met	Tyr	Leu	Gln	Pro	Pro	Ser	Ser	Tyr	Ser	Gln	Asp	Val	Asn	Lys
		260					265					270			
Ser	Ile	Ala	Leu	Phe	Tyr	Thr	Leu	Val	Thr	Pro	Leu	Leu	Asn	Pro	Leu
	275					280						285			
Ile	Tyr	Thr	Leu	Arg	Asn	Lys	Glu	Val	Lys	Gly	Ala	Thr	Lys	Lys	Thr
	290				295						300				
Ser	Gly	Glu	Asp	His	Arg	Cys	Met	Arg	Lys	Leu	Thr	Gln	Gly	Leu	Gln
305				310					315					320	
Phe	Gln	Thr	Phe	Val	His										
			325												

<210> 1531
 <211> 312
 <212> PRT
 <213> Unknown (H38g448 protein)

<220>

<223> Synthetic construct

<400> 1531

```

Met Glu Asn Tyr Asn Gln Thr Ser Thr Asp Phe Ile Leu Leu Gly Leu
 1           5           10           15
Phe Pro Pro Ser Ile Ile Asp Leu Phe Phe Phe Ile Leu Ile Val Phe
           20           25           30
Ile Phe Leu Met Ala Leu Ile Gly Asn Leu Ser Met Ile Leu Leu Ile
           35           40           45
Phe Leu Asp Thr His Leu His Thr Pro Met Tyr Phe Leu Leu Ser Gln
           50           55           60
Leu Ser Leu Ile Asp Leu Asn Tyr Ile Ser Thr Ile Val Pro Lys Met
65           70           75           80
Ala Ser Asp Phe Leu His Gly Asn Lys Ser Ile Ser Phe Thr Gly Cys
           85           90           95
Gly Ile Gln Ser Phe Phe Phe Leu Ala Leu Gly Gly Ala Glu Ala Leu
           100          105          110
Leu Leu Ala Ser Met Ala Tyr Asp Arg Tyr Ile Ala Ile Cys Phe Pro
           115          120          125
Leu His Tyr Leu Ile Arg Met Ser Lys Arg Val Cys Val Leu Met Ile
           130          135          140
Thr Gly Ser Trp Ile Ile Gly Ser Ile Asn Ala Cys Ala His Thr Val
145          150          155          160
Tyr Val Leu His Ile Pro Tyr Cys Arg Ser Arg Ala Ile Asn His Phe
           165          170          175
Phe Cys Asp Val Pro Ala Met Val Thr Leu Ala Cys Met Asp Thr Trp
           180          185          190
Val Tyr Glu Gly Thr Val Phe Leu Ser Ala Thr Ile Phe Leu Val Phe
           195          200          205
Pro Phe Ile Gly Ile Ser Cys Ser Tyr Gly Gln Val Leu Phe Ala Val
           210          215          220
Tyr His Met Lys Ser Ala Glu Gly Arg Lys Lys Ala Tyr Leu Thr Cys
225          230          235          240
Ser Thr His Leu Thr Val Val Thr Phe Tyr Tyr Ala Pro Phe Val Tyr
           245          250          255
Thr Tyr Leu Arg Pro Arg Ser Leu Arg Ser Pro Thr Glu Asp Lys Val
           260          265          270
Leu Ala Val Phe Tyr Thr Ile Leu Thr Pro Met Leu Asn Pro Ile Ile
           275          280          285
Tyr Ser Leu Arg Asn Lys Glu Val Met Gly Ala Leu Thr Arg Val Ser
290          295          300
Gln Arg Ile Cys Ser Val Lys Met
305          310

```

<210> 1532

<211> 312

<212> PRT

<213> Unknown (H38g449 protein)

<220>

<223> Synthetic construct

<400> 1532

```

Met Pro Asn Ser Thr Thr Val Met Glu Phe Leu Leu Met Arg Phe Ser
 1           5           10           15
Asp Val Trp Thr Leu Gln Ile Leu His Ser Ala Ser Phe Phe Met Leu
           20           25           30
Tyr Leu Val Thr Leu Met Gly Asn Ile Leu Ile Val Thr Val Thr Thr
           35           40           45
Cys Asp Ser Ser Leu His Met Pro Met Tyr Phe Phe Leu Arg Asn Leu

```

```

      50      55      60
Ser Ile Leu Asp Ala Cys Tyr Ile Ser Val Thr Val Pro Thr Ser Cys
65      70      75      80
Val Asn Ser Leu Leu Asp Ser Thr Thr Ile Ser Lys Ala Gly Cys Val
      85      90      95
Ala Gln Val Phe Leu Val Val Phe Phe Val Tyr Val Glu Leu Leu Phe
      100      105      110
Leu Thr Ile Met Ala His Asp Arg Tyr Val Ala Val Cys Gln Pro Leu
      115      120      125
His Tyr Pro Val Ile Val Asn Ser Arg Ile Cys Ile Gln Met Thr Leu
      130      135      140
Ala Ser Leu Leu Ser Gly Leu Val Tyr Ala Gly Met His Thr Gly Ser
145      150      155      160
Thr Phe Gln Leu Pro Phe Cys Arg Ser Asn Val Ile His Gln Phe Phe
      165      170      175
Cys Asp Ile Pro Ser Leu Leu Lys Leu Ser Cys Ser Asp Thr Phe Ser
      180      185      190
Asn Glu Val Met Ile Val Val Ser Ala Leu Gly Val Gly Gly Cys
      195      200      205
Phe Ile Phe Ile Ile Arg Ser Tyr Ile His Ile Phe Ser Thr Val Leu
      210      215      220
Gly Phe Pro Arg Gly Ala Asp Arg Thr Lys Ala Phe Ser Thr Cys Ile
225      230      235      240
Pro His Ile Leu Val Ser Val Phe Leu Ser Ser Cys Ser Ser Val
      245      250      255
Tyr Leu Arg Pro Pro Ala Ile Pro Ala Ala Thr Gln Asp Leu Ile Leu
      260      265      270
Ser Gly Phe Tyr Ser Ile Met Pro Pro Leu Phe Asn Pro Ile Ile Tyr
      275      280      285
Ser Leu Arg Asn Lys Gln Ile Lys Val Ala Ile Lys Lys Ile Met Lys
      290      295      300
Arg Ile Phe Tyr Ser Glu Asn Val
305      310

```

<210> 1533

<211> 311

<212> PRT

<213> Unknown (H38g450 protein)

<220>

<223> Synthetic construct

<400> 1533

```

Arg Asn Ala Pro Leu Glu Lys Tyr Asn Gln Thr Ser Thr Asp Phe Ile
1      5      10      15
Leu Leu Gly Ile Phe Pro Pro Ser Arg Ile Gly Phe Leu Leu Phe Ile
      20      25      30
Leu Leu Val Leu Ile Leu Leu Leu Ala Leu Ile Gly Asn Gln Ser Val
      35      40      45
Ile Leu Leu Ile Phe Leu Asp Thr His Leu His Thr Pro Ile Tyr Phe
      50      55      60
Leu Leu Ser Arg Leu Tyr Leu Ile Asp Leu Asn Tyr Ile Ser Thr Ile
65      70      75      80
Val Pro Lys Met Phe Ser Asp Phe Leu Phe Gly Asn Lys Ser Ile Ser
      85      90      95
Phe Ile Gly Cys Gly Ile Gln Ser Phe Phe Phe Val Thr Leu Ala Gly
      100      105      110
Ala Glu Met Leu Pro Leu Thr Ser Met Ala Cys Asp His Tyr Val Ala
      115      120      125
Val Cys Phe Pro Leu His Tyr Pro Ile His Met Ser Lys Ile Val Cys
130      135      140

```

```

Leu Met Ile Ile Gly Ser Trp Ile Met Gly Ser Ile Asp Thr Cys Ala
145                      150                      155                      160
His Ile Ser Tyr Met Pro His Ile Pro Val Cys Ser Ala Arg Ala Cys
                      165                      170                      175
Asp Val Pro Ala Met Val Thr Leu Ala Phe Val Asp Thr Trp Val Tyr
                      180                      185                      190
Glu Cys Thr Val Phe Leu Ser Thr Thr Leu Phe Leu Met Phe Thr Phe
                      195                      200                      205
Ile Gly Ile Ala Cys Ser Tyr Gly Glu Val Leu Leu Thr Val Tyr His
210                      215                      220
Ile Lys Ser Ala Glu Gly Arg Lys Lys Ala Tyr Ser Thr Cys Ser Thr
225                      230                      235                      240
His Leu Thr Val Val Ile Ile Tyr Tyr Ala Met Phe Ala Tyr Thr Tyr
                      245                      250                      255
Leu Tyr Pro Arg Tyr Leu Gln Ser Pro Thr Glu Asp Lys Val Leu Ala
                      260                      265                      270
Val Phe Tyr Thr Ile Leu Thr Ser Met Leu Asn Pro Ile Ile Tyr Ser
                      275                      280                      285
Leu Arg Asn Arg Glu Val Met Gly Ala Leu Thr Arg Val Ser Gln Arg
290                      295                      300
Ile Phe Pro Val Lys Met Lys
305                      310

```

<210> 1534

<211> 192

<212> PRT

<213> Unknown (H38g451 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(192)

<223> Xaa = Any Amino Acid

<400> 1534

```

Arg His Thr Glu Pro Arg Asn Leu Thr Gly Val Xaa Glu Phe Leu Leu
1      5      10      15
Leu Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Leu Leu
20     25     30
Ser Leu Ser Leu Ser Leu Ser Leu Tyr Leu Val Met Val Leu Arg Asn
35     40     45
Leu Leu Ser Ile Leu Ala Val Ser Ser Asp Ser Pro Leu His Thr Pro
50     55     60
Met Tyr Phe Phe Leu Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr
65     70     75     80
Ser Ala Thr Val Pro Lys Val Thr Val Asp Met Gln Ser His Ser Arg
85     90     95
Val Ile Ser His Ala Gly Cys Leu Thr Gln Met Ser Phe Leu Val Leu
100    105    110
Phe Ala Cys Ile Glu Cys Met Leu Leu Thr Val Met Ala Tyr Asp Gly
115    120    125
Phe Val Ala Ile Cys Leu Pro Leu His Tyr Pro Val Ile Met Asn Pro
130    135    140
His Leu Cys Val Phe Phe Val Leu Val Ser Phe Phe Leu Ser Leu Leu
145    150    155    160
Asp Ser Gln Leu His Gly Trp Ile Val Xaa Gln Phe Thr Ile Met Lys
165    170    175
Asn Val Glu Ile Ser His Phe Val Ser Asp Pro Ser Gln Leu Leu Asn
180    185    190

```

<210> 1535
 <211> 317
 <212> PRT
 <213> Unknown (H38g452 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(317)
 <223> Xaa = Any Amino Acid

<400> 1535

```

Met Asp Arg Arg Asn Gln Thr Cys Ile Tyr Glu Phe Leu Leu Met Gly
 1          5          10          15
Phe Ser Glu His Gln Glu Gln Ala Leu Leu Phe Gly Leu Phe Leu
          20          25          30
Val Met Tyr Leu Val Thr Val Leu Glu Asn Leu Leu Ile Ile Leu Ala
          35          40          45
Ile Gly Ser Asp Leu His Leu His Thr Pro Met Tyr Leu Phe Leu Ser
          50          55          60
Asn Leu Ser Phe Leu Asp Ile Gly Phe Ile Ser Thr Ile Ile Pro Lys
          65          70          75          80
Met Leu Asp His Ile Ser Ser Gly Ile Lys Leu Ile Ser Tyr Gly Glu
          85          90          95
Cys Leu Thr Gln Leu Tyr Phe Ser Gly Leu Phe Ala Asp Leu Asp Asn
          100          105          110
Asn Phe Leu Leu Ala Val Met Ala Leu Asp Arg Tyr Val Ala Ile Ser
          115          120          125
His Pro Leu His Tyr Ala Leu Thr Met Asn Ser Gln Arg Cys Val Leu
          130          135          140
Leu Val Ala Val Ser Trp Val Ile Thr Ile Leu His Ala Leu Val His
          145          150          155          160
Thr Leu Leu Val Thr Arg Leu Ser Phe Cys Gly Pro Asn Ile Ile Pro
          165          170          175
His Phe Phe Cys Asp Leu Val Pro Leu Leu Lys Leu Ala Cys Ser Ser
          180          185          190
Thr Cys Val Asn Asp Leu Val Leu Ile Leu Val Ala Gly Thr Leu Leu
          195          200          205
Ile Ala Pro Phe Val Cys Ile Leu Met Ser Tyr Phe Tyr Ile Ala Leu
          210          215          220
Ala Ile Leu Arg Ile Asp Ser Pro Arg Gly Lys Gln Arg Ala Phe Ser
          225          230          235          240
Ser Cys Thr Ser His Leu Ser Val Val Ser Leu Phe Tyr Ser Thr Ala
          245          250          255
Ile Gly Val Tyr Leu Cys Pro Pro Ser Ser His Ser Asp Gly Lys Asp
          260          265          270
Arg Val Phe Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro
          275          280          285
Phe Ile Tyr Ser Leu Arg Asn Arg Asp Met Lys Gly Ala Leu Gly Lys
          290          295          300
Leu Leu Gly Ile Lys Thr Ser Xaa His Pro Tyr Ser Arg
          305          310          315

```

<210> 1536
 <211> 252
 <212> PRT
 <213> Unknown (H38g453 protein)

<220>
 <223> Synthetic construct

<221> VARIANT

<222> (1)...(252)

<223> Xaa = Any Amino Acid

<400> 1536

```

His Leu Xaa Trp Cys Val Phe Arg Tyr Leu Gly Ile Val Val Glu Ile
 1           5           10           15
His Ile Val Phe Xaa Thr Phe Arg Cys Arg Ser Leu Val Ala Gly Tyr
 20           25           30
Val Leu Xaa Thr Phe Val Ala Ile His Leu Arg Arg Asn Ala Ala Phe
 35           40           45
Ser Ile Glu Phe Leu Cys Tyr Lys Xaa Arg Met Gln Asp Ile Asn Xaa
 50           55           60
Thr Lys Xaa Gly Lys Ile Leu Tyr Ser Leu Arg Glu Phe Lys Arg Leu
 65           70           75           80
Leu Ala Thr Ser Leu Tyr Ser Ala Xaa Val Asn Arg Phe Leu Leu Asn
 85           90           95
Lys Leu Leu Pro Gly Leu Val Ser Lys Gln Ile Glu Thr Tyr Phe Arg
 100          105          110
Lys Glu Ile Tyr Ile Leu Ile Ser Thr Ile Arg Phe Ser Tyr Val Glu
 115          120          125
Thr Leu Glu Gly Glu Xaa Gly Val Asn Val Ser Ser Ile Ile Phe Leu
 130          135          140
Leu Ile Pro Phe Ser Met Ile Ser Ala Ser Ser Val Gln Ile Leu Xaa
 145          150          155          160
Gly Val Leu Xaa Met Lys Leu Ser Gln Ala Trp Lys Arg Ser Phe Ser
 165          170          175
Thr Trp Ser Ile Leu Met Ile Ala Val Thr Tyr Trp Asp Ser Phe
 180          185          190
Ile Phe Thr Tyr Val Tyr Glu Thr Xaa Ile Ile His Ile Ser Gly Gln
 195          200          205
Val Lys Phe Leu Glu Ile Phe Tyr Ala Phe Leu Ala Leu Thr Leu Asn
 210          215          220
Pro Val Val Tyr Ser Val Gly Thr Asp Ser Val Leu Val Ala Met Lys
 225          230          235          240
Asn Met Leu Xaa Ser Asn Ile Leu His Lys Lys Lys
 245          250

```

<210> 1537

<211> 313

<212> PRT

<213> Unknown (H38g454 protein)

<220>

<223> Synthetic construct

<400> 1537

```

Met Asp Gln Ile Asn His Thr Asn Val Lys Glu Phe Phe Phe Leu Glu
 1           5           10           15
Leu Thr Arg Ser Arg Glu Leu Glu Phe Leu Phe Val Val Phe Phe
 20           25           30
Ala Val Tyr Val Ala Thr Val Leu Gly Asn Ala Leu Ile Val Val Thr
 35           40           45
Ile Thr Cys Glu Ser Arg Leu His Thr Pro Met Tyr Phe Leu Leu Arg
 50           55           60
Asn Lys Ser Val Leu Asp Ile Val Phe Ser Ser Ile Thr Val Pro Lys
 65           70           75           80
Phe Leu Val Asp Leu Leu Ser Asp Arg Lys Thr Ile Ser Tyr Asn Asp
 85           90           95
Cys Met Ala Gln Ile Phe Phe Phe His Phe Ala Gly Gly Ala Asp Ile

```

```

      100      105      110
Phe Phe Leu Ser Val Met Ala Tyr Asp Arg Tyr Leu Ala Ile Ala Lys
      115      120      125
Pro Leu His Tyr Val Thr Met Met Arg Lys Glu Val Trp Val Ala Leu
      130      135      140
Val Val Ala Ser Trp Val Ser Gly Gly Leu His Ser Ile Ile Gln Val
      145      150      155      160
Ile Leu Met Leu Pro Phe Pro Phe Cys Gly Pro Asn Thr Leu Asp Ala
      165      170      175
Phe Tyr Cys Tyr Val Leu Gln Val Val Lys Leu Ala Cys Thr Asp Thr
      180      185      190
Phe Ala Leu Glu Leu Phe Met Ile Ser Asn Asn Gly Leu Val Thr Leu
      195      200      205
Leu Trp Phe Leu Leu Leu Leu Gly Ser Tyr Thr Val Ile Leu Val Met
      210      215      220
Leu Arg Ser His Ser Gly Glu Gly Arg Asn Lys Ala Leu Ser Thr Cys
      225      230      235      240
Thr Ser His Met Leu Val Val Thr Leu His Phe Val Pro Cys Val Tyr
      245      250      255
Ile Tyr Cys Arg Pro Phe Met Thr Leu Pro Met Asp Thr Thr Ile Ser
      260      265      270
Ile Asn Asn Thr Val Ile Thr Pro Met Leu Asn Pro Ile Ile Tyr Ser
      275      280      285
Leu Arg Asn Gln Glu Met Lys Ser Ala Met Gln Arg Leu Gln Arg Arg
      290      295      300
Leu Gly Pro Ser Glu Ser Arg Lys Trp
      305      310

```

<210> 1538

<211> 309

<212> PRT

<213> Unknown (H38g455 protein)

<220>

<223> Synthetic construct

<400> 1538

```

Met Glu Arg Ile Asn His Thr Ser Ser Val Ser Glu Phe Ile Leu Leu
  1           5           10           15
Gly Leu Ser Ser Arg Pro Glu Asp Gln Lys Thr Leu Phe Val Leu Phe
      20           25           30
Leu Ile Val Tyr Leu Val Thr Ile Thr Gly Asn Leu Leu Ile Ile Leu
      35           40           45
Ala Ile Arg Phe Asn Pro His Leu Gln Thr Pro Met Tyr Phe Phe Leu
      50           55           60
Ser Phe Leu Ser Leu Thr Asp Ile Cys Phe Thr Thr Ser Val Val Pro
      65           70           75           80
Lys Met Leu Met Asn Phe Leu Ser Glu Lys Lys Thr Ile Ser Tyr Ala
      85           90           95
Gly Cys Leu Thr Gln Met Tyr Phe Leu Tyr Ala Leu Gly Asn Ser Asp
      100          105          110
Ser Cys Leu Leu Ala Val Met Ala Phe Asp Arg Tyr Val Ala Val Cys
      115          120          125
Asp Pro Phe His Tyr Val Thr Thr Met Ser His His His Cys Val Leu
      130          135          140
Leu Val Ala Phe Ser Cys Ser Phe Pro His Leu His Ser Leu Leu His
      145          150          155          160
Thr Leu Leu Leu Asn Arg Leu Thr Phe Cys Asp Ser Asn Val Ile His
      165          170          175
His Phe Leu Cys Asp Leu Ser Pro Val Leu Lys Leu Ser Cys Ser Ser
      180          185          190

```

Ile Phe Val Asn Glu Ile Val Gln Met Thr Glu Ala Pro Ile Val Leu
 195 200 205
 Val Thr Arg Phe Leu Cys Ile Ala Phe Ser Tyr Ile Arg Ile Leu Thr
 210 215 220
 Thr Val Leu Lys Ile Pro Ser Thr Ser Gly Lys Arg Lys Ala Phe Ser
 225 230 235 240
 Thr Cys Gly Phe Tyr Leu Thr Val Val Thr Leu Phe Tyr Gly Ser Ile
 245 250 255
 Phe Cys Val Tyr Leu Gln Pro Pro Ser Thr Tyr Ala Val Lys Asp His
 260 265 270
 Val Ala Thr Ile Val Tyr Thr Val Leu Ser Ser Met Leu Asn Pro Phe
 275 280 285
 Ile Tyr Ser Leu Arg Asn Lys Asp Leu Lys Gln Gly Leu Arg Lys Leu
 290 295 300
 Met Ser Lys Arg Ser
 305

<210> 1539

<211> 313

<212> PRT

<213> Unknown (H38g456 protein)

<220>

<223> Synthetic construct

<400> 1539

Met Ala Asn Val Thr Leu Val Thr Gly Phe Leu Leu Met Gly Phe Ser
 1 5 10 15
 Asn Ile Gln Lys Leu Arg Ile Leu Tyr Gly Val Leu Phe Leu Leu Ile
 20 25 30
 Tyr Leu Ala Ala Leu Met Ser Asn Leu Leu Ile Ile Thr Leu Ile Thr
 35 40 45
 Leu Asp Val Lys Leu Gln Thr Pro Met Tyr Phe Phe Leu Lys Asn Leu
 50 55 60
 Ser Phe Leu Asp Val Phe Leu Val Ser Val Pro Ile Pro Lys Phe Ile
 65 70 75 80
 Val Asn Asn Leu Thr His Asn Asn Ser Ile Ser Ile Leu Gly Cys Ala
 85 90 95
 Phe Gln Leu Leu Leu Met Thr Ser Phe Ser Ala Gly Glu Ile Phe Ile
 100 105 110
 Leu Thr Ala Met Ser Tyr Asp Arg Tyr Val Ala Ile Cys Cys Pro Leu
 115 120 125
 Asn Tyr Glu Val Ile Met Asn Thr Gly Val Cys Val Leu Met Ala Ser
 130 135 140
 Val Ser Trp Ala Ile Gly Gly Leu Phe Gly Thr Ala Tyr Thr Ala Gly
 145 150 155 160
 Thr Phe Ser Met Pro Phe Cys Gly Ser Ser Val Ile Pro Gln Phe Phe
 165 170 175
 Cys Asp Val Pro Ser Leu Leu Arg Ile Ser Cys Ser Glu Thr Leu Met
 180 185 190
 Val Ile Tyr Ala Gly Ile Gly Val Gly Ala Cys Leu Ser Ile Ser Cys
 195 200 205
 Phe Ile Cys Ile Val Ile Ser Tyr Ile Tyr Ile Phe Ser Thr Val Leu
 210 215 220
 Lys Ile Pro Thr Thr Lys Gly Gln Ser Lys Ala Phe Ser Thr Cys Phe
 225 230 235 240
 Pro His Leu Thr Val Phe Thr Val Phe Ile Ile Thr Ala Tyr Phe Val
 245 250 255
 Tyr Leu Lys Pro Pro Ser Asn Ser Pro Ser Val Ile Asp Arg Leu Leu
 260 265 270
 Ser Val Ile Tyr Thr Val Met Pro Pro Val Phe Asn Pro Val Thr Tyr

275 280 285
 Ser Leu Arg Asn Asn Asp Met Lys Cys Ala Leu Ile Arg Leu Leu Gln
 290 295 300
 Lys Thr Tyr Gly Gln Glu Ala Tyr Phe
 305 310

<210> 1540

<211> 324

<212> PRT

<213> Unknown (H38g457 protein)

<220>

<223> Synthetic construct

<400> 1540

Met Ala Val Gly Arg Asn Asn Thr Ile Val Thr Lys Phe Ile Leu Leu
 1 5 10 15
 Gly Leu Ser Asp His Pro Gln Met Lys Ile Phe Leu Phe Met Leu Phe
 20 25 30
 Leu Gly Leu Tyr Leu Leu Thr Leu Ala Trp Asn Leu Ser Leu Ile Ala
 35 40 45
 Leu Ile Lys Met Asp Ser His Leu His Met Pro Met Tyr Phe Phe Leu
 50 55 60
 Ser Asn Leu Ser Phe Leu Asp Ile Cys Tyr Val Ser Ser Thr Ala Pro
 65 70 75 80
 Lys Met Leu Ser Asp Ile Ile Thr Glu Gln Lys Thr Ile Ser Phe Val
 85 90 95
 Gly Cys Ala Thr Gln Tyr Phe Val Phe Cys Gly Met Gly Leu Thr Glu
 100 105 110
 Cys Phe Leu Leu Ala Ala Met Ala Tyr Asp Arg Tyr Ala Ala Ile Cys
 115 120 125
 Asn Pro Leu Leu Tyr Thr Val Leu Ile Ser His Thr Leu Cys Leu Lys
 130 135 140
 Met Val Val Gly Ala Tyr Val Gly Gly Phe Leu Ser Ser Phe Ile Glu
 145 150 155 160
 Thr Tyr Ser Val Tyr Gln His Asp Phe Cys Gly Pro Tyr Met Ile Asn
 165 170 175
 His Phe Phe Cys Asp Leu Pro Pro Val Leu Ala Leu Ser Cys Ser Asp
 180 185 190
 Thr Phe Thr Ser Glu Val Val Thr Phe Ile Val Ser Val Val Val Gly
 195 200 205
 Ile Val Ser Val Leu Val Val Leu Ile Ser Tyr Gly Tyr Ile Val Ala
 210 215 220
 Ala Val Val Lys Ile Ser Ser Ala Thr Gly Arg Thr Lys Ala Phe Ser
 225 230 235 240
 Thr Cys Ala Ser His Leu Thr Ala Val Thr Leu Phe Tyr Gly Ser Gly
 245 250 255
 Phe Phe Met Tyr Met Arg Pro Ser Ser Ser Tyr Ser Leu Asn Arg Asp
 260 265 270
 Lys Val Val Ser Ile Phe Tyr Ala Leu Val Ile Pro Val Val Asn Pro
 275 280 285
 Ile Ile Tyr Ser Phe Arg Asn Lys Glu Ile Lys Asn Ala Met Arg Lys
 290 295 300
 Ala Met Glu Arg Asp Pro Gly Ile Ser His Gly Gly Pro Phe Ile Phe
 305 310 315 320
 Met Thr Leu Gly

<210> 1541

<211> 314

<212> PRT

<213> Unknown (H38g458 protein)

<220>

<223> Synthetic construct

<400> 1541

```

Met Thr Asn Gln Thr Gln Met Met Glu Phe Leu Leu Val Arg Phe Thr
 1           5           10           15
Glu Asn Trp Val Leu Leu Arg Leu His Ala Leu Leu Phe Ser Leu Ile
      20           25           30
Tyr Leu Thr Ala Val Leu Met Asn Leu Val Ile Ile Leu Leu Met Ile
      35           40           45
Leu Asp His Arg Leu His Met Ala Met Tyr Phe Phe Leu Arg His Leu
      50           55           60
Ser Phe Leu Asp Leu Cys Leu Ile Ser Ala Thr Val Pro Lys Ser Ile
      65           70           75           80
Leu Asn Ser Val Ala Ser Thr Asp Ser Ile Ser Phe Leu Gly Cys Val
      85           90           95
Leu Gln Leu Phe Leu Val Val Leu Leu Ala Gly Ser Glu Ile Gly Ile
      100          105          110
Leu Thr Ala Met Ser Tyr Asp Arg Tyr Ala Ala Ile Cys Cys Pro Leu
      115          120          125
His Cys Glu Ala Val Met Ser Arg Gly Leu Cys Val Gln Leu Met Ala
      130          135          140
Leu Ser Trp Leu Asn Arg Gly Ala Leu Gly Leu Leu Tyr Thr Ala Gly
      145          150          155          160
Thr Phe Ser Leu Asn Phe Tyr Gly Ser Asp Glu Leu His Gln Phe Phe
      165          170          175
Cys Asp Val Pro Ala Leu Leu Lys Leu Thr Cys Ser Lys Glu His Ala
      180          185          190
Ile Ile Ser Val Ser Val Ala Ile Gly Val Cys Tyr Ala Phe Ser Cys
      195          200          205
Leu Val Cys Ile Val Val Ser Tyr Val Tyr Ile Phe Ser Ala Val Leu
      210          215          220
Arg Ile Ser Gln Arg Gln Arg Gln Ser Lys Ala Phe Ser Asn Cys Val
      225          230          235          240
Pro His Leu Ile Val Val Thr Val Phe Leu Val Thr Gly Ala Val Ala
      245          250          255
Tyr Leu Lys Pro Gly Ser Asp Ala Pro Ser Ile Leu Asp Leu Leu Val
      260          265          270
Ser Val Phe Tyr Ser Val Ala Pro Pro Thr Leu Asn Pro Val Ile Tyr
      275          280          285
Cys Leu Lys Asn Lys Asp Ile Lys Ser Ala Leu Ser Lys Val Leu Trp
      290          295          300
Asn Val Arg Ser Ser Gly Val Met Lys Arg
305          310

```

<210> 1542

<211> 307

<212> PRT

<213> Unknown (H38g459 protein)

<220>

<223> Synthetic construct

<400> 1542

```

Met Asn His Ser Val Val Thr Glu Phe Ile Ile Leu Gly Leu Thr Lys
 1           5           10           15
Lys Pro Glu Leu Gln Gly Ile Ile Phe Leu Phe Phe Leu Ile Val Tyr
      20           25           30
Leu Val Ala Phe Leu Gly Asn Met Leu Ile Ile Ile Ala Lys Ile Tyr

```

```

      35      40      45
Asn Asn Thr Leu His Thr Pro Met Tyr Val Phe Leu Leu Thr Leu Ala
 50      55      60
Val Val Asp Ile Ile Cys Thr Thr Ser Ile Ile Pro Lys Met Leu Gly
65      70      75      80
Thr Met Leu Thr Ser Glu Asn Thr Ile Ser Tyr Ala Gly Cys Met Ser
      85      90      95
Gln Leu Phe Leu Phe Thr Trp Ser Leu Gly Ala Glu Met Val Leu Phe
      100      105      110
Thr Thr Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His
      115      120      125
Tyr Ser Thr Val Met Asn His His Met Cys Val Ala Leu Leu Ser Met
      130      135      140
Val Met Ala Ile Ala Val Thr Asn Ser Trp Val His Thr Ala Leu Ile
145      150      155      160
Met Arg Leu Thr Phe Cys Gly Pro Asn Thr Ile Asp His Phe Phe Cys
      165      170      175
Glu Ile Pro Pro Leu Leu Ala Leu Ser Cys Ser Pro Val Arg Ile Asn
      180      185      190
Glu Val Met Val Tyr Val Ala Asp Ile Thr Leu Ala Ile Gly Asp Phe
      195      200      205
Ile Leu Thr Cys Ile Ser Tyr Gly Phe Ile Ile Val Ala Ile Leu Arg
      210      215      220
Ile Arg Thr Val Glu Gly Lys Arg Lys Ala Phe Ser Thr Cys Ser Ser
225      230      235      240
His Leu Thr Val Val Thr Leu Tyr Tyr Ser Pro Val Ile Tyr Thr Tyr
      245      250      255
Ile Arg Pro Ala Ser Ser Tyr Thr Phe Glu Arg Asp Lys Val Val Ala
      260      265      270
Ala Leu Tyr Thr Leu Val Thr Pro Thr Leu Asn Pro Met Val Tyr Ser
      275      280      285
Phe Gln Asn Arg Glu Met Gln Ala Gly Ile Arg Lys Val Phe Ala Phe
290      295      300
Leu Lys His
305

```

<210> 1543

<211> 270

<212> PRT

<213> Unknown (H38g460 protein)

<220>

<223> Synthetic construct

<400> 1543

```

Met Glu Val Ser Gly Asn His Thr Ser Val Ala Met Phe Val Leu Leu
 1      5      10      15
Gly Leu Ser Asp Glu Lys Glu Leu Gln Leu Ile Leu Phe Pro Val Phe
      20      25      30
Leu Val Ile Tyr Leu Val Thr Leu Ile Trp Asn Met Gly Leu Ile Ile
      35      40      45
Leu Ile Arg Ile Asp Ser His Leu Asn Thr Pro Met Tyr Phe Phe Leu
      50      55      60
Ser Phe Leu Ser Phe Thr Asp Ile Cys Tyr Ser Ser Thr Ile Ser Pro
65      70      75      80
Arg Met Leu Ser Asp Phe Leu Lys Asp Lys Lys Thr Ile Ser Phe Leu
      85      90      95
Ala Cys Ala Thr Gln Tyr Phe Leu Gly Ala Trp Met Ser Leu Ala Glu
      100      105      110
Cys Cys Leu Leu Val Ile Met Ala Cys Asp Arg Tyr Val Ala Ile Gly
      115      120      125

```

Ser Pro Leu Gln Tyr Ser Ala Ile Met Val Pro Ser Ile Cys Trp Lys
 130 135 140
 Met Val Ala Gly Val Cys Gly Gly Gly Phe Leu Ser Ser Leu Val His
 145 150 155 160
 Thr Val Pro Cys Phe Asn Leu Tyr Tyr Cys Gly Pro Asn Ile Ile Gln
 165 170 175
 His Phe Phe Cys Asn Thr Leu Gln Ile Ile Ser Leu Ser Cys Ser Asn
 180 185 190
 Pro Phe Ile Ser Gln Met Ile Leu Phe Leu Glu Ala Ile Phe Val Gly
 195 200 205
 Leu Gly Ser Leu Leu Val Ile Leu Leu Ser Tyr Gly Phe Ile Val Ala
 210 215 220
 Ser Ile Leu Lys Ile Ser Ser Thr Lys Cys Cys Ala Lys Ala Phe Asn
 225 230 235 240
 Thr Cys Ala Ser His Leu Ala Ala Val Ala Leu Phe Tyr Gly Thr Ala
 245 250 255
 Leu Ser Val Tyr Met His Pro Ser Ser Ser His Ser Met Lys
 260 265 270

<210> 1544

<211> 329

<212> PRT

<213> Unknown (H38g461 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(329)

<223> Xaa = Any Amino Acid

<400> 1544

Tyr Ser Lys Glu Ile Ile Glu Xaa Cys Thr Ser Asn Asp Ile Ile Lys
 1 5 10 15
 Cys Gly Xaa His Asn Lys Ile Thr Phe Phe Leu Phe Ile Leu Leu Glu
 20 25 30
 Phe Thr Glu Asp Leu Gly Leu Gln Val Leu Phe Phe Ile Phe Leu
 35 40 45
 Ile Ile Tyr Val Ile Ser Leu Ser Gly Asn Ile Ile Leu Asn Ser Leu
 50 55 60
 Ile Cys Ala Asp Ser Trp Pro Tyr Thr Pro Met Tyr Phe Phe Thr Gly
 65 70 75 80
 Asn Arg Phe Leu Leu Asp Leu Trp Tyr Ser Ser Val His Ile Pro Asp
 85 90 95
 Ile Leu Leu Thr Cys Ile Ser Asp Asp Lys Thr Ile Ser Phe Pro Gly
 100 105 110
 Cys Leu Ala Gln Phe Phe Ser Ala Val Leu Ala Xaa Asn Glu Cys Tyr
 115 120 125
 Met Met Ala Ser Met Ala Tyr Asp Arg Tyr Met Ala Ile Ser Lys Pro
 130 135 140
 Leu Leu Tyr Ser Arg Ala Thr Phe Pro Glu Leu Cys Ala Ser Leu Val
 145 150 155 160
 Glu Ala Ser His Leu Gly Gly Phe Val Asn Ser Thr Ile Ile Thr Ser
 165 170 175
 Glu Thr Pro Thr Leu Ser Phe Cys Gly Ser Asn Ile Ile Asp Asp Phe
 180 185 190
 Phe Cys Asp Leu Pro Pro Leu Val Lys Leu Val Cys Asp Val Lys Glu
 195 200 205
 Arg Tyr Gln Ala Val Leu His Phe Met Leu Ala Ser Asn Ile Thr Pro
 210 215 220
 Thr Ala Leu Ile Leu Ala Ser Tyr Leu Phe Ile Ile Ala Ala Ile Ser

```

225          230          235          240
Lys Ile Arg Ser Ile Lys Gly Arg Leu Gln Val Phe Ser Thr Cys Gly
          245          250          255
Ser Pro Leu Thr Ala Leu Thr Leu Tyr Tyr Gly Ala Ile Phe Phe Ile
          260          265          270
Tyr Ser Gln Pro Arg Thr Ser Tyr Ala Leu Lys Met Asp Lys Leu Gly
          275          280          285
Ser Val Phe Tyr Thr Val Val Ile Pro Met Leu Asn Pro Leu Ile Tyr
          290          295          300
Ser Leu Arg Asn Lys Asp Val Lys Asp Ala Leu Lys Lys Met Leu Asp
305          310          315          320
Arg Leu Gln Phe Leu Lys Glu Lys Tyr
          325

```

<210> 1545

<211> 349

<212> PRT

<213> Unknown (H38g462 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(349)

<223> Xaa = Any Amino Acid

<400> 1545

```

Met Glu Gln Ser Asn Tyr Ser Val Tyr Ala Asp Phe Ile Leu Leu Gly
1          5          10          15
Leu Phe Ser Lys Pro Val Ser Pro Gly Phe Phe Ala Leu Ile Leu Leu
          20          25          30
Val Phe Val Thr Ser Ile Ala Ser Asn Val Val Lys Ile Ile Leu Ile
          35          40          45
His Ile Asp Ser Arg Leu His Thr Pro Met Tyr Phe Leu Leu Ser Gln
          50          55          60
Leu Ser Leu Arg Asp Ile Leu Tyr Ile Ser Thr Ile Val Pro Lys Met
65          70          75          80
Leu Val Asp Gln Val Met Ser Gln Arg Ala Ile Ser Phe Ala Gly Cys
          85          90          95
Thr Ala Gln His Phe Leu Tyr Leu Thr Leu Ala Gly Ala Glu Phe Phe
          100          105          110
Leu Leu Gly Leu Met Ser Cys Asp Arg Tyr Val Ala Ile Cys Asn Pro
          115          120          125
Leu His Tyr Pro Asp Leu Met Ser Arg Lys Ile Cys Trp Leu Ile Val
          130          135          140
Ala Ala Ala Trp Leu Gly Gly Ser Ile Asn Gly Phe Leu Leu Thr Pro
145          150          155          160
Val Thr Thr Gln Phe Pro Phe Cys Ala Ser Arg Glu Ile Asn His Phe
          165          170          175
Phe Cys Glu Val Pro Ala Leu Leu Lys Leu Ser Cys Thr Asp Thr Ser
          180          185          190
Ala Tyr Glu Thr Ala Met Tyr Val Cys Cys Ile Met Met Leu Leu Ile
          195          200          205
Pro Phe Ser Val Ile Ser Gly Ser Tyr Thr Arg Ile Leu Ile Thr Val
          210          215          220
Tyr Arg Met Ser Glu Ala Glu Gly Arg Arg Lys Ala Val Ala Thr Cys
225          230          235          240
Ser Ser His Met Val Val Val Ser Leu Phe Tyr Gly Ala Ala Met Tyr
          245          250          255
Thr Tyr Val Leu Pro His Ser Tyr His Thr Pro Glu Gln Asp Lys Ala
          260          265          270

```

Val Ser Ala Phe Tyr Thr Ile Leu Thr Pro Met Leu Asn Pro Leu Ile
 275 280 285
 Tyr Ser Leu Arg Asn Lys Asp Val Thr Gly Ala Leu Gln Lys Val Val
 290 295 300
 Gly Arg Cys Val Ser Ser Gly Lys Val Thr Thr Phe Lys Gln Ile Ala
 305 310 315 320
 Tyr Ala Ala Arg Asp Leu Lys Xaa Arg Ile Gln Asp Phe Ile Ile Ala
 325 330 335
 Leu Glu Phe Lys Tyr Ser Leu Pro Gly Asn Lys Xaa Pro
 340 345

<210> 1546

<211> 319

<212> PRT

<213> Unknown (H38g463 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(319)

<223> Xaa = Any Amino Acid

<400> 1546

Met Gly Val His Asn Leu Phe Thr Val Thr Gln Phe Ile Leu Ile Gly
 1 5 10 15
 Leu Ser Tyr Phe Ser Asn Glu His Tyr Leu Leu Phe Val Ala Leu Ala
 20 25 30
 Ile Ile Cys Gln Val Phe Leu Val Arg Ser Gly Asp Ile Leu Leu Ala
 35 40 45
 Ile Gly Thr Val Ile Lys Leu His Thr Thr Met Tyr Tyr Phe Leu Ala
 50 55 60
 Asn Val Ser Ile Leu Asp Ile Leu Cys Ser Ser Ala Thr Ile Pro Lys
 65 70 75 80
 Met Pro Lys Ile Leu Xaa Thr Glu Asp His Ser Ile Ser Phe Val Arg
 85 90 95
 Xaa Ala Leu Gln Pro Tyr Phe Leu Val Ala Trp Ala Gly Lys Lys Cys
 100 105 110
 Phe Leu Thr Val Thr Ala Tyr Asp Trp Cys Val Val Thr Cys Phe Ser
 115 120 125
 Leu Cys Tyr Ile Leu Ile Met Asn Lys Leu Val Ser Val Gln Leu Val
 130 135 140
 Tyr Gly Thr Xaa Ala Ala Gly Phe Leu Asn Phe Leu Leu Leu His Val
 145 150 155 160
 Val Ser Thr Leu Cys Leu Ser Phe Cys Lys Pro Asp Arg Val Asn Gln
 165 170 175
 Tyr Tyr Cys Asp Ile Ser Pro Met Gly Ala Leu Leu Cys Gln Ser Met
 180 185 190
 His Leu Ala Asn Met Leu Val Leu Val Glu Ser Val Ile Leu Gly Ile
 195 200 205
 Ser Ala Phe Leu Ala Ala Phe Asn Phe Tyr Ile Tyr Ile Ile Ser Thr
 210 215 220
 Ile Leu Lys Ile Gln Cys Val Glu Trp Ser Ala Lys Cys Phe Ser Thr
 225 230 235 240
 Cys Thr Ser His Leu Leu Thr Val Cys Leu Phe Tyr Gly Ile Leu Thr
 245 250 255
 Phe Thr Tyr Ile Tyr Ser Phe Ser Ser His Thr His Met Ser Lys Ala
 260 265 270
 Ser Pro Asp Leu Ala Thr Asp Arg Leu Ile Ser Met Leu Tyr Arg Val
 275 280 285
 Ile Thr Leu Met Phe Asn Phe Ile Thr Asp Asn Leu Arg Asn Thr Glu

290	295	300
Val Lys Gly Ala Ser Glu Arg Phe Tyr Val Ile Glu His Val Tyr		
305	310	315

<210> 1547
 <211> 280
 <212> PRT
 <213> Unknown (H38g464 protein)

<220>
 <223> Synthetic construct

<400> 1547

Met	Tyr	Leu	Thr	Thr	Val	Leu	Gly	Asn	Leu	Leu	Ile	Met	Leu	Leu	Ile
1				5					10					15	
Gln	Leu	Asp	Ser	His	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Ser	His
			20					25					30		
Leu	Ala	Leu	Thr	Tyr	Phe	Ser	Phe	Ser	Ser	Val	Thr	Val	Pro	Lys	Met
		35					40					45			
Leu	Met	Asp	Met	Arg	Thr	Lys	Tyr	Lys	Ser	Ile	Leu	Tyr	Glu	Glu	Cys
	50					55					60				
Ile	Ser	Gln	Met	Tyr	Phe	Phe	Ile	Phe	Phe	Thr	Asp	Leu	Asp	Ser	Phe
65					70					75				80	
Leu	Ile	Thr	Ser	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Cys	His	Pro
			85						90					95	
Leu	His	Tyr	Thr	Val	Ile	Met	Arg	Glu	Glu	Leu	Cys	Val	Phe	Leu	Val
			100					105					110		
Ala	Val	Ser	Trp	Ile	Leu	Ser	Cys	Ala	Ser	Ser	Leu	Ser	His	Thr	Leu
		115					120					125			
Leu	Leu	Thr	Arg	Leu	Ser	Phe	Cys	Ala	Ala	Asn	Thr	Ile	Pro	His	Val
	130					135					140				
Phe	Cys	Asp	Leu	Ala	Ala	Leu	Leu	Lys	Leu	Ser	Cys	Ser	Asp	Ile	Phe
145				150					155					160	
Leu	Asn	Glu	Leu	Val	Met	Phe	Thr	Val	Gly	Val	Val	Val	Ile	Thr	Leu
			165						170					175	
Pro	Phe	Met	Cys	Ile	Leu	Val	Ser	Tyr	Gly	Tyr	Ile	Gly	Ala	Thr	Ile
		180						185					190		
Leu	Arg	Val	Pro	Ser	Thr	Lys	Gly	Ile	His	Lys	Ala	Leu	Ser	Thr	Cys
	195						200					205			
Gly	Ser	His	Leu	Ser	Val	Val	Ser	Leu	Tyr	Tyr	Gly	Ser	Ile	Phe	Gly
	210				215						220				
Gln	Tyr	Leu	Phe	Pro	Thr	Val	Ser	Ser	Ser	Ile	Asp	Lys	Asp	Val	Ile
225					230					235				240	
Val	Ala	Leu	Met	Tyr	Thr	Val	Val	Thr	Pro	Met	Leu	Asn	Pro	Phe	Ile
			245						250					255	
Tyr	Ser	Ile	Arg	Asn	Arg	Asp	Met	Lys	Glu	Ala	Leu	Gly	Lys	Leu	Phe
		260					265						270		
Ser	Arg	Ala	Thr	Phe	Phe	Ser	Trp								
		275					280								

<210> 1548
 <211> 303
 <212> PRT
 <213> Unknown (H38g465 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(303)
 <223> Xaa = Any Amino Acid

<400> 1548

```

Met Asn Ser Ser Ser Asp Xaa Arg Gln Pro Val Met Asp Gly Val Asn
 1           5           10           15
Asp Ser Ser Leu Gln Gly Phe Val Leu Met Gly Ile Ser Asp His Pro
 20           25           30
Gln Leu Glu Met Ile Phe Phe Ile Ala Ile Leu Phe Ser Tyr Leu Leu
 35           40           45
Thr Leu Leu Gly Asn Ser Thr Ile Ile Leu Leu Ser Arg Leu Glu Ala
 50           55           60
Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser Asn Leu Ser Ser Leu
 65           70           75           80
Asp Leu Ala Phe Ala Thr Ser Ser Val Pro Gln Met Leu Ile Asn Leu
 85           90           95
Trp Gly Pro Gly Lys Thr Ile Ser Tyr Gly Gly Cys Ile Thr Gln Leu
100          105          110
Tyr Val Phe Leu Trp Leu Gly Ala Thr Glu Cys Ile Leu Leu Val Val
115          120          125
Met Ala Phe Asp Arg Tyr Val Ala Val Cys Arg Pro Leu Arg Tyr Thr
130          135          140
Ala Ile Met Asn Pro Gln Leu Cys Trp Leu Leu Ala Val Ile Ala Cys
145          150          155          160
Leu Gly Gly Leu Gly Asn Ser Val Ile Gln Ser Thr Phe Thr Leu Gln
165          170          175
Leu Pro Leu Cys Gly His Arg Arg Val Glu Gly Phe Leu Cys Glu Val
180          185          190
Pro Ala Met Ile Lys Leu Ala Cys Gly Asp Thr Ser Leu Asn Gln Ala
195          200          205
Val Leu Asn Gly Val Cys Thr Phe Phe Thr Ala Val Pro Leu Ser Ile
210          215          220
Ile Val Ile Ser Tyr Cys Leu Ile Ala Gln Ala Val Leu Lys Ile Arg
225          230          235          240
Ser Ala Glu Gly Arg Arg Lys Ala Phe Asn Thr Cys Leu Ser His Leu
245          250          255
Leu Val Val Phe Leu Phe Tyr Gly Ser Ala Ser Tyr Gly Tyr Leu Leu
260          265          270
Pro Ala Lys Asn Ser Lys Gln Asp Gln Gly Lys Phe Ile Ser Leu Phe
275          280          285
Tyr Ser Leu Val Thr Pro Met Val Asn Pro Leu Ile Tyr Thr Leu
290          295          300

```

<210> 1549

<211> 309

<212> PRT

<213> Unknown (H38g466 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(309)

<223> Xaa = Any Amino Acid

<400> 1549

```

Met Gln Arg Ser Asn His Thr Val Thr Glu Phe Ile Leu Leu Gly Phe
 1           5           10           15
Thr Thr Asp Pro Gly Met Gln Leu Gly Leu Phe Val Val Phe Leu Gly
 20           25           30
Val Tyr Cys Leu Thr Val Val Gly Ser Ser Thr Leu Ile Val Leu Ile
 35           40           45
Cys Asn Asp Ser His Leu His Thr Pro Met Tyr Phe Val Ile Gly Asn

```

```

      50              55              60
Leu Ser Phe Leu Asp Leu Trp Tyr Ser Ser Val Tyr Thr Pro Lys Ile
65              70              75              80
Leu Val Thr Cys Ile Ser Glu Asp Lys Ser Ile Ser Phe Ala Gly Cys
      85              90              95
Leu Cys Gln Phe Phe Ser Ala Arg Leu Ala Tyr Ser Glu Cys Tyr Leu
      100              105              110
Leu Ala Ala Met Ala Tyr Asp His Tyr Val Ala Ile Ser Lys Pro Leu
      115              120              125
Leu Tyr Ala Gln Thr Met Pro Arg Arg Leu Cys Ile Cys Leu Val Leu
      130              135              140
Tyr Ser Tyr Thr Gly Gly Phe Val Asn Ala Ile Ile Leu Thr Ser Asn
145              150              155              160
Thr Phe Thr Leu Asp Phe Cys Gly Asp Asn Val Ile Asp Asp Phe Phe
      165              170              175
Cys Asp Val Pro Leu Val Lys Leu Ala Cys Ser Arg Glu Ser Tyr
      180              185              190
Gln Ala Val Leu His Phe Leu Leu Ala Ser Asn Val Ile Ser Pro Thr
      195              200              205
Val Leu Ile Leu Ala Ser Tyr Leu Ser Ile Ile Thr Thr Ile Leu Arg
      210              215              220
Ile His Ser Thr Gln Gly Arg Ile Lys Val Phe Ser Thr Cys Ser Ser
225              230              235              240
His Leu Ile Ser Val Thr Leu Tyr Tyr Gly Ser Ile Leu Tyr Asn Tyr
      245              250              255
Ser Arg Pro Ser Ser Ser Tyr Ser Leu Lys Arg Asp Lys Met Val Ser
      260              265              270
Thr Phe Tyr Thr Met Leu Phe Pro Met Leu Asn Pro Met Ile Tyr Ser
      275              280              285
Leu Arg Asn Lys Asp Met Lys Asp Ala Leu Lys Lys Phe Phe Lys Ser
      290              295              300
Ala Xaa Ser Lys Val
305

```

<210> 1550

<211> 312

<212> PRT

<213> Unknown (H38g467 protein)

<220>

<223> Synthetic construct

<400> 1550

```

Met Asp Gly Val Asn Asp Ser Ser Leu Gln Gly Phe Val Leu Met Ser
1      5      10      15
Ile Ser Asp His Pro Gln Leu Glu Met Ile Phe Phe Ile Ala Ile Leu
      20      25      30
Phe Ser Tyr Leu Leu Thr Leu Leu Gly Asn Ser Thr Ile Ile Leu Leu
      35      40      45
Ser Arg Leu Glu Ala Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser
      50      55      60
Asn Leu Ser Ser Leu Asp Leu Ala Phe Ala Thr Ser Ser Val Pro Gln
65      70      75      80
Met Leu Ile Asn Leu Trp Gly Pro Gly Lys Thr Ile Ser Tyr Gly Gly
      85      90      95
Cys Ile Thr Gln Leu Tyr Val Phe Leu Trp Leu Gly Ala Thr Glu Cys
      100      105      110
Ile Leu Leu Val Val Met Ala Phe Asp Arg Tyr Val Ala Val Cys Arg
      115      120      125
Pro Leu Arg Tyr Thr Ala Ile Met Asn Pro Gln Leu Cys Trp Leu Leu
      130      135      140

```

```

Ala Val Ile Ala Trp Leu Gly Gly Leu Gly Asn Ser Val Ile Gln Ser
145           150           155           160
Thr Phe Thr Leu Gln Leu Pro Leu Cys Gly His Arg Arg Val Glu Gly
           165           170           175
Phe Leu Cys Glu Val Pro Ala Met Ile Lys Leu Ala Cys Gly Asp Thr
           180           185           190
Ser Leu Asn Gln Ala Val Leu Asn Gly Val Cys Thr Phe Phe Thr Ala
           195           200           205
Val Pro Leu Ser Ile Ile Val Ile Ser Tyr Cys Leu Ile Ala Gln Ala
           210           215           220
Val Leu Lys Ile His Ser Ala Glu Gly Arg Arg Lys Ala Phe Asn Thr
225           230           235           240
Cys Leu Ser His Leu Leu Val Val Phe Leu Phe Tyr Gly Ser Ala Ser
           245           250           255
Tyr Gly Tyr Leu Leu Pro Ala Lys Asn Ser Lys Gln Asp Gln Gly Lys
           260           265           270
Phe Ile Ser Leu Phe Tyr Ser Leu Val Thr Pro Met Val Asn Pro Leu
           275           280           285
Ile Tyr Thr Leu Arg Asn Met Glu Val Lys Gly Ala Leu Arg Arg Leu
           290           295           300
Leu Gly Lys Gly Arg Glu Val Gly
305           310

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<210> 1551
 <211> 82
 <212> PRT
 <213> Unknown (H38g468 protein)

<220>
 <223> Synthetic construct

<221> VARIANT
 <222> (1)...(82)
 <223> Xaa = Any Amino Acid

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<400> 1551
Gly Glu Arg Leu Lys Thr Leu Asn Thr Cys Val Ser His Ile Tyr Ala
1           5           10           15
Val Leu Ile Phe Tyr Val Pro Met Val Ser Val Ser Met Val His Arg
           20           25           30
Phe Gly Arg His Ala Pro Glu Tyr Val His Lys Phe Met Ser Phe Val
           35           40           45
Pro Pro Met Leu Tyr Pro Ile Ile Tyr Ser Ile Lys Thr Lys Glu Ile
           50           55           60
Arg Arg Arg Leu His Lys Met Leu Leu Gly Ala Lys Phe Xaa Ser Arg
65           70           75           80
Lys Thr

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<210> 1552
 <211> 312
 <212> PRT
 <213> Unknown (H38g469 protein)

<220>
 <223> Synthetic construct

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<400> 1552
Met Glu Val Gly Asn Cys Thr Ile Leu Thr Glu Phe Ile Leu Leu Gly
1           5           10           15
Phe Ser Ala Asp Ser Gln Trp Gln Pro Ile Leu Phe Gly Val Phe Leu

```

			20					25					30				
Met	Leu	Tyr	Leu	Ile	Thr	Leu	Ser	Gly	Asn	Met	Thr	Leu	Val	Ile	Leu		
		35					40					45					
Ile	Arg	Thr	Asp	Ser	His	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Ile	Gly		
	50					55					60						
Asn	Leu	Ser	Phe	Leu	Asp	Phe	Trp	Tyr	Thr	Ser	Val	Tyr	Thr	Pro	Lys		
65				70						75					80		
Ile	Leu	Ala	Ser	Cys	Val	Ser	Glu	Asp	Lys	Arg	Ile	Ser	Leu	Ala	Gly		
			85						90					95			
Cys	Gly	Ala	Gln	Leu	Phe	Phe	Ser	Cys	Val	Val	Ala	Tyr	Thr	Glu	Cys		
		100						105					110				
Tyr	Leu	Leu	Ala	Ala	Met	Ala	Tyr	Asp	Arg	His	Ala	Ala	Ile	Cys	Asn		
	115						120					125					
Pro	Leu	Leu	Tyr	Ser	Gly	Thr	Met	Ser	Thr	Ala	Leu	Cys	Thr	Gly	Leu		
	130					135					140						
Val	Ala	Gly	Ser	Tyr	Ile	Gly	Gly	Phe	Leu	Asn	Ala	Ile	Ala	His	Thr		
145					150					155					160		
Ala	Asn	Thr	Phe	Arg	Leu	His	Phe	Cys	Gly	Lys	Asn	Ile	Ile	Asp	His		
			165						170					175			
Phe	Phe	Cys	Asp	Ala	Pro	Pro	Leu	Val	Lys	Met	Ser	Cys	Thr	Asn	Thr		
		180						185					190				
Arg	Val	Tyr	Glu	Lys	Val	Leu	Leu	Gly	Val	Val	Gly	Phe	Thr	Val	Leu		
	195					200					205						
Ser	Ser	Ile	Leu	Ala	Ile	Leu	Ile	Ser	Tyr	Val	Asn	Ile	Leu	Leu	Ala		
	210				215						220						
Ile	Leu	Arg	Ile	His	Ser	Ala	Ser	Gly	Arg	His	Lys	Ala	Phe	Ser	Thr		
225				230					235					240			
Cys	Ala	Ser	His	Leu	Ile	Ser	Val	Met	Leu	Phe	Tyr	Gly	Ser	Leu	Leu		
			245						250					255			
Phe	Met	Tyr	Ser	Arg	Pro	Ser	Ser	Thr	Tyr	Ser	Leu	Glu	Arg	Asp	Lys		
		260						265					270				
Val	Ala	Ala	Leu	Phe	Tyr	Thr	Val	Ile	Asn	Pro	Leu	Leu	Asn	Pro	Leu		
	275					280						285					
Ile	Tyr	Ser	Leu	Arg	Asn	Lys	Asp	Ile	Lys	Glu	Ala	Phe	Arg	Lys	Ala		
	290				295						300						
Thr	Gln	Thr	Ile	Gln	Pro	Gln	Thr										
305				310													

<210> 1553

<211> 318

<212> PRT

<213> Unknown (H38g470 protein)

<220>

<223> Synthetic construct

<400> 1553

Met	Pro	Thr	Val	Asn	His	Ser	Gly	Thr	Ser	His	Thr	Val	Phe	His	Leu		
1				5				10					15				
Leu	Gly	Ile	Pro	Gly	Leu	Gln	Asp	Gln	His	Met	Trp	Ile	Ser	Ile	Pro		
		20						25					30				
Phe	Phe	Ile	Ser	Tyr	Val	Thr	Ala	Leu	Leu	Gly	Asn	Ser	Leu	Leu	Ile		
	35					40					45						
Phe	Ile	Ile	Leu	Thr	Lys	Arg	Ser	Leu	His	Glu	Pro	Met	Tyr	Leu	Phe		
	50				55					60							
Leu	Cys	Met	Leu	Ala	Gly	Ala	Asp	Ile	Val	Leu	Ser	Thr	Cys	Thr	Ile		
65				70					75					80			
Pro	Gln	Ala	Leu	Ala	Ile	Phe	Trp	Phe	Arg	Ala	Gly	Asp	Ile	Ser	Leu		
			85					90					95				
Asp	Arg	Cys	Ile	Thr	Gln	Leu	Phe	Phe	Ile	His	Ser	Thr	Phe	Ile	Ser		
		100					105						110				

Glu Ser Gly Ile Leu Leu Val Met Ala Phe Asp His Tyr Ile Ala Ile
 115 120 125
 Cys Tyr Pro Leu Arg Tyr Thr Thr Ile Leu Thr Asn Ala Leu Ile Lys
 130 135 140
 Lys Ile Cys Val Thr Val Ser Leu Arg Ser Tyr Gly Thr Ile Phe Pro
 145 150 155 160
 Ile Ile Phe Leu Leu Lys Arg Leu Thr Phe Cys Gln Asn Asn Ile Ile
 165 170 175
 Pro His Thr Phe Cys Glu His Ile Gly Leu Ala Lys Tyr Ala Cys Asn
 180 185 190
 Asp Ile Arg Ile Asn Ile Trp Tyr Gly Phe Ser Ile Leu Met Ser Thr
 195 200 205
 Val Val Leu Asp Val Val Leu Ile Phe Ile Ser Tyr Met Leu Ile Leu
 210 215 220
 His Ala Val Phe His Met Pro Ser Pro Asp Ala Cys His Lys Ala Leu
 225 230 235 240
 Asn Thr Phe Gly Ser His Val Cys Ile Ile Ile Leu Phe Tyr Gly Ser
 245 250 255
 Gly Ile Phe Thr Ile Leu Thr Gln Arg Phe Gly Arg His Ile Pro Pro
 260 265 270
 Cys Ile His Ile Pro Leu Ala Asn Val Cys Ile Leu Ala Pro Pro Met
 275 280 285
 Leu Asn Pro Ile Ile Tyr Gly Ile Lys Thr Lys Gln Ile Gln Glu Gln
 290 295 300
 Val Val Gln Phe Leu Phe Ile Lys Gln Lys Ile Thr Leu Val
 305 310 315

<210> 1554

<211> 314

<212> PRT

<213> Unknown (H38g471 protein)

<220>

<223> Synthetic construct

<400> 1554

Met Glu Ala Ala Asn Glu Ser Ser Glu Gly Ile Ser Phe Val Leu Leu
 1 5 10 15
 Gly Leu Thr Thr Ser Pro Gly Gln Gln Arg Pro Leu Phe Val Leu Phe
 20 25 30
 Leu Leu Leu Tyr Val Ala Ser Leu Leu Gly Asn Gly Leu Ile Val Ala
 35 40 45
 Ala Ile Gln Ala Ser Pro Ala Leu His Ala Pro Met Tyr Phe Leu Leu
 50 55 60
 Ala His Leu Ser Phe Ala Asp Leu Cys Phe Ala Ser Val Thr Val Pro
 65 70 75 80
 Lys Met Leu Ala Asn Leu Leu Ala His Asp His Ser Ile Ser Leu Ala
 85 90 95
 Gly Cys Leu Thr Gln Met Tyr Phe Phe Ala Leu Gly Val Thr Asp
 100 105 110
 Ser Cys Leu Leu Ala Ala Met Ala Tyr Asp Cys Tyr Val Ala Ile Arg
 115 120 125
 His Pro Leu Pro Tyr Ala Thr Arg Met Ser Arg Ala Met Cys Ala Ala
 130 135 140
 Leu Val Gly Met Ala Trp Leu Val Ser His Val His Ser Leu Leu Tyr
 145 150 155 160
 Ile Leu Leu Met Ala Arg Leu Ser Phe Cys Ala Ser His Gln Val Pro
 165 170 175
 His Phe Phe Cys Asp His Gln Pro Leu Leu Arg Leu Ser Cys Ser Asp
 180 185 190
 Thr His His Ile Gln Leu Leu Ile Phe Thr Glu Gly Ala Ala Val Val

195	200	205
Val Thr Pro Phe Leu Leu Ile Leu Ala Ser Tyr Gly Ala Ile Ala Ala		
210	215	220
Ala Val Leu Gln Leu Pro Ser Ala Ser Gly Arg Leu Arg Ala Val Ser		
225	230	235
Thr Cys Gly Ser His Leu Ala Val Val Ser Leu Phe Tyr Gly Thr Val		
245	250	255
Ile Ala Val Tyr Phe Gln Ala Thr Ser Arg Arg Glu Ala Glu Trp Gly		
260	265	270
Arg Val Ala Thr Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro		
275	280	285
Ile Ile Tyr Ser Leu Trp Asn Arg Asp Val Gln Gly Ala Leu Arg Ala		
290	295	300
Leu Leu Ile Gly Arg Arg Ile Ser Ala Ser		
305	310	

<210> 1555

<211> 316

<212> PRT

<213> Unknown (H38g472 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(316)

<223> Xaa = Any Amino Acid

<400> 1555

Ile Ser Met Phe Ser Cys Asn Thr Ser Thr Ser Gly Gln Ser Thr Phe		
1	5	10
Leu Leu Thr Gly Phe Pro Gly Leu Glu Ala Ser His His Trp Val Ser		
20	25	30
Ile Pro Ile Asn Leu Phe Cys Val Val Ser Ile Leu Gly Asn Asn Ile		
35	40	45
Ile Leu Phe Leu Ile His Thr Asp Pro Ala Leu His Glu Pro Met Tyr		
50	55	60
Ile Phe Leu Ser Met Leu Ala Ala Ser Asp Leu Gly Leu Cys Ala Ser		
65	70	75
Thr Phe Pro Thr Met Val Arg Leu Phe Trp Leu Gly Ala Arg Glu Leu		
85	90	95
Pro Phe Asp Leu Cys Ala Ala Gln Met Phe Phe Ile His Thr Phe Thr		
100	105	110
Tyr Val Glu Ser Gly Val Leu Leu Ala Met Ala Phe Asp Arg Phe Ile		
115	120	125
Ala Ile Arg Asp Pro Leu His Tyr Ala Ile Ile Ile Thr Cys Ser Val		
130	135	140
Thr Ala Glu Val Gly Thr Ala Ile Leu Val Arg Ala Val Leu Leu Asn		
145	150	155
Leu Pro Gly Pro Ile Leu Leu Gln Gln Leu Leu Phe Pro Lys Ile Ser		
165	170	175
Ala Leu Cys His Cys Tyr Cys Leu His Cys Asp Leu Val Gly Leu Ala		
180	185	190
Cys Ser Asp Thr Gln Ile Asn Ser Leu Val Gly Leu Val Ser Ile Leu		
195	200	205
Phe Ser Leu Cys Leu Asp Ser Phe Leu Ile Met Leu Ser Tyr Ala Leu		
210	215	220
Ile Leu Xaa Thr Val Leu Gly Ile Ala Ser Pro Gly Glu Arg Leu Lys		
225	230	235
Ala Leu Asn Thr Cys Val Ser His Leu Cys Ile Val Leu Ile Phe Tyr		
245	250	255

Leu Pro Ile Ile Gly Leu Ser Val Leu His Arg Val Lys Lys His Asp
 260 265 270
 Tyr Pro Ala Leu Ala Val Leu Met Ala Asn Leu His Phe Leu Val Pro
 275 280 285
 Pro Phe Met Asn Pro Ile Val Tyr Cys Ile Lys Ser Arg Gln Ile Arg
 290 295 300
 Gln Ser Leu Leu Lys His Phe Gln Gln Lys Arg Ile
 305 310 315

<210> 1556

<211> 320

<212> PRT

<213> Unknown (H38g473 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(320)

<223> Xaa = Any Amino Acid

<400> 1556

His Thr Glu Pro Trp Asn Leu Thr Gly Val Xaa Glu Phe Leu Leu Leu
 1 5 10 15
 Gly Leu Ser Glu Asp Pro Glu Leu Gln Pro Val Leu Ala Gly Leu Ser
 20 25 30
 Arg Ser Met Tyr Leu Val Met Val Leu Arg Asn Leu Leu Ile Ile Leu
 35 40 45
 Ala Val Ser Ser Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu
 50 55 60
 Ser Asn Leu Cys Trp Ala Asp Ile Gly Phe Thr Ser Ala Met Val Pro
 65 70 75 80
 Lys Met Ile Val Asp Met Gln Ser His Ser Arg Val Ile Ser Tyr Ala
 85 90 95
 Gly Cys Leu Thr Arg Met Ser Phe Leu Val Leu Phe Ala Cys Ile Glu
 100 105 110
 Asp Met Leu Leu Thr Ala Met Ala Tyr Asp Cys Phe Val Ala Ile Cys
 115 120 125
 Arg Pro Leu His Tyr Pro Val Ile Val Asn Pro His Leu Ser Val Phe
 130 135 140
 Leu Val Leu Val Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His
 145 150 155 160
 Ser Xaa Ile Val Leu Gln Phe Thr Phe Phe Lys Asn Val Glu Ile Ser
 165 170 175
 Asn Phe Val Cys Glu Pro Ser Gln Leu Leu Asn Leu Ala Cys Ser Asp
 180 185 190
 Ser Val Ile Asn Ser Ile Phe Leu Tyr Phe Asp Ser Thr Met Phe Gly
 195 200 205
 Phe Leu Pro Ile Ser Arg Ile Leu Leu Ser Tyr Tyr Lys Ile Val Pro
 210 215 220
 Ser Ile Leu Arg Ile Ser Ser Ser Asp Gly Lys Tyr Lys Ala Phe Ser
 225 230 235 240
 Thr Cys Gly Ser His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Gly
 245 250 255
 Ile Gly Val Tyr Leu Thr Ser Ala Val Ser Pro Pro Pro Arg Ser Gly
 260 265 270
 Val Val Ala Ser Val Met Tyr Ala Val Val Thr Pro Met Leu Asn Pro
 275 280 285
 Phe Ile Tyr Ser Leu Arg Asn Arg Asp Ile Gln Ser Ala Leu Trp Arg
 290 295 300
 Leu Arg Ser Arg Thr Val Glu Ser His Asp Leu Phe His Pro Phe Ser

305

310

315

320

<210> 1557

<211> 329

<212> PRT

<213> Unknown (H38g474 protein)

<220>

<223> Synthetic construct

<221> VARIANT

<222> (1)...(329)

<223> Xaa = Any Amino Acid

<400> 1557

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Met Lys Leu Ile Asn His Thr Asp Gln Asn Pro Thr Ser Phe Leu Leu
 1           5           10           15
Met Gly Ile Pro Gly Pro Glu Ala Ser His Phe Trp Ile Ala Phe Pro
          20           25           30
Phe Cys Ser Met Tyr Ala Leu Ala Val Leu Gly Asn Met Val Val Leu
          35           40           45
Leu Val Val His Ser Glu Pro Val Leu His Gln Pro Met Tyr Leu Phe
          50           55           60
Leu Cys Met Leu Ser Thr Ile Asp Leu Val Leu Cys Thr Ser Thr Val
          65           70           75           80
Pro Lys Leu Leu Ala Leu Phe Trp Ala Lys Asp Ala Glu Ile Asn Phe
          85           90           95
Gly Ala Cys Ala Ala Gln Met Phe Phe Ile His Gly Phe Ser Ala Val
          100          105          110
Glu Ser Gly Ile Leu Leu Ala Met Ala Phe Asp Arg Tyr Leu Ala Ile
          115          120          125
Cys Trp Pro Leu His Tyr Gly Ser Leu Leu Ser Pro Glu Ser Val Gly
          130          135          140
Lys Leu Gly Ala Ala Ala Val Leu Arg Gly Leu Gly Leu Met Thr Pro
          145          150          155          160
Leu Thr Cys Leu Leu Ala Arg Leu Ser Tyr Cys Ser Arg Val Val Ala
          165          170          175
His Ser Tyr Cys Glu His Met Ala Val Val Lys Leu Ala Cys Gly Gly
          180          185          190
Thr Gln Pro Asn Asn Ile Tyr Gly Ile Thr Ala Ala Thr Leu Val Val
          195          200          205
Gly Thr Asp Ser Ile Cys Ile Ala Val Ser Tyr Ala Leu Ile Leu Arg
          210          215          220
Ala Val Leu Gly Leu Ser Ser Lys Glu Ala Arg Ala Lys Thr Phe Gly
          225          230          235          240
Thr Cys Gly Ser His Leu Gly Val Ile Leu Leu Phe Tyr Thr Pro Gly
          245          250          255
Leu Phe Ser Phe Tyr Thr Gln Arg Phe Gly Gln His Val Pro Arg His
          260          265          270
Ile His Ile Leu Leu Ala Asp Leu Tyr Leu Val Val Pro Pro Met Leu
          275          280          285
Asn Pro Ile Ile Tyr Gly Met Lys Thr Lys Gln Ile Trp Asp Gly Ala
          290          295          300
Leu Arg Leu Leu Lys Trp Gly Pro Ala Gln Ser Xaa Ser Leu Gln Pro
          305          310          315          320
His Pro Glu Thr Phe Ile Phe Phe Ala
          325

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<210> 1558

<211> 330

<212> PRT